

## Appendix A

RESULT 11	BM690735	675 bp	mRNA	linear	EST 28-FEB-2002
LOCUS	UI-E-CK0-aav-c-12-0-UI-r1	UI-E-CK0	Homo sapiens	CDNA clone	
DEFINITION	UI-E-CK0-aav-c-12-0-UI-5', mRNA sequence.				
ACCESSION	BM690735				
VERSION	BM690735.1	GI:19003993			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 675)				
TITLE	Bonaldo, M.F., Lennon, G. and Soares, M.B.				
JOURNAL	Normalization and subtraction: two approaches to facilitate gene discovery				
MEDLINE	Genome Res. 6 (9), 791-806 (1996)				
PUBMED	97044477				
COMMENT	8899548				
	Contact: Soares, MB				
	Coordinated Laboratory for Computational Genomics				
	University of Iowa				
	375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA				
	Tel: 319 335 8250				
	Fax: 319 335 9565				
	Email: bento-soares@uiowa.edu				
	Tissue procurement: Dr. Gregg Hageman				
	CDNA library preparation: Dr. M. Bento Soares, University of Iowa				
	CDNA library arrayed by: Dr. M. Bento Soares, University of Iowa				
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa				
	Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).				
	Seq primer: M13 Reverse.				
FEATURES	Location/Qualifiers				
source	1..675				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="UI-E-CK0-aav-c-12-0-UI"				
	/issue_type="Retina Foveal and Macular"				
	/dev_stage="adult"				
	/lab_host="DH10B (Life Technologies) (T1 phage resistant)"				
	/clone_lib="UI-E-CK0"				
	/note="Organ: eye; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-CK0 is a cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."				
ORIGIN					
Query Match	17.7%	Score 589.4;	DB 12;	Length 675;	
Best Local Similarity	99.7%	Pred. No. 2.1e-120;			
Matches 601;	Conservative	0; Mismatches	1; Indels	1; Gaps	1;
QY	2728	CAAAATAGAGAGTTCATGTACTTGGCAACACGAGTAATTCCTGAAAAAAGACACTTACT	2787		
Db	8	CAAAATAGAGAG-TCAATGTACTTGGCAACACGAGTAATTCCTGAAAAAAGACACTTACT	66		
QY	2788	TATTATTAAACCCCAATGCAATCATCGGAAACATATTTTACTATTCTTTGGATGATAGT	2847		
Db	67	TATTATTAAACCCCAATGCAATCATCGGAAACATATTTTACTATTCTTTGGATGATAGT	136		

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 12:42:01 ; Search time 12784 Seconds  
(without alignments)  
11290.074 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taacccaagaaggttatcct.....tactatatgacataatcaat 3330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_srs:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_srs:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rtd:\*
- 36: em\_htg\_nam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sv:\*
- 39: em\_hgo\_hum:\*
- 40: em\_hgo\_mus:\*
- 41: em\_hgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	3196	96.0	3268	9	AF047492	AF047492 Homo sapi
2	1713.2	51.4	3552	4	AB047844	AB047844 Bos tauru
3	1375.6	41.3	3668	10	AF266478	AF266478 Mus muscu
4	1366.4	41.0	2924	10	BC022970	BC022970 Mus muscu
5	1287.2	38.7	2850	10	AB047843	AB047843 Rattus no
6	1255.2	37.7	2850	10	AF229929	AF229929 Mus muscu
7	823.6	24.7	90766	9	AL392166	AL392166 Human DNA
8	823.6	24.7	132145	2	AL359817	AL359817 Homo sapi
9	814.2	24.5	1235	9	HSIMPG17	AF017776 Homo sapi
10	535.8	16.1	816	9	HSIMPG13	AF017772 Homo sapi
11	535.8	16.1	160719	2	AL157379	AL157379 Homo sapi
12	481.2	14.5	4953	5	AB070714	AB070714 Gallus ga
13	439	13.2	555	9	AF047491	AF047491 Macaca fa
14	282.6	8.5	171412	2	AC120388	AC120388 Mus muscu
15	274.6	8.2	248573	2	AC096467	AC096467 Rattus no
16	249	7.5	444	9	HSIMPG10	AF017769 Homo sapi
17	236.4	7.1	537	9	HSIMPG02	AF017761 Homo sapi
18	236.4	7.1	132145	2	AL359817	AL359817 Homo sapi
19	236.4	7.1	186301	9	AL356962	AL356962 Human DNA
20	226	6.8	448	9	HSIMPG14	AF017773 Homo sapi
21	210.4	6.3	477	9	HSIMPG15	AF017774 Homo sapi
22	204.6	6.1	310	9	HSIMPG01	AF017760 Homo sapi
23	203.4	6.1	3989	9	AF157624	AF157624 Homo sapi
24	203.4	6.1	4165	9	AF173155	AF173155 Homo sapi
25	200.4	6.0	4368	10	RNU76717	U76717 Rattus norv
26	198.8	6.0	4010	10	AY174061	AY174061 Mus muscu
27	198.8	6.0	6961	10	BC048863	BC048863 Mus muscu
28	169.8	5.1	422	9	HSIMPG03	AF017762 Homo sapi
29	145.6	4.4	159816	2	AC136044	AC136044 Rattus no
30	142.4	4.3	377	9	HSIMPG07	AF017765 Homo sapi
31	110.4	3.3	311	9	HSIMPG06	AF017765 Homo sapi
32	110	3.3	60914	2	AC135246	AC135246 Rattus no
33	103.2	3.1	135646	2	AC119976	AC119976 Mus muscu
34	103.2	3.1	171061	2	AC109266	AC109266 Mus muscu
35	103.2	3.1	227853	2	AC116453	AC116453 Mus muscu
36	103	3.1	1094	9	F271363S12	AF271374 Homo sapi
37	103	3.1	160042	2	AC027757	AC027757 Homo sapi
38	103	3.1	178064	2	AC023311	AC023311 Homo sapi
39	103	3.1	178157	2	AC130436	AC130436 Homo sapi
40	103	3.1	183965	9	AC068764	AC068764 Homo sapi
41	103	3.1	187889	9	AC093008	AC093008 Homo sapi
42	98.4	3.0	222615	2	AC098280	AC098280 Rattus no
43	93.2	2.8	294851	2	EX649242	EX649242 Danio rer
44	90	2.7	203971	2	EX649245	EX649245 Danio rer
45	90	2.7	270051	2	EX649488	EX649488 Danio rer

ALIGNMENTS

RESULT 1  
AF047492  
LOCUS  
DEFINITION Homo sapiens interphotoreceptor matrix proteoglycan 150 (IMPG1)  
ACCSSION AF047492  
VERSION AF047492  
KEYWORDS AF047492.2 GI:6118565  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3268)  
AUTHORS Kuehn,M.H. and Hageman,G.S.  
TITLE Expression and characterization of the IPM 150 gene (IMPG1)

AF047492 3268 bp mRNA linear PRI 26-OCT-1999  
Homo sapiens interphotoreceptor matrix proteoglycan 150 (IMPG1)  
mRNA, complete cds.  
AF047492  
AF047492.2 GI:6118565  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 3268)  
Kuehn,M.H. and Hageman,G.S.  
Expression and characterization of the IPM 150 gene (IMPG1)







REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Bovidae; Bovinae; Bos.  
1 (sites)  
Uehara.F., Onba.N. and Ozawa.M.  
Isolation and characterization of mucinlike glycoprotein associated  
with photoreceptor cells  
Invest. Ophthalmol. Vis. Sci. 41 (9), 2759-2765 (2000)  
20391374  
10937595  
2 (bases 1 to 3552)  
Uehara.F., Onba.N. and Ozawa.M.  
Direct Submission  
Submitted (28-AUG-2000) Fumiyuki Uehara, Kagoshima University  
Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,  
Kagoshima 890-8520, Japan  
(E-mail: fuehara@meds.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5402,  
Fax:81-99-265-4894)

## FEATURES

Location/Qualifiers  
1..3552  
/organism="Bos taurus"  
/mol\_type="rRNA"  
/db\_xref="taxon:9913"  
/cell\_type="retina"  
155..2539  
/standard\_name="core protein of mucinlike glycoprotein  
associated with photoreceptor cells"

## CDS

/codon\_start=1  
/product="MLGAPC core protein"  
/protein\_id="BAB12254.1"  
/db\_xref="GI:9953920"  
translation="MHLEAARVIFPLMIFLQVGKILSIKIYGEIKIDINAPRTBA  
TKNTAKTYKVMRRIIFDLAKHTRKSAFFTVGVKVPQSMEOILASLQAYALRYVC  
EAVWEAVRIFLDRLPPEQVDWVSCQOETFCFLDIGNFNSQBNHLLQORMQK  
ENFLERKDVTKETLGLSGOTPGIQQTLVSHHPCLSLPMTTAQRNLPOLHPSRTP  
VPTREKTEFTDAEADLEQVELSISLANQKFKSELDNSOSPVLVLAASKSLOMOK  
IFKLPFGKBIHVSGFRPKRDGTSSTEMQITAFKKGAKSPASDPLSDSNKI  
ESGDPRTTEEEKORELYPTASERLKLISRALEEDOSLVGTIOFTDEIVGLPSLD  
PDTQLVTLTITDKATLSPPLPGLQPRLETVDRAHSGPPGASPDGWSPPAMST  
SLSETLPFTFASVFPDQDQATDIMSIDQTLVLPRTVPTDDYSALSPVPEISHLP  
TSSEDLWTSQSDWEYLDGVDLTKTPTSSEGRNSVGMFPAMIIFLENITPDPLRY  
ITTSAMTAAGRELVNRSVNVKRPVPAKVPYNLPAKRVLEDFERSFAQOOLDEIDS  
YSLDEPADQDPCKFLAGCFACQVNEWTEAECECRSGSTQALVPIEDCEDIFPK  
GTPCRSLDOSKNQVYEPGVKXFRQODNKNVTKRKFELLITIGYBEFNYQWEGN"

## ORIGIN

Query Match 51.4%; Score 1713.2; DB 4; Length 3552;  
Best Local Similarity 75.1%; Pred No. 0;  
Matches 2558; Conservative 0; Mismatches 638; Indels 212; Gaps 25;

QY 1 TAAACCAAGAGGTTATCTCAATCATCTGGTATCAATATATATATATTTTTCACATTTC 60  
DB 24 TAAAGCCGAGAGGTTATCTCACTCA-GTCAATTCAATATTTTTCATATTTTCATATTC 82  
QY 61 TGT--TACTTTTATGAGATTGAGGTGTCTGTGATTGTATCAGAAATACCAATGC 118  
DB 83 TGTTCATATTTTAA--GTGAGTGTGGGCTGTCTGGGACTATTAICAGAAATATCAATGC 142  
QY 119 ACAAAAGCCAGAGTGTATTGGAAACTAGAGAGCTATTTTGTGTTTGGATTTTCTC 178  
DB 143 ACRAAGCCAGAGTGCATTGGAGCTGCAAGAGTATTTTTCCTTTGGATTTTCTT 202  
QY 179 CAAGTTCAAGGAACCAAGATATCTCCATACATATACCATCTGAACTAAAGACATA 238  
DB 203 CAAGTTCAAGGAATCAAGATCTCTCCATTAAATATACGGTCTGAAATTAAGACATA 262  
QY 239 GACAAATCCCCCAAGAAATGAAACCAACTGAAAGTACTGAAAAAATGTACAAATGTCAACT 298  
DB 263 GATAATGCCCCAGRACTGAGCAACCAAAATACCGCAAAACGTACAAAGTGTCAACC 322  
QY 299 ATGAGACGAATATTCGATTGGCAAGCATCGAACAAAGAGATCCGATTTTCCCAAG 358  
DB 323 ATGAGACGAATATTCGATTGGCAAGCATCGAACAAAGAGATCCGATTTTCCCAACT 382

QY 359 GGGGTTAAAGTCTGTCCACAGGAATCCATGAACAGATTTTAGACAGTCTTCAAGCTTAT 418  
DB 383 GGGGTTAAAGTCTGTCCACAGGAATCCATGAACAGATTTTAGCCAGTCTTCAAGCTTAT 442  
QY 419 TATAGATTGAGAGTGTGTGAGGAAGCAGTATGGAAGCATATCGGATCTTTCTGATGCG 478  
DB 443 TATAGATTGAGAGTGTGTGAGGAAGCAGTATGGAAGCAGTATGGAAGCAGTATCTTCTGATGCG 502  
QY 479 ATCCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCGACAGAGACCTTCTGCG 538  
DB 503 CTCCTCTGAGCCGGGGAATATCAGGACTGGGTGAGCATCTGCGACAGAGACCTTCTGCG 562  
QY 539 CTCCTTTGACATTTGAAAAAATCTTCAAGCAATCTCCAGGAGCAGCTGGAATCTTCTCAGCAG 598  
DB 563 CTCCTTTGACATCGGAAAAATTTTCAACACTCTCCAGGAGCAGCTGGAATCTTCTCAGCAG 622  
QY 599 AGAATAAAACAGAGAGTGTTCCTGACAGAAAGATGAAATATCTGAGAGAGACATTCG 658  
DB 623 AGAATGAAACAGAGAAATCTTCTTGAAGAAAGATGAAGTAGTCACAAAGAGACCTTGA 682  
QY 659 GGAGAGCCTGGTGAACCAATCTGTCATTTTCAACAGCAATCTACATTTCAAGACTTTGGGCA 718  
DB 683 GGAGAGCTTGGTCAAAACCCCTGCTCTCA-- 712  
QY 719 GTATTCTAAGAAAAACCCCTCAGAAGAGCAAAATCAAGATGTTTCCAAAGCTCTCACTGGGC 778  
DB 713 -----CAGACGTTGCCAGTGTCTCACCGGCG 739  
QY 779 CTTTCCTCTCACTCTGTGATGACCCCTCTCAATGAATTTCTGATATACATCAACG 838  
DB 740 CTTTGCTCTCCCTACCGATGAC-CAGTCTCAAGAAATCTCACTACCCCTTCCCG 798  
QY 839 --ACACCAAGATGCTTACACAGAAAGAGAAACAGAAATTCGCTGTGTGG-- 886  
DB 799 GACACCCAGAGTGCCTTACAGAAAGAAATAGAAATTTCACTGATGCTGTGAGGATGC 858  
QY 887 --AGGAGCAGAGGTGGAGCTCAGCGTCTCTCTGTAACAGAAATTTCAAGGCAGAGCT 944  
DB 859 ACTGGAGCAGAAAGTAGAGTAAGTATCTCTGCGCAACCCAGAAAGTTCAGTCAAGCT 918  
QY 945 CGCTGACTCCAGTCCCACTATTTACAGGAGCTAGCAGAGAAAGTCCCAACTTTCAAGTGA 1004  
DB 919 GGATACTCCAGTCCCGGTATTACTCTGAGGTGCGCAGCAAGTCTCAGCTTCAAGTGA 978  
QY 1005 AAAGATATTTAAGAACTTCCAGGATCAAAATAATCCATGTGTAGGATTTAGACCAAA 1064  
DB 979 AAAGATATTTAAGAACTTCCAGGATTTCAAGAGATCCATGTGTCAAGGATTTAGACCAAA 1038  
QY 1065 GAAAGAAAGAGTGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACA 1124  
DB 1039 GAAAGAAAGAGCAGGAGCAAGCTCCACAGAGATGCACTTACAGCCATCTTTAAGAAAG 1098  
QY 1125 CAGTGAGAGCAAAAGCCCTGCAAGTCACTCTCTGTCTTTTGTATTCACAAATAATGA 1184  
DB 1099 CAAGGCAGAAAGCAAAAGCCCTGCCAGTGACCTCTGTCACTTGTATTCACAAATAATGA 1158  
QY 1185 AGTGAGGAGTCTATCATGGRACCATGAGGAGGAGCAAGCAACAGAAATCTATCTCAC 1244  
DB 1159 AAGTGAAGGAGACCCCTCGTGGAAACACGAGGAGAGAGAGAAAGAACTCTATCCAC 1218  
QY 1245 AGCTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGAGGAGAGCAAACTCTTTGGATGT 1304  
DB 1219 AGCTTCAAGAGTCAAGGAGCTGATCAGAGAGCCCTGGAGGAGAGCAGTCTCTGGATGT 1278  
QY 1305 GGGGACAAATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGCCCTTTGGCTCTGACAC 1364  
DB 1279 GGGGACAAATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGCCCTTTGGCTCTGACAC 1338  
QY 1365 CCAATCAGAGCTGCCACATCTTTTCTGTATTAACAGAGGATGCTACTTTGAGTCCAGA 1424  
DB 1339 CCAAGTTGGTGTCTGCCACTCTCTCTACTGATATCAAAAGGATGCTACTCTGAGTCCAGA 1398  
QY 1425 ACTTCTCTCTGTTGAACCCCGAGCTTGAGACAGTGGAGCGGAGCAGAGCATGGTCTACTCTGA 1484

Db 1399 ACTTCTCTTGGTCAACCGAGCTGGAGACAGTGGACAGAGACAGACAGTCCACCTGG 1458  
Qy 1485 CACTTC-----TTGGTCTCCACCTGCTATGSCCTCTACCTCCCTGTGAGAGC 1532  
Db 1459 AGCTTCAACCCAGCGATGGTGGTCTCCACCTGCTATGACCTCTACCTCCCTATCAGAAAC 1518  
Qy 1533 TCCACCTTCTTTATGGGATCAAGCATCTCTCTGACTGATCATCAAGCCACACAGATAC 1592  
Db 1519 TCTACTTTTCTTCTGATCAAGCGTCTTTCTCAGACTGATCAAGTGCCACAGACAT 1578  
Qy 1593 AATGCCACTGACAGACAACTGCTAGTACAGGGCTCACCATCCCAACCAAGTATATTC 1652  
Db 1579 AATGTCCATTGACAGACAGTACTAATCCACGGCTTACTGTCCCACTGATATTC 1638  
Qy 1653 TGCATCAGCCAACTGGCTCTGGGAATTTACATCCACTGATCTTCAGATGACAGCG 1712  
Db 1639 TGCCATCAGCCCAATGGTTCGGGAATTTACATCTTGCTCATCTTCCAGAGA---CTG 1695  
Qy 1713 ATCAAGTGCAGGTGGGAGATATGGTCAGACACCTAGATGAATGGATCTGTCTGACAC 1772  
Db 1696 GTTGAGTACCAGACGACCAAGATACAAATGGAATCTTAGATGGATCTCACTAAGAC 1755  
Qy 1773 TCTGCCCACTGAGGTACCA--GAGCTCAGCGAATATGTTCTGTCCTCCAGATCA-TTT 1829  
Db 1756 TCTACCTCTCTGAAGTCCAGGAATTCAGTGGGTATGTTCCAGCGCTGGATATTTT 1815  
Qy 1830 CTTGAGGATACCACTCTCTGCTCAGCTTACAGTATATCAACCACTAGTCTATGACCAT 1889  
Db 1816 CTTGAGAACATCACTCTGACCCAGGTTGGGCTACATCAACCAAGCGGCTGACTGT 1875  
Qy 1890 TGCCCCAAGGCGAGAGCTGGTAGTGTCTTCTGAGTCTGGGTGCTAACTGAGGCTT 1949  
Db 1876 CGCTCCAGGCGGAGAGTGGTGGTGTCTTCTGAGTGGGTGGGCTATGTCGCCCTT 1935  
Qy 1950 CTCACCAACCTGTCACAGAGCTCTCGAGTACCGAGCTCTGAGCAACAAATTCAC 2009  
Db 1936 CTCACCTGACCTGTTTAAAGAGCTCGCTGGAATATCAAGCTTTGGAGCAGCAATTCAC 1995  
Qy 2010 ACAGCTGCTGTTTCCATATCTACGATCAATCTTACAGGATTAAGCAACTTGAATACT 2069  
Db 1996 ACACTGCTGGTCCAACTCGGATCCAACTTACGGTTTAAAGCACTTGAGTACT 2055  
Qy 2070 TAACCTCAGAAACGGGATGTGATGTGAATAGCAAAATGAAGTTTGAAGTCTGTGCC 2129  
Db 2056 TAACCTCAGAAATGGAGCGTGTGTGAATAGCAAGTGAAGTTTGAATCAAGTGGCC 2115  
Qy 2130 GTATACTCTCACCAGGCTGTGACGGGCTCTTGAGGATTTTCTGCTGTCAGGCCA 2189  
Db 2116 ATATACCTCACCAGGCTGTGCGAGGTCTTGAGGATTTTCTGTCACAGAGCCCA 2175  
Qy 2190 ACACTCCATCTGGAATPAGACAGTACTCTCTCAACATTAAGCACTGATCAAGCAGA 2249  
Db 2176 ACACTTGTATCTGGAATPAGATAGTACTCTCTCGACGTTCAACAGCGGATCAAGCAGA 2235  
Qy 2250 TCCCTGCAAGTCTGGGCTCGGGGATTTGCCAATGTGTAAAGAACGACGACTGA 2309  
Db 2236 TCCCTGCAAAATCTGGCTCGCGGCAATTCGCCAGTGTGTGAGGAATGAGTGGACCGA 2295  
Qy 2310 GGAAGCGAGTGTCTGCTCAAAACAGGATATGACAGCCAGGGGACCTGGACGCTCTGGA 2369  
Db 2296 GGAAGCGAGTGTCTGCTCGATCGGA-----A 2324  
Qy 2370 ACCAGGCTCTGTGGCCCTCGGACAAAGAAATGGAGTCTCTCCAGGAAAGGAGTCC 2429  
Db 2325 CCCAGGCCCTTGTG--CTTCCATAGAGGACTGTGAAGACATCCCGGGGAAGGAAACACC 2382  
Qy 2430 ATGCAAGTTGCGAGATCACTCTGAAATCAAGCATACAAACTAGTGTAAAGTTCCA 2489  
Db 2393 GTGCAGATCACTAGACCAATCTAAATCAAGTGTGAACCTGTTTAAAGTTCCA 2442  
Qy 2490 AAATCAACAAATAACAAAGGTAATCAGTAAAGAAATCTGAATTTACTGACCGGTAGATA 2549

Db 2443 ACCTGACGAGATACACAGTAACTATGAAAAGAAAATTTGAATTTACTGACTATAGGATA 2502  
Qy 2550 TGAAGAATTTAACCAATCAAGATTTGGGAAGAAATTAANAATCTGAAATGTAC-AATTATC 2608  
Db 2503 TGAAGAATTTAACTAATCAAGATTTGGGAAGAAATTAANAATCTGGAAGTGTACAAATTACC 2562  
Qy 2609 ACTTAGGCTATCTCAAGAGAGATGATTTGCCCTTCTCAAG----- 2647  
Db 2563 ACCTAATCTATCTCAAGAGAAATGACTTTCTTTCTCAAGAAAATTTGATTCACCTCTCT 2622  
Qy 2648 -----GAAAATGGAGACAGGCATATTATGGGTCTATCAAAATCCAGACATACAGTC 2698  
Db 2623 CAAAATTTCTGAAAACCTAGCGAGGCATATCCACTGGTCTATCAAAATCCAGGCATGTAATC 2682  
Qy 2699 AACACTGAGANTCAGACACACACATATTTCAATATAGAGAGTCTATGACTTGGCAAC 2758  
Db 2683 AACACAGA-AACCAGACACATCACATTTCAATATAGAGAAGACTTTAGATACCTTTGAAGACC 2741  
Qy 2759 AGTAAATTTCTGAAAATAAAGACACATTTACTTATTTAAACCCCAATGCAATCAGCGAA 2818  
Db 2742 AATAAATTTCTGAAGAAAAG-----CAGCTTATATCAAAACCCAAACACAACTCAGTGAA 2797  
Qy 2819 AC-----ATATTTTACTATTTCTTGGATGATAGTCAAAATGATCAAGCCAGTTTG 2871  
Db 2798 ACATAGTAAATATTTTGGTATTTCTTCTCAGTGCAGTCAAGGTGATGCAAAACCCAGTTT 2857  
Qy 2872 CTTCCACCTTTCCTGAAAATTTTACTTCACAGATCATTTTCAACAAAGCATAGTCTTACTT-- 2929  
Db 2858 TGTCTAGTGCCTTAAATATTTGCTCAGATCATTTACAGTGCACACTTATTTTGG 2917  
Qy 2930 ----ATGTTTGGGACTGAACTTTTGGGAGCAAACTCTTTATATGCTAGAAAT 2985  
Db 2918 GGGCAGGGGGTGGGATTCACCATATACAGGAAATTAAGCTCTTCACTGTTAGGATGT 2977  
Qy 2986 ACATTTAAAGATGACTACTTACGAGGAGATGAGGTCTCTCTAAACGCGATGATGA 3045  
Db 2978 ACAT-----AAAGATTCACATGCAAGAGGTGCA-----GAATGAATGCA 3019  
Qy 3046 TGTAGTGTGTAGGCACTGTAGTGTATATATGCTCCACACTAGCTGTGATAAACACA 3105  
Db 3020 --TAAGGACATGAACTGTGGTGAGCACAATAGTGTCTCCACACTTC-AGTGTCTGTAATC 3076  
Qy 3106 AACCTCAGTATTCAGTTATAGGCACTAGTTTATAGCAACTACTCTTACATAGTA 3165  
Db 3077 CACATACCTCTTCAGTGTCTAGGCATAGTGTATAGAAATTTACTGCTTACACAGTA 3136  
Qy 3166 GACTGTTTGTGCAATAATCTTTGAAATGTTCTTTAAAGAAAACCTGAGGTTCCAGATAC 3225  
Db 3137 GATATTTTGTGCCAATTAATTCCTAGTGTGTTCTTTTCAAGAA-----CTGGGATAT 3189  
Qy 3226 ACATACCATGG-AAAAATCTTACTTTCTGTGTACTACAAAAGCTATTTTAAAGAAAT 3284  
Db 3190 ACATATGATGGAAAAATCTTACTTTCTTGTGTAACTGATAGACCTATTTTAAAGAAAGA 3249  
Qy 3285 GCTATGTT--GGGAGAGGGCGAAGTTGTACTATATGATCAATCAAT 3330  
Db 3250 TATATATCGGGGAAAAAAGTGGGTGTGTTGTTGATCAATCAAT 3297

## RESULT 3

AF266478  
LOCUS 3668 bp mRNA linear ROD 18-AUG-2000  
DEFINITION Mus musculus IPM 150 proteoglycan mRNA, complete cds.  
ACCESSION AF266478  
VERSION AF266478.1 GI:9844921  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kuehn, M.H., Wietacki, D.T. and Hageman, G.S.  
TITLE Molecular characterization of the murine orthologue of the human

retinal proteoglycan IPM 150  
Mol. Vis. 6 (2000) In press  
2 (bases 1 to 3668)  
AUTHORS Kuehn, M.H., Wietek, D.T. and Hageman, G.S.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAY-2000) Ophthalmology, University of Iowa, 2501  
Crosspark Rd., Coralville, IA 52241, USA  
Location/Qualifiers  
1..3668  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
136..2392  
/codon\_start=1  
/product="IPM 150 proteoglycan"  
/protein\_id="AA000796.1"  
/db\_xref="GI:984492"  
/translation="MNFGIKHAFVFGIFLOVQIKDSIKIFSEIKNIDKPRIET  
IESTSVHKVSMKIFDLPLKTRKSLFPAATCPQESLRKQILASQEVYRLVCO  
EYVWEAYRIFLDRIPTPEYQDVSLCOKEFCLPDIGKFNFSOEHDLILQORIKOR  
SPGRKDETASMETLEATEAVPTDYSRSLGFPPLPSDDTLKELSLVLDLQIK  
PTESKTEPIHVSSESEKVEFSLEPNHRFAELTNSGSPYQELVQSQQLQIKI  
FKLPGFGRVILGFRPKBEDSGSSIEIQLMAIFKRDHAEKSPDLSLSDNKIE  
SERIHGVIEDQPTLYLTADLKLIQLLDGLSLVGEKIPFDEVTGLFRPVE  
PDLPLADVTEDATLSPELPEVRELEAVREGSELPMGSKDSMSWPPVSAISRS  
ENLPSTPSIFSLDAGSPPLMTGPTALIPKPTLPTIDYTIROLPLESHWPAISS  
DRELITSHTDRLDMDVSTPALSELGSDYASGOFLMTTPIPTVRLTIS  
SETIATNGELVVFLFSRVANMPFSDYLFNKSLSLEYQALEORFTDLLVPLRSLTGF  
KQELILSPFNGSVI VNSKRVFAKAPFYNLTQAVRVEDLRLSTAAQGLNLEISYLD  
IIPADQADPKLLDCKGFAQKNEWTEAECECRQGHSHGTLDYQTLNLCPPGKTC  
VAGREQATPCRPDHSHTNQAEFGVKLRQKNVYKRNKSLSAIGFBEFEDQDWEGN  
"

Query Match 41.3%; Score 1375.6; DB 10; Length 3668;  
Best Local Similarity 70.7%; Pred. No. 0;  
Matches 2172; Conservative 1; Mismatches 730; Indels 169; Gaps 19;

QY 1 TAAACCAAGAGGTTATCTCAATCATCTGGTATCAATATAATATATTTTCAATTTT 60  
DB 2 TAAACCAAGGAGTCTGTCTACTAGCGGCACCTGGATTGATTATTTTCAATTTT 121  
QY 61 TGTATCTTTT-----AATGAGATTGAGGTGTCTGTGATTTGTTTATCAGATTACC 113  
DB 122 AGTCACCTTATTTCTTTAAGTGTGACTTGTGTTATTTCTGTGATTTT--TCAGATTACC 179  
QY 114 AATGCAAAAGCCAGATGTTTTCGAACTAGAGAGCTATTTTGTGTTTTCGATT 173  
DB 180 AGTATCAGAA--CAGAAATGAAATTTTCAATTAACATGCTATCTTTGTTTGGATT 238  
QY 174 TTCTCCAAGTTCAAGGAACCAAGATATCTCCATTAAACATATACCATTCGAACTAAAG 233  
DB 239 TTCTCCAAGTTCAAGGAATCAAGATACCTCTATTAAATATTCAGTTCTGAAATTAATA 298  
QY 234 ACATAGCAATCCCCAGAAATGAACACTGAAAGTACTGAAATGTAACAAATGT 293  
DB 299 ACATAGCAAAACCCCAAGAAATGAAACAAATGAAAGTACTTCAACAGTGCACAAAGTGT 358  
QY 294 CAACATAGACGAATATTCGATTGCGAAAGCATCGAACAAAGATCCGATTTTTC 353  
DB 359 CAACCATGAACGAATATTCGATTGCGAAAGCTTCGAACCAAGATCAGCACTTTTC 418  
QY 354 CAACGGGGTTAAAGTCTGTCACAGAAATCCATGAACAGATTTTAGACGTCTTCAG 413  
DB 419 CA---GCTGTCAACATCTGTCCAAGAAATCTTTGAGACAGATTTTAGAAGTCTTCAAG 475  
QY 414 CTTATTATAGATTGAGAGTGTGTGAGGAAGCATGTGGGAAGCATATCGGATCTTTCTGG 473  
DB 476 AATATTATAGACTGAGAGTATGTTCAGAAATCTGTGTGGGAGCATATCGTATCTTTCTGG 535  
QY 474 ATCCGATCCCTGACACAGGGGAATATCAGGATCGGGTTCAGCATCTGCCAGCAGGACCT 533  
DB 536 ACCGAATTCCTGACACAGAGGAATATCAAGACTGGGTTCAGCTCTGCCAGAAAGAACCT 595

ORIGIN

QY 534 TGTGCTCTTTTGACATTTGGAAAAAATTCAGCAATTCCTCCAGGAGCACTGGATCTTCTCC 593  
DB 596 TGTGCTCTTTTGACATTTGGAAAAAATTCAGCAATTCCTCCAGGAGCACTGGATCTTCTCC 655  
QY 594 AGCAGAGATAAAAAACAGAGAAGTTTCCCTGACAGAAAAAGATGAAATATCTGCAGAGAAGA 653  
DB 656 AGCAGAGATAAAAAACAGAGAAGTTTCCCTGGGAGGAAGATGAGACAGACTCTCCATGGAGA 715  
QY 654 CATTTGGAGAGCTGTGTGAAACCAATTTGTCATTTCAACAGCAATCTACATTTCAAGACTTT 713  
DB 716 CACTTGAAGCAGCTACTGAAAGCCCTGTGTGTACCCAC----- 752  
QY 714 GGGCAGTATTTCTAAGAAAAACCTCAGAGAGCAAAATCAAGATTTGTCACAAAGTCTCACT 773  
DB 753 -----AGATGTTTCCAGGATGTCCCT 773  
QY 774 TGGGCTCTTCTCTCTCATCTCTGATGACACCTCTCTCAATGAAATTTCTCGATTAATCACT 833  
DB 774 GGGGCTCTTCTCTCTCTCTGATGACACAGACCTCAAGGAGATTTCTCAGTGTCTACCT 833  
QY 834 CAACGACACCAGATGCTTACACAGAAAGAGAGAAACAGAA-----TTGCTGT 881  
DB 834 CAAGGACATTTCAAAAGCCCAACAAAGAAAGTAAACAGAACTATTTCACTGTCTGAAT 893  
QY 882 GTTGGAGGAGCAGAGGTGGAGCTCAGCGTCTCTCTGTTAAACCAAGATTCAGGCGAGA 941  
DB 894 CTATCAGAGAGAGAGGTGGAAATTCAGCATCTCTCTGCCAAACACAGAGTTCAAGGCGAGA 953  
QY 942 GCTGCTGACTCTCCAGTCCCTCATTTTACCAGGAGCTTAGCAGGAAAGTCCCAACTTCAGAT 1001  
DB 954 GCTCACCACCTCTGGGTCCACCATACCTACCAAGAACTGGTGGGACAGTCCCACTGAGTT 1013  
QY 1002 GCAAAAGATATTTAAGAAAACTTCCAGGATTTCAAAAAATTCATGTGTAGGATTTAGACC 1061  
DB 1014 GCAAAAGATATTTAAGAAAACTTCCAGGATTTCCGAGAAATTCGTTGATTTAGATTTAGACC 1073  
QY 1062 AAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAG 1121  
DB 1074 AAAGAAAGAAAGATGGTTCAAGCTCCACAGAAATACAGCTATGCGCCATCTTTAAGAG 1133  
QY 1122 ACACAGTGCAGAGAGCAAAAAAGCCCTGCAAGTGAACCTCTGTCTTTGATTTCCAAACAAAT 1181  
DB 1134 GGACCATGAGAGCAAAAAAGCCCTGATAGTATCTACTGTCTCTTGTATTTCCAAACAAAT 1193  
QY 1182 TGAAGTGAGAGAGTCTATCATGGAACCATGAGAGGAGGACAGCAACCAAGATCTATCT 1241  
DB 1194 TGAAGTGAAGAGATCCATCATGGAAGTATAGAA-----GACAAAACCAACCAAGAACTACCT 1250  
QY 1242 CACAGCTACAGACTCAAAAGGCTGATCAGCAAGCACTAGAGAGAAACAAATCTTTGGA 1301  
DB 1251 CACAGCTACAGACTCAAAAGCTCAAAACATCATCAACACTAGATGAGACCTGTCTTGGT 1310  
QY 1302 TGTGGGACAAATTCAGTTCTCATGTAATTTGCTGGATCACTGCCAGCTTTGGTCTGTA 1361  
DB 1311 AGAAGGAAAAATTCATTCGTTGATGAAGTTACTTGGGACACT-----CTTCAGACCTGT 1364  
QY 1362 CACCAATCAGAGCTGCCACATCTTTTGTGTTTATAACAGAGATGCTACTTCTTGTAGTCC 1421  
DB 1365 CACTGAACCAAGATCTGCCAAGCCCTTGTCTGATGTTCAGAGAGATGCCATTTGTAGTCC 1424  
QY 1422 AGAATCTTCTCTGTTGAAACCCAGCTTTGAGACAGTGGACGGAGCAGAGCATGTTTACC 1481  
DB 1425 AGAATCTTCTCTGTTGAAACCCAGCTTTGAGGAGCTGGACAGAGAGATCTGAGTGGCC 1484  
QY 1482 T-----GACACTCTTCTGCTCCACTGCTATGGCTCTACCTCCCTCTC 1526  
DB 1485 TGGAAATGCTCTCCAAAGACAGATTTCTGCTCTCCACTGTTATCAGCTCAATTTCCCATC 1544  
QY 1527 AGAAGCTCCACTTCTTTTATGGCATCAAGCATCTTCTCTCTGACTGATCAAGCAGCAC 1586  
DB 1545 AGAAGCTACCTTCGTTTA---CACCTAGCATCTTCTCTCTAGATGCTCAAGGCCCTCC 1601



QY 1587 AGATACAAATGGCCACTGACACAGCAAAATGCTAGTACACAGGGCTACCAATCCCAACCAAGTGA 1646  
 Db 1602 TCCCTTGATGACCACTGGCCCAACAGCACTCATCCCAAGGCCACTCTCCCACTATCGA 1661  
 QY 1647 TTATCTGCAATCAGCAACTGGCTCTGGGAATTTACATCCACCTGATCTTTCAGATGA 1706  
 Db 1662 TTATCTACCACTCCGCAATGGCTCTGGATCTGCAATGGCTGATCTCTCAAGTGA 1721  
 QY 1707 CAGCGATCAAGTGGAGTGGGGAAGATATGGTTCAGACACCTTAGATGAAATGGATCTGTC 1766  
 Db 1722 CAGAGAGCTGATCACAAGCAGCCATGACACCAATCCGAGACCTAGATGATGATGGATGTC 1781  
 QY 1767 TGCACTCTCTGCCCATCTGAGGTACAGAGCTCAGCGAATATGTTCTGTCGCCAGATCA 1826  
 Db 1782 TGACAGCCAGCTTGTGAGAATATCAGAACTGAGTGATACGATCTGCTCGGGTCA 1841  
 QY 1827 TTCTTGAGGATACCACTCTCTGCTCAGCTTTACAGTATATCACCACCTAGTCTTATGAC 1886  
 Db 1842 GTTCTTGAGATGACACACACCATCCCAACAGTACGGTTCTATCACCACCTCGGAGAC 1901  
 QY 1887 CATTGCCCCAGGGCCAGAGCTGGTAGTGTCTTCACTCTGGTGTGGTATCATATGCG 1946  
 Db 1902 CATTGCCACCAAGGGCCAGGAGCTAGTGGTATCTTCAAGCTGCGGTGTTGCTAACATGCC 1961  
 QY 1947 TTCTTCCCAACGACCTGTTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATT 2006  
 Db 1962 GTTCTTCTTACCTGTTCAACAAGAGTCTCTGGAGTATCAAGCTCTGGAGCAAGATT 2021  
 QY 2007 CACAGCTGCTGTTTCCATATCTACGATCOAATCTTACAGGATTTAAGCAACTGAAAT 2066  
 Db 2022 CACAGCTGCTGTTTCCATATCTACGATCOAATCTTACGAGGATTTAAGCAACTGAAAT 2081  
 QY 2067 ACTTAATCTCAGAAACGGAGTGTGATTTGCAATAGCAAAATGAAGTTTGTCTAAGTCTGT 2126  
 Db 2082 ACTCAGCTTCAGAAACGAAAGTGTGATCTGACAGCAAAAGTGGGTTTGCAGAGCGGT 2141  
 QY 2127 GCCGTATTAACCTCACAAGGTGTGCACGGGTCTTGGAGGATTTCTTCTGCTGAGC 2186  
 Db 2142 ACCCTTACAACCTCACCAGCGCGTGGCGGGTCTTGGAGGATCTCGGTCCACCGCAGC 2201  
 QY 2187 CCAACAATCCATCTGGAATATAGACAGCTACTCTCAACATTCAGCACTGATCAAGC 2246  
 Db 2202 TCAAGGCTCAATCTGGAATATGAAAGTACTCTCCCTCAGCATGAACAGCTGATCAGC 2261  
 QY 2247 AGATCCCTGCAAGTTCTCGGCTCGGGCGAATTTGCCAATGTGTAAAGAACGACGAC 2306  
 Db 2262 GGATCCCTGCAAACTCTAGACTGTGGCAATTTGCCAGTGTCTAAGATGATGAGTGCAC 2321  
 QY 2307 TGAGAACCGAGTGTCTGCTGAAACCAAGATATGACAGCCAGGGAGCTTGGAGCTGT 2366  
 Db 2322 AGAGGAAGCAGAGTGTCTGCTGACAGAGGACATGAGAGCCACGGGACCTTGGACTACCA 2381  
 QY 2367 GGAACCGGCTCTGTGGCTCTGGCCACAAAGGAATGGAGGTCTCTCAGGGAAGGGAGC 2426  
 Db 2382 GACCTGAACTCTGTCTCCCTCG---AAAGCTGTGTGGCCGGCCAGACCAAGCAAC 2438  
 QY 2427 TCCATGAGGTGCGAGTACTCTGAAATCAGACATACAAATAGTGTGTTAAAGTT 2486  
 Db 2439 TCCATGAGGCGCCAGATCACTCTACAAACCAAGCTCAGGAACCTGGTGTAAAGCT 2498  
 QY 2487 CCAAAATCAACAATACRAGGTATCAGTAAAGAAATTCGAATCTACTGACCGTGA 2546  
 Db 2499 ACGTCAGCA-----AATAGGTAGTCAAGAAAGAAATTCGAATCTACTGACGTATAGG 2552  
 QY 2547 ATATGAAGATTTAACCATCAAGATTGGGAAGGAAATTAATAACTGAAA----- 2595  
 Db 2553 ATTTGAAGATTTGAAGACCAAGAGCTGGAGGGAATTAAGAGCTGAATCATATGCAATT 2612  
 QY 2596 -----ATGTACAATATCATAGTCTATCTCAGAGAGATGATTTGCT 2640  
 Db 2613 ATGTTGCAAACTGTGTGAAGAGGAATTTATTTCTTAAAGAAAGGTGTATCTGTTCTGT 2672  
 QY 2641 TCTCAAGGAAATGGAGACAGGCATTTCTATGGGTCTCAATAATCCAGACATACAGTCAA 2700

Db 2673 TAACTTCTGAAAAACAGAGGGAGAGATTTCAGTGGTCAATTGGAATACAGGCAATGTAATCAA 2732  
 QY 2701 CACTGAGATCAGACACACACCACTATTTCAAATATAGAGAGTCATCTACTTGGCAACCAAG 2760  
 Db 2733 CTTTGAGACTCAG-----CATGCTTGACAGAGCACAGGGGTGATTTGATGA-CAG 2784  
 QY 2761 TAAATCTGAAAAAAGACACTTACTTATTA--AAACCCCAATCAATCAGCGAA 2818  
 Db 2785 TTAAGCTGTTGGGGGGGGGCAATATTTTGTAGTCAAAATCTCAAGCAATCATTTGGA 2844  
 QY 2819 ACATATTTTACTTATTTCTGGATGATGATCAAAATGATCATAGCCAGCTTGTCTTCCAC 2878  
 Db 2845 ACACA-TTTGACTATTTTGGACAGTACTC--AAGTAGCAAAAGATAAGGTATAGCTTTTT 2901  
 QY 2879 CTTCCCTGAAAATTTTACTCACAGATCATTTGCACAACAGCATAGCTTACTTATTTGTTAG 2938  
 Db 2902 CTTCTTTTAAATTTATFACATAAARCTATTTCAAATAAATACAAC-----TTGTTTAG 2954  
 QY 2939 GGACTGAAATTTATTTGGGAAGCAACTCTTTATATGCTAGAAAGTACATTTAAAGAT 2998  
 Db 2955 TGGGTTGTACAATATTTGAGGATCTGATCTTTATATGTTAGATATACAGTTAAAGAT 3014  
 QY 2999 GACTACTTACGC 3010  
 Db 3015 TATCATTTGGGC 3026

## RESULT 4

BC022970

LOCUS

DEFINITION

Mus musculus interphotoreceptor matrix proteoglycan 1, mRNA (cdna

clone MGC:35847 IMAGE:5366008), complete cds.

ACCESSION

BC022970

VERSION

BC022970.1

KEYWORDS

MGC.

SOURCE

Mus musculus

ORGANISM

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 2924)

Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Schetz, J.E., Brownstein, M.J., Udén, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smillius, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED

12477932

REFERENCE

2 (bases 1 to 2924)

Straussberg, R.

Direct Submission

Submitted (04-FEB-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk



1184 AAAGTGAGGAGTCTATCATGGAACCATGAGGAGGACAAAGCAACAGAAATCTATCTCA 1243  
1138 AAAGTGAAAGAAATCCATCATGAGTCAAT...AGAAAGCAAAACCAAGCAACCTACCTCA 1194  
1244 CAGCTACAGACCTCAAAAGGCTGATCAGCAAGACCTAGAGGAGAAACAATCTTTGGATG 1303  
1195 CAGCTACAGACCTCAAAAGGCTGATCAGCAAGACCTAGAGGAGAAACAATCTTTGGATG 1254  
1304 TGGGAGCAATTCAGTTCATCTGATGAAATGCTGGATCATCTGCCAGCCTTTGGTCTGACA 1363  
1255 AAGGGAAATTCATCTGGTGTATGAATTAATCTGGGACACT...CTTCAGACCTGTCA 1308  
1364 CCCATCAGAGCTGCCACATCTTTTCTGTATTAACAGAGATGCTACTTTGATGCCAG 1423  
1309 CTGAACCAATCTGCCAGAGCCCTTGTGTATGTCACAGAGATGCCACTTTGATGCCAG 1368  
1424 AACTTCTCTCTGTTGAACCCCAAGCTTGAGACAGTGGAGGAGCAGAGCATGGTCTACCT- 1482  
1369 AACTTCTCTCTGTTGAGCCTAGGCTTGAGGAGTGGACAGAGAGATCTGAGCTGCCCTG 1428  
1483 -----GACACTTCTTGGTCTCACCTGCTATAGGCTCTTACCTCCCTGTGAG 1528  
1429 GAATGTCTCTCAAGACAGATCTTGGTCTCCACCTGTATCAGCCTCAATTTCCGATCAG 1488  
1529 AAGCTCCACCTTCTTTTATGAGCATCAAGCATCTTCTCTGACTGATCAAGGCAACCAAG 1588  
1489 AATATCTACCTCTGTTTA---CACCTAGCATCTTCTCTGATGCTCAAAAGCCCCCTC 1545  
1589 ATCAATGGCCACTGACAGCAATGCTAGTACAGAGGCTCACCATCCCAACCAAGTATT 1648  
1546 CTTGATGACCACTGGCCCAACAGCACTCATCCCAAGCCCACTCTCCCACTATCGATT 1605  
1649 ATTCTGCAATCAGCACTGCTGCTGGAATTTACATCCCACTGATCTTCAGATGACA 1708  
1606 ATTCTACCACTGCGCAATGCTCTGGAATGCTCATATGGCCTGCACTCTCCAGTGA 1665  
1709 GCGCATCAAGTGCAGGTGCGAAGATATGTCAGACACCTAGATGAATGATCTGCTG 1768  
1666 GAGAGCTGATCAACAGCAGCATACACAATCCGAGACCTAGATGGCATGCTGCTG 1725  
1769 ACATCTCTGCCCCATCTGAGTACAGAGCTCAGGCAATATGTTCTGCTCCAGATCAT 1828  
1726 ACAGCCCAAGCTTGTGAGAAATATCAGAACTGAGTGGATACGATTTCTGCTCGGGTCA 1785  
1829 TCTTGAGGATACCACTCTGCTGCTGATATACAGTATATCACCACCTAGTTCTATGACCA 1888  
1786 TCTTGAGATGACCAACACCCATCCCAACAGTACAGTTCATCACCACAGCTCCGAGACCA 1845  
1889 TTGCCCCCAAGGCGGAGAGCTGATGTTCTTTCAGTCTCGGTGTTGCTAACATGCGCT 1948  
1846 TTGCCCCCAAGGCGGAGAGCTGATGTTCTTTCAGTCTCGGTGTTGCTAACATGCGCT 1905  
1949 TCTTCAACAGCTGTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTC 2008  
1906 TCTTCTATGACCTGTTCAACAGAGTCTCTGGAGTATCAAGCCCTGGAAACAGATTC 1965  
2009 CACAGCTGCTGTTCCATATCTACGATCCAATCTTACAGGATTTAAGCACTTGAATATC 2068  
1966 CAGAGCTGCTGTTCCATATCTACGATCCAATCTTACGGGATTTAAGCACTGGAATATC 2025  
2069 TTAACCTTCAGAAACGGAGTGTGATGTAATAGCAAAATGAATTTGCTTAAGTCTGTC 2128  
2026 TCAGTTTCAGAAACGGAGTGTGATGTAATAGCAAAATGAATTTGCTTAAGTCTGTC 2085  
2129 CGTATAACCTTCAACAGGCTGTGACGCGGCTCTTGGAGGATTTTCGTTCTGCTCGAGCCC 2188  
2086 CTTCAACCTTCAACAGGCTGTGACGCGGCTCTTGGAGGATTTTCGTTCTGCTCGAGCCC 2145  
2189 ACAACTTCATCTGAATATGACAGCTACTCTCAATGTAACAGGCTGATCAAGCAG 2248  
2146 AAGGGCTCAATCTGAATATGAAAGCTACTCTCCCTGCAATTTGAACAGGCTGATCAGGCG 2205  
2249 ATCCCTGCAAGTCTCTGGGCTCGCGCAATTTGCCCAATGTTGTAAGAAAGCAAGGAGCTG 2308

2206 ATCCCTGCAAACTCTAGACTGTGGCAATTTGCCAGTGTGTAAAGAAATAGTGGACAG 2265  
2309 AGAAGCGGAGTCTGCTGCTGCAACACAGGATATGACAGCCAGGAGGCTTGGAGCTTGG 2368  
2266 AGAAGCAGAGTGTGCTGCGACAGAGGATCAGAGCCACGAGCCCTGGAGTACACAGA 2325  
2369 AACAGGCTCTGCTGGCCCTGGCCACAAAGGAATGCGAGGTCCTCCAGGGAAGGAGCTC 2428  
2326 CCCTGAACCTCTGCTGCCCTGG---AAAGACTTGTGTGGCCGCGAGAACAGCAACTC 2382  
2429 CATGCAAGTTCAGAGTCACTCTGAAATTCNAGCATACAAACTAGTGTGTAAGGTTC 2488  
2383 CATGCAAGGCGCAGAGTCACTCTACAAACCAAGCTCAGAACTGCTGTGTTAAAGACTAC 2442  
2489 AAAATCAACAAATAACAAGGTAATCAGTAAAGAAATTTCTGAATTTACTGACCGTAGAAT 2548  
2443 GTCAGCAA-----ATAAGGTAGTCAAGAAAGAAATTTCTAACTATCAGCTATAGGAT 2496  
2549 ATGAAGAAATTAACCATCAAGATTGGGAAGGAATTTAAAACTGAAA----- 2595  
2497 TTGAAGAAATTTGAAGACCCAGGACTGGAGGAGAAATTTAAAGCTGGAATCATATGCATTAT 2556  
2596 -----ATGTACAAATTTATCAGTCTAGCTATCTCAAGAGAGATGATTTGCTTTC 2642  
2557 GTTGCAAACTCTGTTGAAAGGAACTTTATTTCTTAAAGAAAGGTATCTGTTCTGTTA 2616  
2643 TCAAGGAAATGGAGACAGGCATATTCATGGGTCAATCAAAATCCAGACATACAGTCAACA 2702  
2617 ACTTCTGAAAAACAGAGGAGAGATTCAGTGTGTCATTTGGAATACAGGCATGTAATCAACT 2676  
2703 CTGAGATCAGACACACCATATTTCAATATAGAGAGTCTATGTTGGCAACCAAGTGA 2762  
2677 TTGAGACTCAGCATGC-----TTGAAACAGAGACAGAGCGTGTATTTGATGA-CAGTT 2728  
2763 AATTCGAAAAAAGAGACACTTACTTATTATTA--AAACCCCAATGCAATCAGCGAAAC 2820  
2729 AAGCTGTGTTGGGCGGGGCGACATATTTTAGTCAAACTCNAAGCAATCATTTGGAAC 2788  
2821 ATATTTTACTATTCTTGATGATAGTCAAAATGATCATAGCCAGGTTTGTCTCCACT 2880  
2789 ACA-TTTGACTATTTTGGACAGTACTC--AGTAGCAAGATAAGGTTAGCTTTTTCT 2845  
2881 TCCTGAAAAATTTTACTCAGATCATTTGCAACAGCATGCTTACTTATTGTTTAG 2938  
2846 TCTTTAAATTTATACATAAGCTTATTTCAATAAATACACTGTTTAGTGGGTTG 2903

## RESULT 5

AB047843

LOCUS

DEFINITION

Rattus norvegicus

AB047843

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

AB047843 2850 bp mRNA linear ROD 30-AUG-2000  
Rattus norvegicus mRNA for MLGAPC core protein, complete cds.

AB047843.1 GI:9955917

Rattus norvegicus (Norway rat)

Rattus norvegicus

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (sites)

Uehara, F., Ohba, N. and Ozawa, M.

Core Protein of rat Mucinlike Glycoprotein Associated with

Photoreceptor Cells

Published Only in DataBase (2000)

2 (bases 1 to 2850)

Uehara, F., Ohba, N. and Ozawa, M.

Direct Submission

Submitted (28-AUG-2000) Fumiyuki Uehara, Kagoshima University

Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,

Kagoshima 890-8520, Japan

(E-mail: f.uehara@med5.kufm.kagoshima-u.ac.jp, Tel: 81-99-275-5402,

Fax: 81-99-265-4894)



Qy	15	TATCTCAATCATCTGTAATCAATATATAATATATTTTCATTTC-----TGTTACTTTT	69
Db	7	TGTACTCAGCGACGCGCACCTAGGCTTAATATATTTTCATATTTTCAGTCAATTTATTTTC	66
Qy	70	TTAATGAGATTTGAGGTTGTTCTCTGATTTGTTATTCAGAAATACCAATGCACAAAGCCAG	129
Db	67	TTTAAAGTGTGACTTGGTATTTGTTCTGAGACTTTTCAGAAATACCAAGTACACAG-AGCCAG	125
Qy	130	AATGTATTTGGAAACTAGAGAGCTATTTTGTGTTTTTGGATTTTTTCTCAAAGTTCAAAGG	189
Db	126	GATGAAATTTGGAGATTTAAACATGCTATCTTTGGTTTTTGTGGATTTTTTCTCAAAGTTCAAAGG	185
Qy	190	AACCAAGATATCTCCATTTAACTATACCATCTGAAACTTAAGACATAGACATATCCCCC	249
Db	186	AATCAAGATACCTCTCTACTAAACACACAGTCTTGGAACTTAAAAACATAGACAAAGCCCC	245
Qy	250	AAGAAATGAACAACACTGAAAGTCTGAAAAAATCTGACAAATGTCAACTATGAGACCAAT	309
Db	246	AAGAAATGAACAACACTGAAAGCATTTGAGAGTGCACAAAGCGTCACCATGAAACCAACT	305
Qy	310	ATTTCGATTTTGGCAAAAGCATCGAAACAAAAGATTCGCGCATTTTTCCTCAAGGGGGTTAAAGT	369
Db	306	GTTTCGCTCTGSCAAAGCTTCGAAACAAAAGATCGCGCTGTTCCCA--GCTGTGAACAT	362
Qy	370	CTGTCCACAGGAATCCATGAAACAGATTTTACACAGCTTTCAGAGTTATATAGATTTGAG	429
Db	363	CTGTCCGCGGGAATCCTTTGAGGCGAGATTTTAAAGTCTTCAAGAAATATATTCGACATGAG	422
Qy	430	AGTCGTGCAGAACGATATGGGAAGCATATCGGATCTTTCTGGATCGCATCTCCCTGCACAC	489
Db	423	AGTATGTCAAGAAATAGTGTGGGAAGCATATCGGATCTTTCTGGATCGCGTCTCTGCACAC	482
Qy	490	AGGGGAATATCAGGACTGGGTTCAGCATCTGCCAGCAGGAGACCTTCTGCGCTTTTGACAT	549
Db	483	AGAGGAATATCAAGACTGGGTTCAGCCTCTGCCAGAAAGGAGACCTTCTGCGCTTTTGACAT	542
Qy	550	TGSAAAAAAATCTCAGCAATTTCCAGGAGACACTGGATCTTCTCCAGCGAGAGAAATAACA	609
Db	543	TGGGAAAAAATCTCAGCAACTCCAGGAGACACTGGATCTTCTCAGCAGAGAAATTTTTC	602

QY	1690	CCTGCATCTT	CAGATGACAG---	CCGATCAAGTGCAGGTGGCGAAGATATGGTCAAGACAC	1746
DB	1630	CCTGAGTCTT	TCCAGTGACAGAGAGATT	GTGCGACACCAAGACAGCCACGACACAATCAGAGAC	1689
QY	1747	CTAGATGAAT	TGGATCTGTCTG	CACATCTCTGCCCATCTCAGCTACCCAGAGCTCAGCGAA	1806
DB	1690	CTAGATGAAT	TGGATGTGTC	CGACACGCCCTGCCTTGTCCGAATAGCAGAACTGAGTGG	1749
QY	1807	TATGTTTCTGT	CCGAGATCAATTTCT	TGGAGGATACACATCCTCTCTCAGCTTTACAGTAT	1866
DB	1750	TATGACTCT	CCCCCGGATCGGTTTT	TGGAGATGACACCGCCCATCCCGCAATTTACAGTAT	1809
QY	1867	ATCACCACTAGT	TCTATGACATTTGCC	CCCCCAAGCGCCGACAGCTGGTAGTGTCTTTCAGT	1926
DB	1810	GTCAACCEC	AGCTCTGAGACCAATG	CCGCCCAAGGCCACGAGCTAGTGGTATTTCTTCAGT	1869
QY	1927	CTCGGTGTCT	TAAATATGCGCTTCT	CAACGACCTGTTTCAACAGAGCTCTCTGGAGTAC	1986
DB	1870	CTCGGTGTCT	TAAATATGCGCTTCT	CAATGATGCTTTGTTCAATAGAGTTCCTCTGGAGTAC	1929
QY	1987	CGAGCTCTG	GAGCAACAATTTACAC	AGCTCTCTGGTTCATATCTAGCATCCAATCTTACA	2046
DB	1930	CAAGCCTT	GGAAACAACGATTTCA	CAGACCTGTTGGTTCATATCTACGATCGAATCTTACG	1989
QY	2047	GGATTTAAG	CAACTTGAATTACTTAA	CTTCAGAAACGGGAGTGTGATTTGCAATAGCAAA	2106
DB	1990	GGCTTTAAG	CAACTGGAAATACTCAG	CTTCAGAAACGGAAAGTGTGATCGTGAACAGCAAA	2049
QY	2107	ATGAAGTTT	GCTTAAGTCTGTCGGT	ATAACCTCACCAAGGCTGTGCACGGGTCTTGGAG	2166
DB	2050	GTGGGTTC	CGCCAAAGGCGTACCT	CAACCTCACCAAGGCGTGGCGGGGTCTTGGAG	2109
QY	2167	GAATTTTGGT	TCTGCTGAGCCCAACAA	CTCATCTTGGAAATAGACAGCTACTCTCTCAAC	2226
DB	2110	GATCTTCGGT	CCACTGCAGCTCAAG	AGCTCAACCTTGGAAATCGAAAGTTACTCTCTTGAT	2169
QY	2227	ATTGAACCA	GCTGATCAAGCAGAT	CCCTGCAAGTTCTGTGCGCTTCCGGCGAATTTGCCCAA	2286
DB	2170	ATCGAACCA	GCTGATCAGGCAGAT	CCCTGCAAAATTTCTAGACTGTGGCAAAATTCGCCCCAG	2329
QY	2287	TGTGTAAAG	AACGAAACGGAATG	AGGAAGCGGAGTGTGCTTGCAAAACAGGATATGACAGC	2346
DB	2230	TGTATAAAG	ATGATGTGACAGAGG	AAGCAGAGTGTGCTTGACAGAGGACATGAGAGC	2289
QY	2347	CAGGGAGCCT	TGAGCGGTGTGGAA	ACAGGCGCTGTGTGGCCCTGCGCAAAAGGAATCGGAG	2406
DB	2290	CACGGGACCT	TGGAATATACAGGA	ACCTGAACTCTGTCTCTCTCG--AAAGACTTGTGAA	2346
QY	2407	GTCTCCAGG	GAAGGGAGCTCCAT	GCAGGTGTGCAGATCACTCTGAAAATCAAGCATAC	2466
DB	2347	GCCAGTCA	AGGACAGGAAACCC	ATGACGGCCACCGATCACTCTCAAAACCAAGCTCGG	2406
QY	2467	AAAACCTAG	TTTAAAAGTTTCCAA	AAATTCAAACAAATTAACCAAGGTATTCAGTAAAAAGAAAT	2526
DB	2407	CAACCTAGT	TTTAAAAGCTTACAC	CGTACAGCAAAAT---AAGGTGGTTCAGAGAAAAGAAAT	2463
QY	2527	TCTGAAAT	TACTGACCGTAGAAT	ATGAGAAATTTAAACCATCAAGATTGGGAAGGAAATTA	2586
DB	2464	TCTGAACT	CTCAGCTACAGATTT	TGAAGAAATTTGATGACCAAGATTTGGGAGGGAAATTA	2523
QY	2587	AAACTGAAA	ATGTA	2600	
DB	2524	AGGCTGGA	ATCATA	2537	

RESULT 6  
AF229929  
LOCUS  
DEFINITION  
AF229929  
Mus musculus stialoprotein associated with cones and rods SPACR  
3675 bp mRNA linear  
mRNA, complete cds.  
ACCESSION  
AF229929  
VERSION  
AF229929.1 GI:11177167  
KEYWORDS

ORIGIN	Query Match	Score	DB 10;	Length
Mus musculus (house mouse)	37.7%	1255.2;	DB 10;	3675;
Mus musculus	Best Local Similarity	69.0%;	Pred. No. 4.5e-293;	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 3675)	Matches 2007; Conservative	2;	Mismatches 746;	Indels 155; Gaps 15;
REFERENCE				
AUTHORS				
Lee J.W., Chen Q., Rayborn M.E., Shadrach K.G., Crabb J.W., Rodriguez I.R. and Hollyfield J.G.				
TITLE				
SPACR in the interphotoreceptor matrix of the mouse retina: molecular and biochemical characterization				
JOURNAL				
REFERENCE				
AUTHORS				
Rodriguez, I.R., Lee, J.W. and Hollyfield, J.G.				
TITLE				
Direct Submission				
JOURNAL				
Submitted (31-JAN-2000) LRCWB, NEI-NIH, 6 Center Drive MSC2740 6/304, Bethesda, MD 20892, USA				
FEATURES				
source				
1..3675				
Location/Qualifiers				
/organism="Mus musculus"				
/mol_type="mRNA"				
/db_xref="taxon:10090"				
229..2457				
/note="retina specific protein present in the interphotoreceptor matrix"				
/codon_start=1				
/product="sialoprotein associated with cones and rods SPACR"				
/protein_id="AAG32162.1"				
/db_xref="GI:1177168"				
/translation="MKRIFDLPKLRYSALFPAANICQBSLRQILASLOEYRLRVQEVWVEAYRIFLDRIPDEPTFADVSVLCOKETFCFLDIGKFNSSQKHLDDLLQRIKQSFQKQDEBTASMETLEAPFVPTDVRMSLGFPLPSDDDDTLKSLSTLTKDIQKPTSLIPETHVFSSESEKVEFSISLPHNRFKALNTSGSPYYQELVGOSQLQKIPKPLTGFEIRVLGFRPKBEZGSSSTEIQLMALFKRDHAEAKSPSHLLSLDNLKISERITHGVIEDQPEVTLTDLKLLIQLLDGSLVGEKIPGDEVTGTLPRPVTEPDLKPIADVEDATLSPELFVPEVLEADVRSSELPKGSXSSSPVVASISRZNLSPFTPSFSLDAQSPPLMTGCTPALIPKPLTPIDYSTRQLBLESHPWASSTRELLITSSHDTRLDGDVSDTPALSEISLSDYSASGQFLDMTTPIPTRVLTTSDELTATQKGLVFLSRVANMPPSYDLFNKSLSEYQALQRFDTLLVPVYLRSLTGFKLEILDFRNGSVNKSVEFAKAPVNLTAQVRGVLEDRSTAAQGLNLEIESYQDLPADQDPCKLLDCGFAQCNKEMTEBAECRCROGHESHGTLDTQTLNLCPPGKTCVAGREQATPCRPDPHSINQAQEPGVKLRQKNVKKRNKLSAIGFEEPDQDWE GN"				
ORIGIN				
Query Match	37.7%	Score 1255.2;	DB 10;	Length 3675;
Best Local Similarity	69.0%;	Pred. No. 4.5e-293;		
Matches 2007; Conservative	2;	Mismatches 746;	Indels 155;	Gaps 15;
Qy	154	TATTTTGTGTTTGGATTTTCTTCCAGTTCAGGAACCAAGATATCTCCATTACAT	213	
Db	84	TGTTCTGTGATTTTTCAGAAATACCAAGTATACAGAACCAAGATGAATTTTCAAAATAAAC	143	
Qy	214	ATACCAATTCGAACTAAAGACATAGACAATCCCCAAGAAATGAAACCAACTGAAAGTAC	273	
Db	144	ATGCTATCTTGTGTTGGATTTTCTCCAAGTTCAGGAATCAACAATGAAAGTAC	203	
Qy	274	TGAAAAATGTACAAAATGTCAACTATGAGACGAATATTCGATTGGCAGAGCATCGAC	333	
Db	204	TTCAACAGTGCACAAAGTGTCAACCAATGAAAGCAATATTCGATTGCCAAGCTTCCAAC	263	
Qy	334	AAAAAGATCGCATTTTCCCAACGGGGTTAAAGTCTGTCCACAGGAATCCATGAAACA	393	
Db	264	CAAAAGATCAGCACTTTTCCCA---GCTGCTAACATCTGTCCCAGGAATCTTTGAGACA	320	
Qy	394	GATTTTAGACAGCTCTTCAAGCTTATTATAGATTGAGAGTGTGTFCAGGAAGCATATGGGA	453	
Db	321	GAITTTAGCAAGTCTTCAGAAATATTATAGCTGAGAGTATGTCAAGAAAGTCTGTGGGA	380	
Qy	454	AGCATATCGATCTTTCTTGATCGCATCCCTGACACAGGGGAATATCAGACTGGGTTCAG	513	
Db	381	AGCATATCGTATCTTTCTTGACCGAATCTCTGACACAGAGGAATATCAAGACTGGGTTCAG	440	
Qy	514	CATCTGCCACAGGAGACCTTCTGCTCTTTGTGATTTGGAAAAAAGCTTCAGCAATTTCCCA	573	

Db 441 CCTCTGCCAGAAAGAAACCTCTCTGCTCTTTGACATTTGGGAAAAAATTTCAGCAACTCCCA 500  
Qy 574 GGAGCACTGGATCTCTCCAGCAGAGAAATAAACAAGAGAGTTTCCCTTGACAGAAAAAGA 633  
Db 501 GGAGCACTGGATCTCTCTCCAGCAGAGAAATAAACAAGAGAGTTTCCCTTGAGGAGAAAGA 560  
Qy 634 TGAATATCTGACAGAGAAAGACATTTGGAGAGAGCTGCTGAAACCAATGCTATTTCAACAGC 693  
Db 561 TGAGACAGCCTCCATGGAGACACTGGAAGCACCCTACTGAAAGCCCTGTGTGTAACCCAC--- 617  
Qy 694 AATCTACATTTCAAGACCTTGGCAGCTATTCFAAGAAACCCCTCAGAGAGCAATTCAA 753  
Db 618 -----A 618  
Qy 754 GATGTTGCCAACGTCCTCACTTGGGCTTTCCCTCTCACTCCTGATGACACCCCTCTCTCAAT 813  
Db 619 GATGTTGCCAGGATGCTCTGGGCTTCCCACTTCTCTGATGACACAGACCTCAAG 678  
Qy 814 GAAATCTCGATATATACATCAACGACACCAAGATGCTTACACAGAGAGAAAGACAGAA 873  
Db 679 GAGATTTCTCAGTGTCACTTCAAGGACATTTCAAAAGCCCAACACAGAAAGTATACAGAA 738  
Qy 874 -----TTGCTGTGTTGGAGGACAGAGGTTGGAGCTCAGCGTCTCTCTGTGTA 921  
Db 739 CCTATTCACGTCTGAAATCTCATCAGAGGAGAGGTGGAGTTCAGCATCTCTTGCCA 798  
Qy 922 AACCGAAGTTCAAGGACAGAGCTGGTGACTCCAGTCCCATATTTACAGAGAGCTAGCA 981  
Db 799 AACCAAGGTTCAAGGACAGAGCTCACCACCTCTGGGTCACTACTACCAGGAAGTGGTG 858  
Qy 982 GGAAGTCCCACTTCAGATGCAAAAGATATTTAAGAAATCTCCAGGATTCAAAAAATC 1041  
Db 859 GGACAGTCCCACTGCTAGTTGCAAAAGATATTTAAGAAATCTCCAGGATTCGAGAAATC 918  
Qy 1042 CATGTGTTAGGATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAA 1101  
Db 919 CGTGATTTAGGATTTAGACCAAGAAAGAAAGATGGTTCAAGCTCCACAGAAATACAG 978  
Qy 1102 CTTAGGCGCATTTTAGAGACACAGTGCAGAGAGCAAAAGCCCTCAAGTGAACCTCTG 1161  
Db 979 CTTATGGCCATCTTTAAGAGGACCATGCAGAGAGCAAAAGCCCTGATAGTCTATCTG 1038  
Qy 1162 TCTTTTGAATCCAAACAAAATGAAAGTGAAGAGTCTATCATGGAACCATGGAGGAGAC 1221  
Db 1039 TCTCTTGAATCCAAACAAAATGAAAGTGAAGAGTCCATCATGAGTCAAT---AAGAGAC 1095  
Qy 1222 AAGCAACAGAAATCTATCTCAAGCTACAGACCTCAAGAGGCTGATCAGCAAGCACTA 1281  
Db 1096 AAACAACAGAAACCTACCTACAGCTACAGACCTCAAAAGAACTCATATCAACTACTA 1155  
Qy 1282 GAGGAAGAACAACTTTTGGATGTGGGACAAATTCAGTTCACTGATGAAATTTGCTGGATCA 1341  
Db 1156 GATGGAGACCTGCTCTTGGTAGAGGAGAAATTCATTCGGTGTAGGATTACTGGGACA 1215  
Qy 1342 CTGCCAGCCTTTGGTCTCGACACCCATCAGAGCTGCGCCACATCTTTTGGTGTATTAACA 1401  
Db 1216 CT-----CTTCAGACCTGTCTCACTGAACACAGATCTGCCCAAGCCCTTGTGTATGCACA 1269  
Qy 1402 GAGGATGCTATTTGAGTCCAGAACTCTCTCTGTGAAACCCAGCTTGAGACAGTGGAC 1461  
Db 1270 GAGGATGCTATTTGAGTCCAGAACTCTCTCTGTGAGCCTAGGCTTGAGGAGTGGAC 1329  
Qy 1462 GGAGCAGAGCAGTGTCTACCT-----GACACTCTTGGTCTCCACCTGCT 1506  
Db 1330 AGAGAAGGATCTGAGTCTGCTGGAATGTCTCCAAAGACAGATCTTGGTCTCCACCTGTA 1389  
Qy 1507 ATGGCTCTACTCTCTGAGAGCTCCAGCTCTCTTTATGGCATCAAGCATCTCTCT 1566  
Db 1390 TCAGCCTCAATTTCCGATCAGAAATCTACTCTTGTTA---CACCTAGCATCTCTCT 1446  
Qy 1567 CTGACTGATCAAGGACCAACAGATACAAATGGCCACTGACACAGAAATGCTAGTACCAAGG 1626

Db 1447 CTAGATGCTCAAGACCCCTCCCTTGATGACCACTGGCCCAACAGCACTCATCCCCAAG 1506  
Qy 1627 CTCAACATCCCCACCACTGATTAATCTGCAATCAGCAACTGGCTCTGGAAATTTACAT 1586  
Db 1507 CCCACTCTCCCACTACTGCAATTTCTACCATCCGCAATTTGCTCTGGAATCGTCACAT 1566  
Qy 1687 CCACCTGATCTTCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGATATGGTCAGACAC 1746  
Db 1567 TGGCTCTGATCTCTCCAGTGACAGAGCTGATCACAAGCAGCCATGACACAATCCGAGAC 1626  
Qy 1747 CTAGATGAAATGGATCTGCTGACACTCTTCCCACTCTGAGGTACAGAGCTCAGGGAA 1806  
Db 1627 CTAGATGGCATGGATGTCTGACAGCCAGCTTGTGAGAAATATCAGAACTGAGTGGGA 1686  
Qy 1807 TATGTTTCTGCTCCAGATCATTTCTTGGAGGATACCACTCTCTCTCAGCTTTACAGTAT 1866  
Db 1687 TACGATTTCTGCTCGGTCTGATTTCTTGGAGATGACCAACCCATCCCAACAGTACGTTTC 1746  
Qy 1867 ATCACCACTAGTTCTATGACCATTTGCCCAAGGGCGAGAGTGGTGTGTTCTTCAGT 1926  
Db 1747 ATCACCACTAGTCTCGAGACCATTTGCCCAAGGGCGAGAGTGGTGTGTTCTTCAGC 1806  
Qy 1927 CTGGTGTGCTTAACATGGCTTCTCCACGACTGTTTCAACAGAGCTCTCTGGAGTAC 1986  
Db 1807 CTGGTGTGCTTAACATGGCTTCTCTATGACTGTTTCAACAGAGTCTCTCTGGAGTAT 1866  
Qy 1987 CGACTCTGGAGCAACAAATTCACACAGCTGCTGTTCCATATCTTACGATCCAATCTTTACA 2046  
Db 1867 CAAGCCCTGAGACAAAGATTCACAGACTGCTGTTGTTCCCTCTATCAGATCGAATCTTACG 1926  
Qy 2047 GGATTTAAGCAACTTTGAAATATCTTAACCTCAGAAACGGGAGTGTGATTTAGATAGCAAA 2106  
Db 1927 GGATTTAAGCAACTTTGAAATATCTCAGCTTCAAGAACGGAAAGTGTGATCGTGAACAGCAAA 1986  
Qy 2107 ATGAGTTGCTAAGTCTGTGCGGTATAAATCTACCAAGGCTGTGCACGGGGTCTTGGAG 2166  
Db 1987 GTGGGTTTGAAGGGGTACCTTACAACTCACCCAGGCGTGTGCGGGGTCTTGGAG 2046  
Qy 2167 GATTTTCTGCTGTGAGCCCAACAACTCCATCTGGAATTCGAAGCTACTCTCCCTCGAC 2226  
Db 2047 GATCTTGGTCCACCGGAGCTCAAGGGCTCAATCTGGAATTCGAAGCTACTCTCCCTCGAC 2106  
Qy 2227 ATTGAACAGCTGATCAGCAGATCCCTGCAAGTCTCTGGCTCGCGCAATTTGCCCAA 2286  
Db 2107 ATTGAACAGCTGATCAGCAGATCCCTGCAAGTCTCTGCAACTCTAGACTGTGGCAATTTGCCCA 2166  
Qy 2287 TGTGTAAAGAACGAAACGAGCTGAGAGAGCGAGTGTCTGTCAAAACGAGGATATGACAGC 2346  
Db 2167 TGTGTAAAGATGAGTGGACAGAGAGAGTGTCTGTCAGACAGGAGCATGAGAGC 2226  
Qy 2347 CAGGGAGCCTGGAGGCTGTGAAACAGGCTCTGTGGCCCTGTCGCAAAAGAAATGGAG 2406  
Db 2227 CAGGGAGCCTGGAGTACAGACCTTGAACCTCTGTCCCTCTG---AAGACTTGTGTG 2283  
Qy 2407 GTCTCCAGGAAAGGAGCTCCATGCAAGTGTGCGATCTCTGAAATTCAGAGCATAC 2466  
Db 2284 GCGGCCCGAGAACAGCACTCCATGAGGCCACCACTGATCTCTCAAAACCAAGCTCAG 2343  
Qy 2467 AAAACTAGTGTAAAGTCCAAAATCAACAAATTAACAGGTAATCAGTAAAGAAAT 2526  
Db 2344 GAACTGTGTAAAGTCTAGCA---AATAAGGTAGTCAAGAAAGAAAT 2397  
Qy 2527 TCTGAAATTAACCGTAGAATATGAAGAAATTAACCATCAAGATTTGGGAGGAAATTA 2586  
Db 2398 TCTAACTATCAGCTATAGGATTTGAAGAAATTTGAGACACAGGACTGGGAGGAAATTA 2457  
Qy 2587 AAACCTGAAA-----ATGTACAATATCATTAGCTATC 2620  
Db 2458 AAGCTGGAATCATATGCAATATTTGCAAACTCTGTTGAAAGGAACTTTATTTCTTAAA 2517  
Qy 2621 TCAAGAGAGATGATTTGCTCTCAAGGAAATTTGAGACAGGATATTCATGGGGTCATCA 2680  
Db 2518 GAAAGGTGTATCTGTCTGTAACTTCTGAAACAGAGGAGAGATTCAGTGGTCAATG 2577

QY 2681 AAATCCAGATACAGTCACACTGAGAATCAGCACACACATATTTCAATATAGAAGA 2740  
 |||||  
 Db 2578 GAATACAGGATGTAATCAACTTTGAGACTCAGCATGC-----TTGAACAAGACGACAGGC 2633  
 |||||  
 QY 2741 GTCATGTAATCTGGCAACACAGTAATCTGAAAAAAGACACTTACTTATTTATAAAC 2800  
 |||||  
 Db 2634 GTGTATTGTATGACAGTATAGCTGGTGGGGGGGGGGGACATATTTTGTAGCAAACT 2693  
 |||||  
 QY 2801 CCAATCAATCAGCGAAACATATTTTACTATTTCTTGGATGATAGTCAAAATGATCAT 2860  
 |||||  
 Db 2694 C--AAAGCAATCATTTGAMCACA-TTTGACTATTTTGGVCAGTACTC--AAGTAGCAA 2748  
 |||||  
 QY 2861 AGCCAGTTTCTTCCACCTTCCCTGAAATTTTACTCACAGATCATTTCCACACAGCAT 2920  
 |||||  
 Db 2749 GATAGGTTAGCTTTTCTTCTTTAAATTTATACATAAGCTTATTTCAATAA--- 2804  
 |||||  
 QY 2921 AGCTTACTTATTTGTTAGGAGTCAACAATTTATTTGGAAAGCAAACTTTTATATGCTAG 2980  
 |||||  
 Db 2805 ---ATACAACCTTGTAGTGGTGTGACATATTTGAGGATCTGATCTTTTATATGTAG 2861  
 |||||  
 QY 2981 AAAGTACATTTAAAGATGACTACTTAGCC 3010  
 |||||  
 Db 2862 AATATACAGTTAAAGATTATCATTTGGCC 2891  
 |||||

## RESULT 7

AL392166/c AL392166 90766 bp DNA linear PRI 17-MAR-2001  
 LOCUS Human DNA sequence from clone RP11-758J17 on chromosome 6, complete  
 DEFINITION sequence.  
 ACCESSION AL392166  
 VERSION AL392166.19 GI:13396652  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 90766)

REFERENCE 1 Direct Submission  
 Sanger Centre, Hinxton, Cambridgeshire,  
 Submitted (15-MAR-2001) humquery@sanger.ac.uk  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

## AUTHORS

## JOURNAL

## COMMENT

On Mar 20, 2001 this sequence version replaced gi:13234983.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em: EMBL; Sw:  
 SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP  
 database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping  
 Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr6>  
 RP11-758J17 is from the library RP11-11.3 constructed by the group  
 of Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBACE3.6  
 IMPORTANT: This sequence is not the entire insert of clone  
 RP11-758J17 It may be shorter because we sequence overlapping

sections only once, except for a 100 base overlap.  
 The true left end of clone RP11-62J18 is at 24864 in this sequence.  
 The true right end of clone RP11-453C2 is at 90667 in this sequence.  
 The true right end of clone RP3-472A9 is at 100 in this sequence.

## FEATURES

Location/Qualifiers  
 1..90766  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="6"  
 /clone="RP11-758J17"  
 /clone\_lib="RP11-11.3"  
 64..483  
 /note="match: GSS: Em:AQ037329"  
 171..463  
 /note="Alusq repeat: matches 1..294 of consensus"  
 464..666  
 /note="L1PB3 repeat: matches 5941..6140 of consensus"  
 1963..2000  
 /note="19 copies 2 mer gt 84% conserved"  
 2002..2285  
 /note="Alusx repeat: matches 1..285 of consensus"  
 5357..5715  
 /note="L1MA6 repeat: matches 5423..5788 of consensus"  
 5720..6039  
 /note="160 copies 2 mer ta 55% conserved"  
 5732..6097  
 /note="6 copies 61 mer 59% conserved"  
 5896..6073  
 /note="Weak data. Digests checked and match."  
 6105..6587  
 /note="L1MA6 repeat: matches 5785..6293 of consensus"  
 6878..6992  
 /note="AluJo/FLAM repeat: matches 1..115 of consensus"  
 6996..7297  
 /note="Alusx repeat: matches 1..305 of consensus"  
 9105..9153  
 /note="12 repeat: matches 2645..2698 of consensus"  
 9525..9807  
 /note="Alusx repeat: matches 25..308 of consensus"  
 9846..9955  
 /note="HY1 repeat: matches 1..110 of consensus"  
 9875..10328  
 /note="match: GSS: Em:AQ407990"  
 10385..10760  
 /note="L1ME repeat: matches 5303..5714 of consensus"  
 10761..11036  
 /note="L1P24 repeat: matches 5867..6146 of consensus"  
 11037..11094  
 /note="29 copies 2 mer aa 72% conserved"  
 11096..11316  
 /note="L1M4 repeat: matches 4823..5039 of consensus"  
 12031..12187  
 /note="MERSA repeat: matches 5..186 of consensus"  
 12708..12880  
 /note="MERSA repeat: matches 1..179 of consensus"  
 14029..14333  
 /note="Alusq repeat: matches 1..305 of consensus"  
 15129..15266  
 /note="MIR repeat: matches 114..251 of consensus"  
 16761..17159  
 /note="match: GSS: Em:AQ018572"  
 17011..17215  
 /note="ORSL repeat: matches 203..443 of consensus"  
 17794..17851  
 /note="12 repeat: matches 2648..2705 of consensus"  
 complement(18194..18664)  
 /note="match: GSS: Em:AQ728325"  
 18506..18856  
 /note="match: GSS: Em:AQ493517"  
 18514..18752  
 /note="match: GSS: Em:AQ825405"  
 18582..18939

misc_feature	/note="match: GSS: Em:AQ090573" complement(19695..19209) /notes="match: GSS: Em:AQ698147" 18945..19146 /notes="match: GSS: Em:AQ692558" 19864..20173 /note="AluX repeat: matches 1..311 of consensus" 20195..20238 /note="MER67D repeat: matches 1..44 of consensus" 20236..20471 /note="AluJb repeat: matches 1..1295 of consensus" 20545..20946 /note="L1PA4 repeat: matches 5742..6142 of consensus" 20947..21190 /note="MER67C repeat: matches 60..331 of consensus" 21224..21616 /note="L2 repeat: matches 1263..1720 of consensus" 22472..22537 /note="L2 repeat: matches 2685..2750 of consensus" 22644..22720 /note="L1R37B repeat: matches 2..79 of consensus" 22749..22828 /note="MER58 repeat: matches 21..101 of consensus" 22839..22926 /note="MER58 repeat: matches 2363..2459 of consensus" 24580..24968 /note="MER7B repeat: matches 20..405 of consensus" 26574..26983 /note="AluX repeat: matches 1..312 of consensus" 29375..29520 /note="MIR repeat: matches 3..146 of consensus" 30097..30357 /note="MLT1J repeat: matches 108..393 of consensus" complement(30363..30542) /notes="match: GSS: Em:AQ470494" 30465..31008 /note="MER41A repeat: matches 1..554 of consensus" 33124..33278 /note="AluSg/x repeat: matches 132..286 of consensus" 33956..34319 /note="MIR1A1 repeat: matches 1..365 of consensus" 34615..34930 /note="L1PA7 repeat: matches 5814..6140 of consensus" 34957..38245 /note="L1PA7 repeat: matches 3084..6143 of consensus" 38246..39550 /note="AluSg repeat: matches 1..305 of consensus" 38551..41663 /note="L1PA7 repeat: matches 4..3084 of consensus" 41796..41889 /note="MER53 repeat: matches 1..96 of consensus" 42126..42355 /note="match: GSS: Em:AQ067266" complement(42655..43132) /note="match: GSS: Em:AQ442060" 42731..43105 /note="L2 repeat: matches 2379..2750 of consensus" 43131..43364 /note="HAI1 repeat: matches 757..1038 of consensus" 43460..43753 /note="AluJb repeat: matches 2..293 of consensus" 43763..43807 /note="L1NA9 repeat: matches 6263..6307 of consensus" 43828..43998 /note="HAI1 repeat: matches 864..1043 of consensus" 44030..44091 /note="HAI1 repeat: matches 1161..1225 of consensus" 44092..44391 /note="AluX repeat: matches 1..300 of consensus" 44392..44425 /note="HAI1 repeat: matches 1224..1257 of consensus" 44458..44780 /note="HAI1 repeat: matches 1332..1669 of consensus"
--------------	--

repeat_region	44781..44846	/notes="LIMD2 repeat: matches 6271..6336 of consensus"
repeat_region	44847..45544	/notes="LIM4 repeat: matches -10..721 of consensus"
repeat_region	45557..45727	/notes="LIMB5 repeat: matches 6004..6176 of consensus"
repeat_region	45730..46038	/notes="AluSg repeat: matches 1..310 of consensus"
repeat_region	46044..46936	
Query Match	24.7%;	Score 823.6; DB 9; Length 90766;
Best Local Similarity	97.8%;	Pred. No. 2.3e-188;
Matches 835; Conservative	0;	Mismatches 19; Indels 0; Gaps 0;
Qy	2477	TTAAAAAGTTCAAAATCAACAAAATAACAGGTAAATCAGTAAAGAAATCTCGAATTAC 2536
Db	3531	TTCTTAAGTCTTAAAACTATTTCTCTTTTCAGGTAAATCAGTAAAGAAATCTCGAATTAC 3472
Qy	2537	TGACCGTAGAATATGAAGAAATTTAACCATCAAGATTGGGAAGCAATTTAAAACTGAAAA 2596
Db	3471	TGACCGTAGAATATGAAGAAATTTAACCATCAAGATTGGGAAGCAATTTAAAACTGAAAA 3412
Qy	2597	TGTCAAATTATCACTTAGGCTATCTCAAGAGAGATGATTTGGCTTCTCAAGGAAAATGGA 2656
Db	3411	TGTACAAATTATCAATTAGGCTATCTCAAGAGAGATGATTTGGCTTCTCAAGGAAAATGGA 3352
Qy	2657	GACAGCATATTCATCGGTCATCAAAATCCAGACATACAGTCAACACTGAGAAATCAGCAC 2716
Db	3351	GACAGGCATATTCATCGGTCATCAAAATCCAGACATACAGTCAACACTGAGAAATCAGCAC 3292
Qy	2717	ACACCATATTTCAAATATAGAAGAGTCATGTACTTTGGCAACCAAGTAAATCTCGAAAAAA 2776
Db	3291	ACACCATATTTCAAATATAGAAGAGTCATGTACTTTGGCAACCAAGTAAATCTCGAAAAAA 3232
Qy	2777	AGACACTTACTTATTTAAACCCCAATGCAATCAGCGAAACATATTTTACTATTCT 2836
Db	3231	AGACACTTACTTATTTAAACCCCAATGCAATCAGCGAAACATATTTTACTATTCT 3172
Qy	2837	TGATGATAGTCAAAATGATCAAGCCAGGTTTGCTTCCACCTTCCCTGAAAAATTTTAC 2896
Db	3171	TGATGATAGTCAAAATGATCAAGCCAGGTTTGCTTCCACCTTCCCTGAAAAATTTTAC 3112
Qy	2897	TCACAGATCATTTGCAACAGCATAGCTTACTTATTTAGGACTGCAAAATTTATTG 2956
Db	3111	TCACAGATCATTTGCAACAGCATAGCTTACTTATTTAGGACTGCAAAATTTATTG 3052
Qy	2957	GGAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGACTACTTTACGCGAGGAG 3016
Db	3051	GGAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGACTACTTTACGCGAGGAG 2992
Qy	3017	ATCGAGTCTCTCTAAACCGCATGAATGTATGTAGTGTAGGCACTGTAGTGTAGTGTATA 3076
Db	2991	ATCGAGTCTCTCTAAACCGCATGAATGTATGTAGTGTAGGCACTGTAGTGTAGTGTATA 2932
Qy	3077	TATGCTCCACACTACGCTCTGATAAAACACAACTCAGTATTCAGTATTTAGGCACACTAG 3136
Db	2931	TATGCTCCACACTACGCTCTGATAAAACACAACTCAGTATTCAGTATTTAGGCACACTAG 2872
Qy	3137	TTTATACGCAACTACTGCTTACATAGTAGACTGTTTGTGTGCAATAATCTTTGAATTG 3196
Db	2871	TTTATACGCAACTACTGCTTACATAGTAGACTGTTTGTGTGCAATAATCTTTGAATTG 2812
Qy	3197	TTCTTTAAAGAAACTGAGGTTCCAGATACACATACCATGGAATAATCTTACTTTCTTGT 3256
Db	2811	TTCTTTAAAGAAACTGAGGTTCCAGATACACATACCATGGAATAATCTTACTTTCTTGT 2752
Qy	3257	TACTACACAAGCTATTTTAAAGAAATGCTATGTTGGGAAGAGGCGAAGTTGTACTAT 3316
Db	2751	TACTACACAAGCTATTTTAAAGAAATGCTATGTTGGGAAGAGGCGAAGTTGTACTAT 2692
Qy	3317	ATGACATAATCAAT 3330
Db	2691	ATGACATAATCAAT 2678

## RESULT 8

AL359817 LOCUS  
 DEFINITION Homo sapiens chromosome 1 clone RP11-505B21, 26 unordered pieces.  
 ACCESSION AL359817  
 VERSION AL359817.6 GI:12225447  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_CANCELLED.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

## REFERENCE

1 Melay, K.

## AUTHORS

## TITLE

Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk

## COMMENT

On Jan 14, 2001 this sequence version replaced gi:12214326.

----- Genom Center

Center: Sanger Centre

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: bA505B21

----- Summary Statistics

Assembly program: XGAP4, version 4.5

Sequencing vector: plasmid; 108752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 117761 bases at least Q40

Consensus quality: 123343 bases at least Q30

Consensus quality: 126505 bases at least Q20

Insert size: 129645; sum-of-contigs

Insert size: 168195; 8.3% error; agarose-fp

Quality coverage: 2.65x in Q20 bases; sum-of-contigs Quality

coverage: 2.65x in Q20 bases; agarose-fp

-----

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 26 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1  
 \* 8912: contig of 8912 bp in length  
 \* 9013: gap of 100 bp  
 \* 12665: contig of 3553 bp in length  
 \* 12666: gap of 100 bp  
 \* 12766: 16825: contig of 4060 bp in length  
 \* 16826: 16925: gap of 100 bp  
 \* 16926: 22958: contig of 6033 bp in length  
 \* 22959: gap of 100 bp  
 \* 23059: 23058: gap of 100 bp  
 \* 25081: 25080: contig of 2022 bp in length  
 \* 25181: gap of 100 bp  
 \* 27272: contig of 2092 bp in length  
 \* 27373: gap of 100 bp  
 \* 40755: 40754: contig of 13382 bp in length  
 \* 40855: 40854: gap of 100 bp  
 \* 45148: 45147: contig of 4293 bp in length  
 \* 45248: gap of 100 bp  
 \* 45493: contig of 3246 bp in length  
 \* 48494: 48593: gap of 100 bp  
 \* 48594: 52881: contig of 4288 bp in length  
 \* 52882: 52981: gap of 100 bp  
 \* 52982: 57112: contig of 4131 bp in length  
 \* 57113: gap of 100 bp  
 \* 57212: contig of 3425 bp in length  
 \* 60638: 60737: gap of 100 bp  
 \* 60738: 62745: contig of 2008 bp in length  
 \* 62746: 62845: gap of 100 bp

\* 62846 70684: contig of 7839 bp in length  
 \* 70685 70784: gap of 100 bp  
 \* 70785 74560: contig of 3776 bp in length  
 \* 74561 74560: gap of 100 bp  
 \* 74561 77342: contig of 2582 bp in length  
 \* 77343 77342: gap of 100 bp  
 \* 81105 81104: contig of 3762 bp in length  
 \* 81205 81204: gap of 100 bp  
 \* 81205 83750: contig of 2546 bp in length  
 \* 83751 83750: gap of 100 bp  
 \* 83751 92962: contig of 9112 bp in length  
 \* 92963 92962: gap of 100 bp  
 \* 93063 106092: contig of 13030 bp in length  
 \* 106093 106192: gap of 100 bp  
 \* 106193 110395: contig of 4803 bp in length  
 \* 110396 110395: gap of 100 bp  
 \* 110396 114862: contig of 3767 bp in length  
 \* 114863 114862: gap of 100 bp  
 \* 114863 118927: contig of 3865 bp in length  
 \* 118928 118927: gap of 100 bp  
 \* 118928 124084: contig of 5157 bp in length  
 \* 124085 124184: gap of 100 bp  
 \* 124185 128603: contig of 4419 bp in length  
 \* 128604 128703: gap of 100 bp  
 \* 128704 132145: contig of 3442 bp in length.

FEATURES  
 source  
 1..132145  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="1"  
 /clone="RP11-505B21"  
 /clone\_lib="RPC1-11.2"  
 1..8912  
 /note="assembly\_fragment:00016  
 clone\_end:SP6  
 vector\_side:left"  
 9013..12665  
 /note="assembly\_fragment:00251  
 fragment\_chain:1"  
 12766..16825  
 /note="assembly\_fragment:00570  
 fragment\_chain:1"  
 16926..22958  
 /note="assembly\_fragment:01358  
 fragment\_chain:1"  
 23059..25080  
 /note="assembly\_fragment:01072  
 fragment\_chain:2"  
 25181..27272  
 /note="assembly\_fragment:01212  
 fragment\_chain:2"  
 27373..40754  
 /note="assembly\_fragment:01200  
 fragment\_chain:2"  
 40855..45147  
 /note="assembly\_fragment:01131  
 fragment\_chain:3"  
 45248..48493  
 /note="assembly\_fragment:01273  
 fragment\_chain:3"  
 48594..52881  
 /note="assembly\_fragment:01215  
 fragment\_chain:3"  
 52982..57112  
 /note="assembly\_fragment:00099  
 fragment\_chain:4"  
 57213..60637  
 /note="assembly\_fragment:00140  
 fragment\_chain:4"  
 60738..62745  
 /note="assembly\_fragment:00161  
 fragment\_chain:5"



```
misc_feature 62846..70684
              /note="assembly fragment:01222
              /fragment_chain:5"
misc_feature 70785..74560
              /note="assembly fragment:00675
              /fragment_chain:6"
misc_feature 74661..77242
              /note="assembly fragment:00556
              /fragment_chain:6"
misc_feature 77343..81104
              /note="assembly fragment:00676
              /fragment_chain:7"
misc_feature 81205..83750
              /note="assembly fragment:00946
              /fragment_chain:7"
misc_feature 83851..92962
              /note="assembly fragment:01026
              /fragment_chain:8"
misc_feature 93063..106092
              /note="assembly fragment:00881
              /fragment_chain:8"
misc_feature 106193..110995
              /note="assembly fragment:00353"
misc_feature 111096..114862
              /note="assembly fragment:00726"
misc_feature 114963..118827
              /note="assembly fragment:00964"
misc_feature 118928..124084
              /note="assembly fragment:01042"
misc_feature 124185..128603
              /note="assembly fragment:01274"
misc_feature 128704..132145
              /note="assembly fragment:01290"

ORIGIN
Query Match      24.7%; Score 823.6; DB 2; Length 132145;
Best Local Similarity 97.8%; Pred. No. 2.3e-188;
Matches 835; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2477 TTAATAAGTCTCAAAATCAACAAATAACAAGGTAATCAGTAAAGAAATCTGAATTAC 2536
DB 39723 TCTTAAAGTCTTAAACTATTCTCTTTCAGGTAATCAGTAAAGAAATCTGAATTAC 39782

QY 2537 TCACGCTAGATCAAGATTTACCATCAAGTTGGGAGGAAATTAATAAAGTGAATA 2596
DB 39783 TGACGCTAGATCAAGATTTACCATCAAGTTGGGAGGAAATTAATAAAGTGAATA 39842

QY 2597 TGTACAATATCACTTAGGCTATCTCAAGAGAGATGATTGCTTCTCAAGGAAATGGA 2656
DB 39843 TGTAACAATATCACTTAGGCTATCTCAAGAGAGATGATTGCTTCTCAAGGAAATGGA 39902

QY 2657 GACAGGCTATTCATGGGTCAATCAAAATCCAGACATACAGTCAACATGAGAAATCAGCAC 2716
DB 39903 GACAGGCTATTCATGGGTCAATCAAAATCCAGACATACAGTCAACATGAGAAATCAGCAC 39962

QY 2717 ACACCATATTTCAATATAGAGAGTCAATGACTTGGCAACACAGTAAATCTGAAAAAAA 2776
DB 39963 ACACCATATTTCAATATAGAGAGTCAATGACTTGGCAACACAGTAAATCTGAAAAAAA 40022

QY 2777 AGACACTTACTTATTATTAATAACCCCAATGCAATCAGCGAAACATATTTTACTATCT 2836
DB 40023 AGACACTTACTTATTATTAATAACCCCAATGCAATCAGCGAAACATATTTTACTATCT 40082

QY 2837 TGGATGATAGTCAAAATGATCATAGCCAGGTTTCTTCCACCTTCCCTGAAATTTTAC 2896
DB 40083 TGGATGATAGTCAAAATGATCATAGCCAGGTTTCTTCCACCTTCCCTGAAATTTTAC 40142

QY 2897 TCACAGATCATTTGCAACAGCATAGCTTACTTATTGTTTAGGGACTGAACAATTTATTG 2956
DB 40143 TCACAGATCATTTGCAACAGCATAGCTTACTTATTGTTTAGGGACTGAACAATTTATTG 40202

QY 2957 GGAAGCAAACTTTATATGCTAGAAAGTACATTTAAAGATGACTACTTACGAGGAG 3016
DB 40203 GGAAGCAAACTTTATATGCTAGAAAGTACATTTAAAGATGACTACTTACGAGGAG 40262

QY 3017 ATGCAGGCTCTCTCTAAACGCATGATGTATGTAGTGTGAGCAGCTAGTGTAGTGTATA 3076
DB 40263 ATGCAGGCTCTCTCTAAACGCATGATGTATGTAGTGTGAGCAGCTAGTGTAGTGTATA 40322

QY 3077 TATGCTCCACACTACGCTCTGATAAACACAAACCTCAGTATTTCAGTTATTAGCACACTAG 3136
DB 40323 TATGCTCCACACTACGCTCTGATAAACACAAACCTCAGTATTTCAGTTATTAGCACACTAG 40382

QY 3137 TTTTATACGCACTACTGCTTACATAGTAGACTGTTTGTGGCAATATCTTTCAATTG 3196
DB 40383 TTTTATACGCACTACTGCTTACATAGTAGACTGTTTGTGGCAATATCTTTCAATTG 40442

QY 3197 TTTCTTTAAAGAAACTGAGGTTTCAGATACATACATACATACATACATACATACATACAT 3256
DB 40443 TTTCTTTAAAGAAACTGAGGTTTCAGATACATACATACATACATACATACATACATACAT 40502

QY 3257 TACTACAAAGCTATTTTAAAGAGATGCTATGTTGGAGAGAGGCGAAGTTGACTAT 3316
DB 40503 TACTACAAAGCTATTTTAAAGAGATGCTATGTTGGAGAGAGGCGAAGTTGACTAT 40562

QY 3317 ATGACATATCAAT 3330
DB 40563 ATGACATATCAAT 40576

RESULT 9
HSIMPG17
LOCUS 1235 bp DNA linear PRI 28-OCT-1998
DEFINITION Homo sapiens interphotoreceptor matrix gene (IPM150), exon 17 and complete cds.
ACCESSION AF017776
VERSION AF017776.1 GI:3800731
KEYWORDS
SEGMENT
SOURCE 17 of 17
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 1235)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Fehrig, U., Gehrig, A., Sauer, C.G., Marguardt, A., Kohler, M., Schmid, M. and Weber, B.H.
TITLE Genomic organization and chromosomal localization of the interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate for 6q-linked retinopathies
JOURNAL Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
MEDLINE 98358139
PUBMED 9691169
REFERENCE 2 (bases 1 to 1235)
AUTHORS Gehrig, A., Fehrig, U., Kelsell, R., Hunt, D.M., Maumenee-Hussels, I.E. and Weber, B.H.F.
TITLE Assessment of a novel interphotoreceptor matrix gene (IPM150) localized to eq14.2-q15 in autosomal dominant Stargardt-like macular dystrophy, progressive bifocal choriorretinal atrophy (PB CRA), and North Carolina macular dystrophy (MCDRL)
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1235)
AUTHORS Fehrig, U., Kuehn, M., Hageman, G.S. and Weber, B.H.F.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am Hubland, Wuerzburg D-97074, Germany
FEATURES
source 1..1235
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="6"
            /map="6q14.2-q15"
            /order=(AF017760.1:1..310,AF017761.1:1..537,AF017762.1:1..422,AF017763.1:1..300,AF017764.1:1..304,AF017765.1:1..311,AF017766.1:1..377,AF017767.1:1..300,AF017768.1:1..294,AF017769.1:1..444,AF017770.1:1..347,
```

```

AF017771.1:1..438,AF017772.1:1..816,AF017773.1:1..448,
AF017774.1:1..477,AF017775.1:1..380,1..5490)
/gene="IPM150"
join(AF017760.1:1..223,AF017761.1:97..330,
AF017762.1:112..278,AF017763.1:82..110,
AF017764.1:107..171,AF017765.1:139..242,
AF017766.1:163..303,AF017767.1:98..154,
AF017768.1:153..173,AF017769.1:92..339,
AF017770.1:148..224,AF017771.1:271..349,
AF017772.1:144..676,AF017773.1:111..330,
AF017774.1:171..269,AF017775.1:94..166,413..490)
/gene="IPM150"
/product="interphotoreceptor matrix"
join(AF017760.1:157..223,AF017761.1:97..330,
AF017762.1:112..278,AF017763.1:82..110,
AF017764.1:107..171,AF017765.1:139..242,
AF017766.1:163..303,AF017767.1:98..154,
AF017768.1:153..173,AF017769.1:92..339,
AF017770.1:148..224,AF017771.1:271..349,
AF017772.1:144..676,AF017773.1:111..330,
AF017774.1:171..269,AF017775.1:94..166,413..490)
/gene="IPM150"
/codon_start=1
/product="interphotoreceptor matrix"
/protein_id="AAC68835.1"
/db_xref="GI:3800733"
/translation="MWLETRAI FVWIFLQVQGTQKDISINVIHSETKIDNPPRNET
TESTEKYKMTMRI EDLAKHRTKSAFPTGVKVCPOSKQLDLSLOAYRLVC
QEAWEAVRIFELDRIPDTGEVDWVSIQOETFCLEFDIGKFNSENQHLDLQRIKQ
RSPDRKDEISAEKTEFIVISIDVANVLSGPPFPDDTLNLEILNDLNTK
METTEREFPELBEQREVSILVNQKFAELADSPYQBELAGSLOLMOKIFKK
LPFGKHLVGRKXKDGSSMTQMTAI FKHSREAKSPASDLLSPDSNKIESEE
VYHGMEDKQPEYLVATDLKRLISKALBEEQSLDVGTQFIDEAGSLPAFGPDQ
SELPSPAVITEDATLSPELPPVPOLETVDGAHGLPDTWSGPAMASTLSGAPPF
PMASISLITQGTDMATQTMVPLGATPDSYSAI SOLAIGISHPASDDRS
SAGDEWVHDEMDLSDTPASEVPSELSEVSPDFLEDTPFVSLQIITSSWTI
APKRELVFVFSRVANVAFNDFNKSLEYRALEQQFTQLLYPLRSNLTGKQLE
ILNFNGSVINSKKFASVPYNLTKAVHGVLEDFRSAQAQHLHEDISYLSNIPA
DQADPCFKLACEAQCKYKNTBEACRCKPYDQSGSLDGLPGLCGPTECEVY
QKGAPCLRPDHSENQAYKTSVKKFNQNNKVIKRNSELLTVEYEEFNHQDWEGN"
413..490
/gene="IPM150"

ORIGIN
Query Match 24.5%; Score 814.2; DB 9; Length 1235;
Best Local Similarity 97.8%; Pred. No. 3.4e-186;
Matches 836; Conservative 0; Mismatches 18; Indels 1; Gaps 1;
QY 2477 TTAAGAGCTCCAAATCAACAATAACAGAGTAATCAGTAAAGAAATCTCAANTAC 2536
DB 381 TTCTTAAGTCTTAAAGATTTCTCTTTTCAGGTAATCAGTAAAGAAATCTCAANTAC 440
QY 2537 TGACCGTAGAATATGAAGAAATTAACCAATCAAGATTGGGAAGGAAATTAAGAACTGAAA 2596
DB 441 TGACCGTAGAATATGAAGAAATTAACCAATCAAGATTGGGAAGGAAATTAAGAACTGAAA 500
QY 2597 TGTAACAATATCACTTAGGCTATCTCAAGAGAGATGATTGCTTCCTCAAGGAAATGGA 2656
DB 501 TGTAACAATATCACTTAGGCTATCTCAAGAGAGATGATTGCTTCCTCAAGGAAATGGA 560
QY 2657 GACAGGCATATTCATGGGTCTCAAAATCCAGACATACAGTCAACACTGAGAATCAGCAC 2716
DB 561 GACAGGCATATTCATGGGTCTCAAAATCCAGACATACAGTCAACACTGAGAATCAGCAC 620
QY 2717 ACACCATATTTCAATATAGAGAGTCAATGACTTGGCAACAGTAAATTCGAA-AAAA 2775
DB 621 ACACCATATTTCAATATAGAGAGTCAATGACTTGGCAACAGTAAATTCGAAAGAAA 680
QY 2776 AAGACACTTACTTATTTATAAACCCTCAATGCAATCAGCGAACAATATTTTACTATTC 2835
DB 681 AAGACACTTACTTATTTATAAACCCTCAATGCAATCAGCGAACAATATTTTACTATTC 740
QY 2836 TTGGATGATAGTCAAAATGATCATAAAGCCAGGTTTGCTTCCACCTTCCCTGAAAAATTTTA 2895

```

```

|||||
741 TTGGATGATAGTCAAAATGATCATAGCCAGGTTTGCTTCCACCTTCCCTGAAAAATTTTA 800
|||||
2896 CTCACAGATCATTTGCAACAAGCATAGCTTACTTATTGTTTGGGACTGAACAAATTTATT 2955
|||||
801 CTCACAGATCATTTGCAACAAGCATAGCTTACTTATTGTTTGGGACTGAACAAATTTATT 860
|||||
2956 GGGAGCAACTCTTTATATGCTAGCAAGTACATTTAAAGATGACTACTTACGAGGGA 3015
|||||
861 GGGAGCAACTCTTTATATGCTAGCAAGTACATTTAAAGATGACTACTTACGAGGGA 920
|||||
3016 GATGCAAGTCTCTCTAAACGCATGAATGATGCTAGTGTAGGCACTGTAGTGAAGTAT 3075
|||||
921 GATGCAAGTCTCTCTAAACGCATGAATGATGCTAGTGTAGGCACTGTAGTGAAGTAT 980
|||||
3076 ATATGCTCCACTAGTCTGTATTAACACCAACCTCAGTATTCACTTATTAGGCACACTA 3135
|||||
981 ATATGCTCCACTAGTCTGTATTAACACCAACCTCAGTATTCACTTATTAGGCACACTA 1040
|||||
3136 GTTTTATAGCAACTACTGCTTACATAGTAGACTGTTTGTGTCCTCAATAATCTTTGAATT 3195
|||||
1041 GTTTTATAGCAACTACTGCTTACATAGTAGACTGTTTGTGTCCTCAATAATCTTTGAATT 1100
|||||
3196 GTTCTTTAAAGAACTGAGGTTTCAGATACATACCATGGAATAATCTTACTTTCTTG 3255
|||||
1101 GTTCTTTAAAGAACTGAGGTTTCAGATACATACCATGGAATAATCTTACTTTCTTG 1160
|||||
3256 TTACTACACAAAGCTATTTTAAAGAAAGATGCTATGTTGGGAGAGGGGAGGTTGTACTA 3315
|||||
1161 TTACTACACAAAGCTATTTTAAAGAAAGATGCTATGTTGGGAGAGGGGAGGTTGTACTA 1220
|||||
3316 TATGACATATCAAT 3330
|||||
1221 TATGACATATCAAT 1235
|||||

RESULT 10
HSIMPG13 816 bp DNA linear PRI 28-OCT-1998
LOCUS Homo sapiens interphotoreceptor matrix gene (IPM150), exon 13.
ACCESSION AF017772
VERSION AF017772.1 GI:3800727
KEYWORDS
SEGMENT 13 of 17
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 816)
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Zelbor,U., Gehrig,A., Sauer,C.G., Marquardt,A., Kohler,M.,
Schmid,M. and Weber,B.H.
Genomic organization and chromosomal localization of the
interphotoreceptor matrix proteoglycan-1 (IMPG1) gene: a candidate
for 6q-linked retinopathies
CYTOGENET. Cell Genet. 81 (1), 12-17 (1998)
JOURNAL 98358139
MEDLINE 2691169
PUBMED 2691169
REFERENCE 2 (bases 1 to 816)
AUTHORS Gehrig,A., Zelbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.B.
and Weber,B.H.F.
Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like
macular dystrophy, progressive bifocal choriorretinal atrophy
(PBCRA), and North Carolina macular dystrophy (MCDRL)
Unpublished
REFERENCE 3 (bases 1 to 816)
AUTHORS Zelbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
Direct Submission
JOURNAL Submitted (09-AUG-1997) HumanGenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
FEATURES
source
1..816
/organism="Homo sapiens"

```



/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/map="6q14.2-q15"  
144..676  
/gene="IPM150"

## ORIGIN

```
Query Match      16.1%; Score 535.8; DB 9; Length 816;
Best Local Similarity 99.6%; Pred. No. 1.e-118;
Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1481 CTGACACTTCTTGGTCTCCACCTGTATGGCTCTACTCCTCTGTCAGAGCTCCACCTT 1540
Db 141 CAGACACTTCTTGGTCTCCACCTGTATGGCTCTACTCCTCTGTCAGAGCTCCACCTT 200
QY 1541 TCTTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGCAACCAAGATGAGCA 1600
Db 201 TCTTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGCAACCAAGATGAGCA 260
QY 1601 CTGACCAAGATGCTAGTACAGGGCTCAACATCCCAACAGTGAATTTCTGCAATCA 1660
Db 261 CTGACCAAGATGCTAGTACAGGGCTCAACATCCCAACAGTGAATTTCTGCAATCA 320
QY 1661 GCCAATGGCTCTGGGAATTTTCATCTCCACCTGCTATTCAGATGACAGCCGATCAAGTG 1720
Db 321 GCCAATGGCTCTGGGAATTTTCATCTCCACCTGCTATTCAGATGACAGCCGATCAAGTG 380
QY 1721 CAGTGGCAAGATATGCTGACACCTAGATGAATGATGCTGTCGACTCTCTGCGCC 1780
Db 381 CAGTGGCAAGATATGCTGACACCTAGATGAATGATGCTGTCGACTCTCTGCGCC 440
QY 1781 CATCTGAGTACAGAGCTCAGCGAATATGTTTCTGTCCAGATCATTTCTGGAGGATA 1840
Db 441 CATCTGAGTACAGAGCTCAGCGAATATGTTTCTGTCCAGATCATTTCTGGAGGATA 500
QY 1841 CCACTCTGCTCAGCTTTACAGTATATCAACACTAGTTCTATGACCATTTGCCCCCAAGG 1900
Db 501 CCACTCTGCTCAGCTTTACAGTATATCAACACTAGTTCTATGACCATTTGCCCCCAAGG 560
QY 1901 GCGAGAGCTGGTAGTGTCTTCAGTCTGGTGTCTTAACATGGCTTCTCCACAGACC 1960
Db 561 GCGAGAGCTGGTAGTGTCTTCAGTCTGGTGTCTTAACATGGCTTCTCCACAGACC 620
QY 1961 TGTTCACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACAGCTGGTG 2019
Db 621 TGTTCACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACAGCTGGTG 679
```

## RESULT 11

AL157379/c  
LOCUS Homo sapiens chromosome 6 clone RPL-62L18. linear HTG 11-SEP-2001  
DEFINITION  
ACCESSION AL157379  
VERSION AL157379.14 GI:15590763  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_CANCELLED.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1.  
Wall M.  
Direct Submission  
Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk  
On Sep 12, 2001 this sequence version replaced gi:11991356.

## COMMENT

----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information

Center project name: dj62L18  
----- Summary Statistics  
Sequencing program: XGAP4; version 4.5  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 160382 bases at least Q40  
Consensus quality: 160493 bases at least Q30  
Consensus quality: 160578 bases at least Q20  
Insert size: 160719; sum-of-contigs  
Insert size: 158939; 9.3% error; agarose-fp  
Quality coverage: 8.32x in Q20 bases; sum-of-contigs Quality  
coverage: 8.41x in Q20 bases; agarose-fp

-----  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

## FEATURES

## source

Location/Qualifiers  
1..160719  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/clone="RPL-62L18"  
/clone\_lib="RPC1-1"

## misc\_feature

1..160719  
/note="assembly\_fragment:02758  
vector\_side:left  
clone\_end:T7  
vector\_side:right"

## ORIGIN

```
Query Match      16.1%; Score 535.8; DB 2; Length 160719;
Best Local Similarity 99.6%; Pred. No. 1.4e-118;
Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1481 CTGACACTTCTTGGTCTCCACCTGTATGGCTCTACTCCTCTGTCAGAGCTCCACCTT 1540
Db 7764 CAGACACTTCTTGGTCTCCACCTGTATGGCTCTACTCCTCTGTCAGAGCTCCACCTT 7705
QY 1541 TCTTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGCAACCAAGATGAGCA 1600
Db 7704 TCTTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGCAACCAAGATGAGCA 7645
QY 1601 CTGACCAAGATGCTAGTACAGGGCTCAACATCCCAACAGTGAATTTCTGCAATCA 1660
Db 7644 CTGACCAAGATGCTAGTACAGGGCTCAACATCCCAACAGTGAATTTCTGCAATCA 7585
QY 1661 GCCAATGGCTCTGGGAATTTTCATCTCCACCTGCTATTCAGATGACAGCCGATCAAGTG 1720
Db 7584 GCCAATGGCTCTGGGAATTTTCATCTCCACCTGCTATTCAGATGACAGCCGATCAAGTG 7525
QY 1721 CAGTGGCAAGATATGCTGACACCTAGATGAATGATGCTGTCGACTCTCTGCGCC 1780
Db 7524 CAGTGGCAAGATATGCTGACACCTAGATGAATGATGCTGTCGACTCTCTGCGCC 7465
QY 1781 CATCTGAGTACCAAGCTCAGCGAATATGTTTCTGTCCAGATCATTTCTTGGAGGATA 1840
Db 7464 CATCTGAGTACCAAGCTCAGCGAATATGTTTCTGTCCAGATCATTTCTTGGAGGATA 7405
QY 1841 CCACTCTGCTCAGCTTTTACAGTATATCAACACTAGTTCTATGACCATTTGCCCCCAAGG 1900
Db 7404 CCACTCTGCTCAGCTTTTACAGTATATCAACACTAGTTCTATGACCATTTGCCCCCAAGG 7345
QY 1901 CCGAGAGCTGGTAGTGTCTTCTGAGTCTGGTGTGCTACATGGCCCTTCTCCAGAGACC 1960
Db 7344 CCGAGAGCTGGTAGTGTCTTCTGAGTCTGGTGTGCTACATGGCCCTTCTCCAGAGACC 7285
QY 1961 TGTTCACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACAGCTGGTG 2019
Db 7284 TGTTCACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACAGCTGGTG 7226
```



```

QY 1179 AATTGAAGTGAAGAGTCTATCATGGAACCATGGAGGAGGACACGACCAAGAAATCTA 1238
Db 1209 GGTGAAATGAAGAGGTACCACTCTCTGCAAGGAGAGAGGAAATATCAGCAACCAA 1268
QY 1239 TCTCAGAGCTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGAGGAAGA-----ACA 1292
Db 1269 ACTCAGAGTAACAGACCTTCAGCAGCTGGTGGCCACAGCACTCCATGAAGACAGATCCCT 1328
QY 1293 ATCTTTGGATGGGACAAATTCAGTCTCAGTCACTGATGAATTCGTGGATCACTGCCAGCCTT 1352
Db 1329 ACCAGTGGACCTTGGGACACTTCGGTTTACTGAGCAACCTATTAACCACTCAAGTGATTT 1388
QY 1353 TGGTCTGTGACACCAATCAGAGCTGCCACATCTTTTGTGCTTATTAACAGAGAGTGCTAC 1412
Db 1389 TGATAATGACATCAAGGCACTGCTACTATTCCTCTGGCAGGCCCTGATTTGGATGACAC 1448
QY 1413 TTTTGGTCCAGAACTCTCTCTCTGAAACCCAGCTTGAGACAGTGGAGCGAGC 1466
Db 1449 CATAAGCGCAGAACTCCCACTGGTTTATCCAGCCCAATAACAGTGGACCAAC 1502

RESULT 13
AF047491
LOCUS
DEFINITION
Macaca fascicularis interphotoreceptor matrix proteoglycan 150
mRNA, partial cds.
ACCESSION
AF047491
VERSION
AF047491.1 GI:2906229
KEYWORDS
Macaca fascicularis (crab-eating macaque)
SOURCE
Macaca fascicularis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.
REFERENCE
1 (bases 1 to 555)
Kuehn, M.H. and Hageman, G.S.
Characterization And Complete cDNA Sequence Of IPM 150, A Novel
Human Photoreceptor Cell-Associated Chondroitin-Sulfate
Proteoglycan
Unpublished
REFERENCE
2 (bases 1 to 555)
Kuehn, M.H. and Hageman, G.S.
Direct Submission
Submitted (10-FEB-1998) Ophthalmology and Visual Sciences,
University of Iowa, 200 Hawkins Drive, 11190E PFP, Iowa City, IA
52240, USA
FEATURES
source
1..555
location/qualifiers
/organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xref="taxon:9541"
/tissue_type="retina"
<1..>555
/notes="IPM 150"
/codon_start=1
/product="interphotoreceptor matrix proteoglycan 150"
/protein_id="AAC03788.1"
/db_xref="GI:2906230"
/translatability="IFPPNGVKVCPQESMKQILASLQAYRURVCOEAWBAYRIFLD
RIPDTGEYQDWSFCQQTFCFLDIGNFNSQEBLIDLQQRKQKSPFRDEYSTE
KTGEPSEITVSTDVASVSLGPPVPTPDTLLNELNDNALNDTKMPTTERETELAS
EEQRVELSISLNRKFABELADQS"
ORIGIN
Query Match 13.2%; Score 439; DB 9; Length 555;
Best Local Similarity 85.8%; Pred. No. 3e-95;
Matches 526; Conservative 0; Mismatches 25; Indels 62; Gaps 1;

QY 347 TTTTCCACAGCGGGGTAAAGTCTGTCACAGGAATCATGAACAGAGATTTAGACAGT 406
Db 4 TTTTCCGACAGCGGGGTAAAGTCTGTCACAGGAATCATGAACAGAGATTTAGCCAGT 53

```

```

QY 407 CTTCAAGCTTATTATAGATTGAGAGTGTGTGTCAGGAAGCAGTATGGGAAGCATATCGGATC 466
Db 64 CTTCAAGCTTATTATAGATTGAGAGTGTGTGTCAGGAAGCAGTATGGGAAGCATATCGGATC 123
QY 467 TTTCTGGATCCGATCCCTGACAGAGGGGAATATCAGGACTGGGTGAGCATCTCCAGCAG 526
Db 124 TTTCTGGATCCGATCCCTGACAGAGGGGAATATCAGGACTGGGTGAGCATCTCCAGCAG 183
QY 527 GAGACCTCTTGGCTCTTGGACATTTGGAATAAATTTGAGCAATTTCCAGGAGCAGCTGGAT 586
Db 184 GAGACCTCTTGGCTCTTGGACATTTGGAATAAATTTGAGCAATTTCCAGGAGCAGCTGGAT 243
QY 587 CTTCTCCAGCAGAGAAATAAAGAGAGAGTTCCTTGACAGAAAAGATGAATATCTGCA 646
Db 244 CTTCTCCAGCAGAGAAATAAAGAGAGAGTTCCTTGACAGAAAAGATGAATATCTGCA 303
QY 647 GAGAGACATTTGGAGAGCCTGGTGAACCATTTGTCATTTCAACGCAATCTCAATTTCA 706
Db 304 GAGAGACATTTGGAGAGCCTGGTGAACCATTTGTCATTTCAACGCAATCTCAATTTCA 347
QY 707 AAGACTTTGGGAGTATTCTTAAGAAAACCTTCAGAGAGCAAAATTCAGAGTGTGCCAAG 766
Db 348 -----AGATGTTGCCAGCG 361
QY 767 TCTCACTTGGGCTTTTCCCTCTCCTCTGATGACACCCCTCTCAATGAATTCGATA 826
Db 362 TCTCACTTGGGCTTTTCCCTCTCCTCTGATGACACCCCTCTCAATGAATTCGATA 421
QY 827 ATACACTCAACGACCAAGATGCTTACACAGAGAGAAACAGAAATTCGCTGTGTGG 886
Db 422 ATGCACTCAACGACCAAGATGCTTACACAGAGAGAAACAGAAATTCGCTGTGTGG 481
QY 887 AGGAGCAGAGGGTGGAGCTCAGCGTCTCTTGTTAAACAGAAAGTTCAGGAGAGCTCG 946
Db 482 AGGAGCAGAGGGTGGAGCTCAGCGTCTCTTGTTAAACAGAAAGTTCAGGAGAGCTCG 541
QY 947 CTGACTCCGAGTC 959
Db 542 CTGACTCCGAGTC 554

RESULT 14
AC120388
LOCUS
DEFINITION
Mus musculus chromosome 9 clone RP24-300P2 map 9, *** SEQUENCING IN
PROGRESS ***, 3 unordered pieces.
ACCESSION
AC120388.4 GI:39930692
VERSION
HTG; HTGS PHASE1; HTGS FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 171412)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 9, clone RP24-300P2
Unpublished
REFERENCE
2 (bases 1 to 171412)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguski, L.,
Boukhalil, B., Brown, A., Camarata, J., Campolongo, A., Chang, J.,
Chazaro, B., Choquet, Y., Colangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faroo, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gordon, J., Hulme, W., Iliiev, I., Johnson, R., Jones, C.,
Hogson, B., Horton, J., Kells, C., Lakocque, K., Lamazares, R.,
Lander, S., Lechoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunhkhong, P., Pierre, N., Pollara, V.,

```



Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpthy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowitz, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensukewa, L., Louleghed, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankarvis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokeleneh, O., Okwuonu, G., Olarnpunsoo, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plapper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Raches, R., Quiroz, J., Rachlin, B., Reeves, K., Regier, M.A., Reigh, R., Rellis, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, I., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, D., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wood, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

## TITLE

Direct Submission

## JOURNAL

Unpublished

## REFERENCE

2 (bases 1 to 248573)

## AUTHORS

Worley, K.C.

## TITLE

Direct Submission

## JOURNAL

Submitted (17-SEP-2001)

Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## REFERENCE

3 (bases 1 to 248573)

## AUTHORS

Rat Genome Sequencing Consortium.

## TITLE

Direct Submission

## JOURNAL

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:23264514. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GPCR

Center clone name: CH230-85A18

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 236654 bases at least Q40

Consensus quality: 238781 bases at least Q30

Consensus quality: 240212 bases at least Q20

Estimated insert size: 249458; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length

\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 247402: contig of 247402 bp in length

\* 247502: gap of unknown length

\* 247503 248573: contig of 1071 bp in length.

## FEATURES

## source

1..248573

/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clones="CH230-85A18"

3167..3839

/note="clone boundary"

clone end:T7

site:ECORI

end\_sequence: BH302159"

95023..95328

/note="clone boundary"

clone end:Sp6

site:ECORI

end\_sequence: BH302192"

## ORIGIN

Query Match	8.2%	Score 274.6	DB 2	Length 248573
Best Local Similarity	70.8%	Pred. No. 3e-55		
Matches 380	Conservative 0	Mismatches 154	Indels 3	Gaps 1

  

QY	1483	GACACTCTTGGTCTCCACCTGCTATGGCTCTACCTCCCTGTGAGAGTCCACCTTTC	1542
DB	213183	GACAGTCTTGGTCTTGGCTGTAAACAGCTCGACTTCGGAGTGGAAATCTACCTTC	213124
QY	1543	TTTATGGATCAAGATCTTCTCTGACTGATCAAGGACCAAGATCAATGGCCACT	1602
DB	213123	TTTACGCT--AGCATCTTGGCTCTGGATGATCAAGCTCCCTCCCTTGTATGGCCACT	213067
QY	1603	GACCAGCAATGCTAGTACAGGGCTCACCATCCCACTGATTTCTGCAATCAGC	1662
DB	213066	GGCCACAGCATCTATCCCACTGCTCTGCTCCCTCTCGATTTCTACCGTCCGC	213007
QY	1663	CAACTGGCTCTGGAAATTCATCCCTCCATCTTTCAGATGACGCGATCAAGTCA	1722
DB	213006	CAATGGCGCTAGAAAGTGTCAATTCGCTGAGTCTTCCAGTGCAGAGATTGACCACA	212947
QY	1723	GCTGGCAGATATGTTGTCAGACACCTAGTGAATGATCTGCTGACATCTCCGCCCCA	1782
DB	212946	AGCAGCCACGACACAATCAGAGACCTAGTGAATGATGTCGACACGCTGCTTG	212887
QY	1783	TCTGAGTACAGAGCTCAGCGAATATGTTTCTCTCCAGATCAATTTCTTGGAGATACC	1842
DB	212886	TCGGAATAGCAGAACTGAGTGGATGATGACTCTCCCGGATCGTCTTGGAGATGACC	212827
QY	1843	ACTCTGTCTGCTTACAGTATATACCACTAGTCTTATGACCATGCCCCAAGGCG	1902
DB	212826	ACGCCATCCCGACATACAGTATGTCAACCACTGAGCTTGCAGCATGCGCCCAAGGCG	212767
QY	1903	CGAGAGCTGGTAGTGTCTTCTCAGTCTGGTGTGCTAACATGGGCTTCTCCAAAGAGCTG	1962
DB	212766	CACGAGCTAGTGTATTTCTTTCAGTCTGGCGGTGCTAACATGGGCTTCTCTATGACTTG	212707
QY	1963	TTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACAGACTGCTG	2019
DB	212706	TTCAATAAGAGTTCCTCGAGTACCAAGCTTGAACAACAGATTTCACAGACTGCTG	212650

Search completed: March 1, 2004, 18:13:25

Job time : 12825 secs

---

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 14:08:16 ; Search time 8150 Seconds  
(without alignments)

12201.357 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taaaccaagaaggtatcct.....tactatatcacataatcaat 3330

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_man:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pig:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1642.4	49.3	1665	29 AY415971	AY415971 Homo sapi
2	943.6	28.3	1647	29 AY415973	AY415973 Mus muscu
3	739.2	22.2	1587	29 AY415972	AY415972 Pan trogl
4	716.2	21.5	801	12 BG196799	BG196799 RST16026

5	640.2	19.2	836	12	BI752112	BI752112 603022362
6	634	19.0	690	13	EX510244	EX510244 DXF2P686P
7	628.8	18.9	633	12	BM695987	BM695987 UI-E-CL1-
8	626	18.8	626	13	BQ639265	BQ639265 hd33D04.Y
9	617.2	18.5	622	13	BQ638902	BQ638902 hd29a06.Y
10	615.6	18.5	653	12	BM685921	BM685921 UI-E-CKO-
11	589.4	17.7	675	12	BM690735	BM690735 UI-E-CKO-
12	577.6	17.3	598	13	BQ636596	BQ636596 hd11h02.Y
13	498.4	15.0	508	14	CA333958	CA333958 c844g04.Y
14	472	14.2	472	13	EX097138	EX097138 BX097138
15	459.6	13.8	561	14	W26960	W26960 16h10 Human
16	442.2	13.3	698	13	BU729227	BU729227 UI-E-CL1-
17	433	13.0	683	13	BU732814	BU732814 UI-E-CQ1-
18	429.6	12.9	824	12	BI738733	BI738733 603358767
19	418.2	12.6	963	13	BU506195	BU506195 AGENCOURT
20	409	12.3	422	12	BM726533	BM726533 UI-E-EJO-
21	386	11.6	448	12	BM681190	BM681190 UI-E-EJO-
22	385.6	11.6	851	12	BI733865	BI733865 603353151
23	380.2	11.4	393	13	BQ636351	BQ636351 hd07h06.Y
24	376.2	11.3	641	13	BU734170	BU734170 UI-E-CK1-
25	363.2	10.9	368	12	BM694699	BM694699 UI-E-CI1-
26	354.4	10.6	405	14	H38604	H38604 YD48e04.r1
27	327	9.8	510	9	AL713229	AL713229 DXF2P686P
28	323	9.7	618	14	CA391789	CA391789 csi8h07.Y
29	317	9.5	322	9	AA326863	AA326863 EST30113
30	298.8	9.0	309	14	H38594	H38594 YP48c06.r1
31	298.2	9.0	701	29	AG128736	AG128736 Pan trogl
32	292.4	8.8	797	11	AK020862	AK020862 Mus muscu
33	291	8.7	298	9	AA296278	AA296278 EST10795
34	282.4	8.5	521	12	BM691879	BM691879 UI-E-CL1-
35	282.4	8.5	548	13	BU728582	BU728582 UI-E-CL1-
36	274.4	8.2	340	9	AV656968	AV656968 AV656968
37	271	8.1	753	12	BI735383	BI735383 603356869
38	268	8.0	515	13	BU726282	BU726282 UI-E-CKO-
39	262	7.9	527	13	BU731220	BU731220 UI-E-CI1-
40	262	7.9	567	28	AZ974344	AZ974344 2M0243F20
41	253.2	7.6	886	14	CF549501	CF549501 AGENCOURT
42	238	7.1	802	12	BI735091	BI735091 603356230
43	226.2	6.8	678	28	AZ876525	AZ876525 2M0191104
44	224.2	6.7	813	13	BX743512	BX743512 BX743512
45	222.4	6.7	481	9	AI510373	AI510373 mp95e12.Y

## ALIGNMENTS

RESULT 1	AY415971	1665 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY415971	1665 bp	DNA	linear	GSS 17-DEC-2003
DEFINITION	Homo sapiens IMPG1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY415971				
VERSION	AY415971.1				
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1665)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1665)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				







TITLE	QUERY MATCH	BEST LOCAL SIMILARITY	SCORE	DB	LENGTH
JOURNAL PUBLISHED	922	AAACAGAGTTCAAGGCGAGCTGGTGTACTCCAGCTCCCACTATATACCAAGAGCTAGCA	981		
REFERENCE	1	AAACAGAGTTCAAGGCGAGCTCACCACCTCTGGGTCACTACTACCAAGAACTGGTG	60		
AUTHORS	982	GGAAAGTCCCAACTTCAGATGCAAGAGATATTTAAGAACTTCCAGGATTCAAAATAATC	1041		
	61	GGACAGTCCCAACTGCGAGTTGCAAGAGATATTTAAGAACTTCCAGGATTCGGAATTC	120		
TITLE	1042	CATGTGTTTAGGATTTAGACAAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAA	1101		
JOURNAL	121	CGTGATTTAGGATTTAGNN	180		
PUBLISHED	1102	CTTAGCGGCATCTTTAGAGACACAGTGGAGAGCAAAAAGCCCTGCAAGTGCCTCGT	1161		
REFERENCE	181	CTTATGGGCATCTTTAAGAGGGACCATGCAAGAGCAAAAAGCCCTGATAGTCATCTAGT	240		
AUTHORS	1162	TCCTTTGATTCACAAAAATTTGAAAGTGAGGAGTCTATCATGGAACCATGGAGGAGAC	1221		
	241	TCTCTTGATTCACAAAAATTTGAAAGTGAGGAGTCCATCATGGAGTCAT---AGAAGAC	297		
TITLE	1222	AGCAACACAGAAATCTATCTCACAGTACAGACCTCAAAGGCTGATCAGCAAGCACTA	1281		
JOURNAL	298	AAACACACAGAAACCTACCTCACAGCTACAGACCTCAAAGAACTCATCATCAACTACTA	357		
PUBLISHED	1282	GAGGAAGACAACTTTTGGATGTGGGACAAATTCAGTTCACCTGATGAAATTCCTGGATCA	1341		
REFERENCE	359	GATGAGACCTGTCTCTGGTAGAAGGGAAATTTCCATTCGGTGATGAAAGTACTGGGACA	417		
AUTHORS	1342	CTGCAGGCTTTGGTCTCTGACACCCATCAGAGCTGCCACATCTTTTGGTGTATAACA	1401		
	418	CT-----CTTCAGACCTGTCACTGAACACAGATCTGCCCAAGCCCTTGGTGTCACTA	471		
TITLE	1402	GAGGATGCTACTTTGAGTCAGAACTTCTCTCTGTTGAAACCCAGCCTTGAGACAGTGGAC	1461		
JOURNAL	472	GAGGATGGCACTTTGAGTCAGAACTTCTCTCTGTTGAGCCTTAGGCTTGAGCAGTGGAC	531		
PUBLISHED	1462	GGACAGAGCATGGTCTACCTGACACTTCTTGGTCTCCACCTGCTATGGCTCTACCTCC	1521		
REFERENCE	532	AGAGAGAGATCTGAGCTGCGCTGACAGTCTTGTGTCTCCACCTGTATGAGCTCAATTTCC	591		
AUTHORS	1522	CTGTGAGAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGC	1581		
	592	CGATCAGAAATCTACCTTCTGTTA---CACCTAGCATCTTCTCTAGATGCTCAAGC	648		

Qy	1582	ACCACAGATACAATGGCCACTGACACAGACAAATGCTAGTATACACGGGCTCACCATCCTCCACCC	1641
Db	649	CCCCCTCCCTTGATGACCACTGGCCCCAACAGCACTCATCCCCAAAGGCCACTCTCCTCCCACT	708
Qy	1642	AGTGATTATTCTGCAATCAGCAACTGGGTCTGGGAATTTACATCCACCTGCAATCTTCA	1701
Db	709	ATCGATTATTCTACCATCCGCCAATTGGCTCTGGATCGTCAATTGGCCTGCATCCTCC	768
Qy	1702	GATGACAGCCGATCAAGTGCAGGTGGCGGAAGATATGGTGCAGACACCTAGATGAATGGAT	1761
Db	769	AGTGACAGAGAGCTGATCAACAAGCAGCCATGACACAATCCGAGACCTAGATGGCATTGGAT	828
Qy	1762	CTGTCTGCACTCTCGCCCATCTGAGGTACCAAGCTCAGCGAAATATGTTTCTGTGCCCA	1821
Db	829	GTGTCTGACACGCCAGCCCTGTGCAGAAATACAGAACTGAGTGGATACGATTCTGCCTCG	888
Qy	1822	GATCAATTTCTTGAGGATACCACTCTCTGTCTGACGTTTACAGTATATCAACACTAGTTCT	1881
Db	889	GGTCAGTTCTTGAGATGACCAACCCATCCCAACAGTAGTCGGTTCATCAACACACAGCTCC	948
Qy	1882	ATGACCAATTGCCCCCAAGGCCGAGAGCTGGTAGTGTCTTTCAGTCTGCGTGTGCTTAAC	1941
Db	949	GAGACCAATTGCCACCAAGGCCAGGAGCTAGTGGTATTCTTCAGCCTGCGTGTGCTAAC	1008
Qy	1942	ATGGCTTCTTCCAAACGACTGTTTCAACAGAGCTCTCTGGAGTACCGAGTCTTGGAGCAA	2001
Db	1009	ATCCGCTTCTCTATGACCTGTTTCAACAAGAGTTCTCTGGAGTATCAAGGCCCTTGGACAA	1068
Qy	2002	CAATTTCACACAGCTGCTGGTTTCCATATCTACGATCCAAATCTTACAGGATTTTAAGCAACTT	2061
Db	1069	CGATTTCACAGACTGCTGGTTCCCTATCTACGATCGAATCTTACGGGATTTTAGCAACTG	1128
Qy	2062	GAATACTTAACTTCAGAAACGGGAGTGTGATGTGAAATAGCAAAATGAAGTTTGCTAAG	2121
Db	1129	GAATACTCAGCTTCAGAAACGGAGTGTGATCGTGAACAGCAAAAGTGGGTTTGCAAAAG	1188
Qy	2122	TCGTGCGGTATAAATCTCACCAGGCTGTGCACGGGTCTTTGGAGGATTTTCGTTCTGCT	2181
Db	1189	CGGGTACCTTACAACTTCAACCGCCGTGGCGGGTCTTGGAGGATCTTCGGTCCACC	1248
Qy	2182	GCAGCCCAACAATCCATCTGGAATATGACAGCTACTCTCTCAACATTGAACACAGCTGAT	2241
Db	1249	GCAGCTCAAGGGCTCAATCTGGAATTCGAAGGCTATCCCTCGACATGAACACAGCTGAT	1308
Qy	2242	CAAGCAGATCCCTGCAAGTTCTGGCTCGCGGGAATTTGCCCAATGTGTAAAGAACGAA	2301
Db	1309	CAGGCGATCCCTGCAACTTCTAGACTGTGCAAAATTTGCCCACTGTGTAAAGATGAG	1368
Qy	2302	CGGACTGAGGAACGGAGTGTGCTGTCAAAACGAGGATATGACAGCCAGGGAGCCTGGAC	2361
Db	1369	TGGACAGAGGAGCAGAGTGTGCTGACAGACGGGACATGAGAGCCACGGGACCTCTGGAC	1428
Qy	2362	GGTCTGGAAACCGGCTCTGTGGCCCTGCGACAAAGGAATGCGAGTCTCTCCAGGGAAAG	2421
Db	1429	TACCAGACCTGAACTCTGTGCCCTTGG---AAGACTTGTGTGGCCGGCCGAGAACAA	1485
Qy	2422	GGAGCTCCATGCAGGTGTCAGATCACTCTGAAATCAAGCATACAAAATAGTGTAAA	2481
Db	1486	GCAACTCCATGCAGGCCAACAGATCACTCTACAAACCAAGCTCAGGAACCTGGTGTAAA	1545
Qy	2482	AGTTCCTCAAAATCAACAAATTAACAGGTAATCAGTTAAAGAAATCTCGAAATCTAGTACC	2541
Db	1546	AAG---CTACGTCAGCAAAATAGGTAGTGCAGAAAGAAATTTCTAACTATCAGCT	1602
Qy	2542	GTAGAATATGAAGAATTTTAACCATCAAGATTGGGAAGGAAATTTAA	2596
Db	1603	ATAGGATTTGAAGAAATTTCAAGACACAGGACTGGAGGGAAATTTAA	1647

RESULT 3  
AY415972  
LOCUS

AY415972	1587 bp	DNA	linear	GSS 17-DEC-2003
----------	---------	-----	--------	-----------------



```
QY 2560 AACCATCAGATTGGGAAGGAATTA 2586
Db 1561 AACCATCAGATTGGGAAGGAATTA 1587

RESULT 4
LOCUS BGI96799 801 bp mRNA linear EST 21-APR-2001
DEFINITION R516026 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BGI96799
VERSION BGI96799.1 GI:13718486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 801)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cochren,K., Lo,K.,
Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 11329013
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 474.

FEATURES
source
1..801
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

ORIGIN
Query Match 21.5%; Score 716.2; DB 12; Length 801;
Best Local Similarity 97.7%; Pred. No. 1.2e-148;
Matches 757; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

QY 2449 TCTGAAATCAAGCATACAAACTAGTGTAAAGTTCCAAATCAACAAATAACAAG 2508
Db 23 TCTGAATATCAAGCATACAAACTAGTGTAAAGTTTCAAATCAACAAATATCAAG 81

QY 2509 GTAATCAGTAAAGAAATTCGAATCTACTGACCTAGAGTATGAGAAATTAACCATCAA 2568
Db 82 GTAATCAGTAAAGAAATTCGAATCTACTGACCTAGAGTATGAGAAATTAACCATCAA 141

QY 2569 GATTGGGAGGAATTAATACTGAAATGACAAATATCACTAGGCTATCTCAAGAGA 2628
Db 142 GATTGGGAGGAATTAATACTGAAATGACAAATATCACTAGGCTATCTCAAGAGA 201

QY 2629 GATGATTGGCTTCTCAAGGAAATGGAGACAGGCATATTCATGGGTCACTCAAAATCCAG 2688
Db 202 GATGATTGGCTTCTCAAGGAAATGGAGACAGGCATATTCATGGGTCACTCAAAATCCAG 261

QY 2689 ACATACAGTCAACCTGAGATCGACACACCATATTTCAATATAGAGACTCATGA 2748
Db 262 ACATACAGTCAACCTGAGATCGACACACCATATTTCAATATAGAGACTCATGA 321
```

```
QY 2749 CTTGGCAACCAAGTAATTTCTGAAAAAAGACACTTACTTATTATTAACCCCAATGC 2808
Db 322 CTTGGCAACCAAGTAATTTCTGAAAAAAGACACTTACTTATTATTAACCCCAATGC 381

QY 2809 AATCAGCGAAACATATTTTACTATTTCTGGATGATAGTCAAAATGATCATAAAGCCAGGT 2868
Db 382 AATCAGCGAAACATATTTTACTATTTCTGGATGATAGTCAAAATGATCATAAAGCCAGGT 441

QY 2869 TTGCTTCACACCTTCCTCGAAAAATTTTACTTCACAGATCAATTTGCGAACAGCATAGCTTACT 2928
Db 442 TTGCTTCACACCTTCCTCGAAAAATTTTACTTCACAGATCAATTTGCGAACAGCATAGCTTACT 501

QY 2929 TATTGTTTAGGACGTGAACAATTTATTGGGAAGCAAACTCTTTATATGCTGAGAAAGTACA 2988
Db 502 TATTGTTTAGGACGTGAACAATTTATTGGGAAGCAAACTCTTTATATGCTGAGAAAGTACA 561

QY 2989 TTTAAAAAGATGACTACTTACGACGAGAGATGACAGTCTCTCTAAACGATGAATGTATGT 3048
Db 562 TTTAAAAAGATGACTACTTACGACGAGAGATGACAGTCTCTCTAAACGATGAATGTATGT 621

QY 3049 AGTGCTAGGACACTGAGTGTATATATGCTCCACACTACGCTCTGATAAACACAAAC 3108
Db 622 AGTGCTAGGACACTGAGTGTATATATGCTCCACACTACGCTCTGATAAACACAAAC 681

QY 3109 CTCAGTATTCACTTATTAGGCACACTAGTCTTTATACGCAACTACTGCTTACATAGTAGAC 3168
Db 682 CTCAGTATTCACTTATTAGGCACACTAGTCTTTATACGCAACTACTGCTTACATAGTAGAC 741

QY 3169 TGTGTTTGGCAATAATCTTTGAATTTGTTCTTTAAAGAACTGAGGTTTCAGAT 3223
Db 742 TGTGTTTGGTG-CAATAANTCTTTGAATTTGTTCTTT-AAAGAACTGAGGTTTAAAT 794

RESULT 5
LOCUS B1752112
DEFINITION B1752112 836 bp mRNA linear EST 25-SEP-2001
ACCESSION B1752112
VERSION B1752112.1 GI:15743690
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 836)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11482 row: 1 column: 16
High quality sequence stop: 822.

FEATURES
Location/Qualifiers
1..836
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5192991"
/lab_host="DH10B"
/clone_lib="NIH MGC 114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
```

range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."

```
ORIGIN
Query Match      19.2%; Score 640.2; DB 12; Length 836;
Best Local Similarity 96.8%; Pred. No. 1e-131;
Matches 693; Conservative 0; Mismatches 18; Indels 5; Gaps 4;
QY 2232 ACCAGCTGATCAAGCAGATCCCTGCAAGTTCCTGGCTGGGGGAAATTTGCCCAATGTGT 2291
DB 122 AACACCTGATCAAGCAGATCCCTGCAAGTTCCTGGCTGGGGGAAATTTGCCCAATGTGT 181
QY 2292 AAAGAACGACGAGCTGAGGAAGCGGAGTGTGGTGCAGAACCGAGATATGACAGCCAGGG 2351
DB 182 AAAGAACGACGAGCTGAGGAAGCGGAGTGTGCACTGCAAAACCGAGATATGACAGCCAGGG 241
QY 2352 GAGCTGGACGGTCTGGAACGAGGCTCTGTGGCCCTGGCACAAGGAATGCCAGGTCT 2411
DB 242 GAGCTGGACGGTCTGNAACGAGGCTCTGTGGCCCTGGCACAAGGAATGCCAGGTCT 301
QY 2412 CCAGGAAAGGAGCTCCATCCAGGTTCGCGATCATCTTGAAATCAAGCATACAAAAC 2471
DB 302 CCAGGAAAGGAGCTCCATCCAGGTTCGCGATCATCTTGAAATCAAGCATACAAAAC 361
QY 2472 TAGTGTAAAAAGTCCAAATCAACAAATCAACAGGTATCATGTAAGAAATTCGA 2531
DB 362 TAGTGTAAAAAGTCCAAATCAACAAATCAACAGGTATCATGTAAGAAATTCGA 421
QY 2532 ATTACTGACCGTAGAATATGAAGAAATTTAACCATCAAGATTGGGAAGAAATTAAGAACT 2591
DB 422 ATTACTGACCGTAGAATATGAAGAAATTTAACCATCAAGATTGGGAAGAAATTAAGAACT 481
QY 2592 GAAATGTACAAATATCATCTTAGCTATCTCAAGAGAGATGTTGCTCTTCAAGGAAA 2651
DB 482 GAAATGTACAAATATCATCTTAGCTATCTCAAGAGAGATGTTGCTCTTCAAGGAAA 541
QY 2652 ATGAGACAGGCATATTCATGGGTTCATCAAAATCCAGACATACAGTCAACACATGAGATC 2711
DB 542 ATGAGACAGGCATATTCATGGGTTCATCAAAATCCAGACATACAGTCAACACATGAGATC 601
QY 2712 AGCACAACCATATTTCAATATAGAGAGTCATGTCCTGGCAACAGATAATCTGAA 2771
DB 602 AGCACAACCATATTTCAATATAGAGAGTCATGTCCTGGCAACAGATAATCTGAA 661
QY 2772 -AAAAAGACACTTACTTATTTATTAACCCCAATGCAATCAGCGAAACATATTTTAC 2830
DB 662 GAACAAAGACACTTACTTATTTATTT--ACCAAAATGCAATCAGCGGAAACATATTTTAC 719
QY 2831 TATTTCTCGATGATAGTCAAAA--TGATCATAGCCAGGTTTGTTCACCTTCCCTGAAA 2889
DB 720 TATTTCTCGATGATAGTCAAAAATGATCATAGCCAGGTTTGTTCACCTTCCCTGAAA 779
QY 2890 ATTTTACTCACAGATCAATTCACACAGCATTA-GCTTACTTATTTGTTTGGGACTG 2944
DB 780 ATTTTACTCACAGATCAATTTGCAACAGCATAGGCTTACTTATTTGTTAAGGACTG 835
```

```
RESULT 6
BX510244
LOCUS      690 bp      mRNA      linear      EST 04-SEP-2003
DEFINITION DKFZp686P2496_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION  BX510244
VERSION     BX510244.1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 690)
AUTHORS   Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
```

Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.  
EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., et al.)  
Unpublished (2003)  
Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp686P2496) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERVANY; Email: clone@rzpd.de.  
Location/Qualifiers  
1..690  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686P2496"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlcc3)"  
/note="Vector: pTriplex2; Site\_1: SfiI; Site\_2: SfiI; cDNA-collection"

#### FEATURES

source

#### ORIGIN

```
Query Match      19.0%; Score 634; DB 13; Length 690;
Best Local Similarity 100.0%; Pred. No. 2.4e-130;
Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAAACCAAGAGGTTATCTCAATCATCTGTCATCATATATATATATATTTTTCACATTC 60
DB 57 TAAACCAAGAGGTTATCTCAATCATCTGTCATCATATATATATATATTTTTCACATTC 116
QY 61 TGTACTTTTTTAATGAGATTTGAGGTTTCTGTGATTTATCATAGATTTACCAATGCAC 120
DB 117 TGTACTTTTTTAATGAGATTTGAGGTTTCTGTGATTTATCATAGATTTACCAATGCAC 176
QY 121 AAAAGCCAGATGTATTTGGAACTAGAGAGCTATTTTGTGTTTTCGATTTTCTCCA 180
DB 177 AAAAGCCAGATGTATTTGGAACTAGAGAGCTATTTTGTGTTTTCGATTTTCTCCA 236
QY 181 AGTTCAGAGAACCAAGATATCTCCATTAACATATACCATTCTGAAACTAAAGACATAGA 240
DB 237 AGTTCAGAGAACCAAGATATCTCCATTAACATATACCATTCTGAAACTAAAGACATAGA 296
QY 241 CAATCCCCCAAGAAATGAAACAACTGAAAGTACTGAAAAAATGTACAAAATGTCAACTAT 300
DB 297 CAATCCCCCAAGAAATGAAACAACTGAAAGTACTGAAAAAATGTACAAAATGTCAACTAT 356
QY 301 GAGAGCATATTCGATTTGGCAAGCATCGAACAAAAAGATCCGATTTTCCCAACGGG 360
DB 357 GAGAGCATATTCGATTTGGCAAGCATCGAACAAAAAGATCCGATTTTCCCAACGGG 416
QY 361 GGTTAAAGTCTGTCCACAGGAATCCATGAACAGATTTTAGACAGCTTCTCAAGCTTATTA 420
DB 417 GGTTAAAGTCTGTCCACAGGAATCCATGAACAGATTTTAGACAGCTTCTCAAGCTTATTA 476
QY 421 TAGATTGAGAGTGTCTCAGGAGCAGTATGGAGCATATCGGATCTTCTTGGATCGCAT 480
DB 477 TAGATTGAGAGTGTCTCAGGAGCAGTATGGAGCATATCGGATCTTCTTGGATCGCAT 536
QY 481 CCTGTACACAGGGGAATATCAGGACTGGGTTCAGCATCTGCCAGCAGGAGACCTTCTGCT 540
DB 537 CCTGTACACAGGGGAATATCAGGACTGGGTTCAGCATCTGCCAGCAGGAGACCTTCTGCT 596
QY 541 CTTTGTGATTTGAAAAAATCTTCAGCAATCCAGAGGACCTTGGATCTTCTCCACAGAG 600
```

```

Db      597 CTTTGACATTGGRAAACTTCAGCAATTCAGGAGCAGCTGATCTTCTCCAGCAGAG 656
        601 AATPAAACAGAGAGTTTCCCTGACAGAAAGAT 634
        657 AATPAAACAGAGAGTTTCCCTGACAGAAAGAT 690

RESULT 7
BM695987
LOCUS      633 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-CL1-afa-m-11-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone
ACCESSION  BM695987
VERSION     BM695987.1 GI:19009245
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 633)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED    889548
COMMENT   Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
            Location/Qualifiers
                1..633
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="UI-E-CL1-afa-m-11-0-UI"
                    /tissue_type="human retina"
                    /dev_stage="adult"
                    /lab_host="PH10B (Life Technologies) (T1 phage resistant)"
                    /clone_lib="UI-E-CL1"
                    /note="Organ: eye; Vector: p773-Pac (Pharmacia) with a
                    modified polylinker; Site 1: EcoR I; Site 2: Not I;
                    UI-E-CL1 is a normalized cDNA library containing the
                    following tissue(s): retina. The library was constructed
                    according to Bonaldo, Lennon and Soares, Genome Research,
                    6:791-806, 1996. First strand cDNA synthesis was primed
                    with an oligo-dT primer containing a Not I site. Double
                    stranded cDNA was ligated to an EcoR I adaptor, digested
                    with Not I, and cloned directionally into p773-Pac
                    vector. The oligonucleotide used to prime the synthesis of
                    first-strand cDNA contains a library tag sequence that is
                    located between the Not I site and the (dT)18 tail. The
                    sequence tag for this library is CCGCG. This library was
                    created for the program, Gene Discovery in the Visual
                    System, supported by National Eye Institute (NEI)."
```

## ORIGIN

```

Query Match      18.9%; Score 628.8; DB 12; Length 633;
Best Local Similarity 99.5%; Pred. No. 3 5e-129;
Matches 630; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2529 TGAATTACTGACCGTAGATATGAGAAATTAAACATCAAGATTGGGAGGAAATTAATA 2589
        |||||

```

```

Db      1 TGAATTACTGACCGTAGATATGAGAAATTAAACATCAAGATTGGGAGGAAATTAATA 60
        2589 ACTGAAAATGTACAAATTATCACTTAGGCTATCTCAAGAGAGATGATTTGGCTTCTCAAGG 2648
        61 ACTGAAAATGTACAAATTATCACTTAGGCTATCTCAAGAGAGATGATTTGGCTTCTCAAGG 120
        2649 AAAATGGAGAGCAGGCATATTCAATGGGGTCATCAAAATCCAGACATACAGTCAACACTCAGA 2708
        121 AAAATGGAGAGCAGGCATATTCAATGGGGTCATCAAAATCCAGACATACAGTCAACACTCAGA 180
        2709 ATCAGCACACACCATATTTCAAAATATAGAAGTCAATGTTGGCAACACCAAGTAAATTCCT 2768
        181 ATCAGCACACACCATATTTCAAAATATAGAAGTCAATGTTGGCAACACCAAGTAAATTCCT 240
        2769 GAAAAAAGACACTTACTTATTATTAACCCCAATGCAATCAGCGAACAATATTTTT 2828
        241 GAAAAAAGACACTTACTTATTATTAACCCCAATGCAATCAGCGAACAATATTTTT 300
        2829 ACTATTCTTGGATGATAGTCAAAATGATCAATAAGCCAGGTTTGGCTTCCACCTTCCCTGAA 2888
        301 ACTATTCTTGGATGATAGTCAAAATGATCAATAAGCCAGGTTTGGCTTCCACCTTCCCTGAA 360
        2889 AATTTTACTCAGATCATTTTGAAACAGCATAGCTTACTTATTTAGGGACTGAACA 2948
        361 AATTTTACTCAGATCATTTTGAAACAGCATAGCTTACTTATTTAGGGACTGAACA 420
        2949 ATTTATTGGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGAGTCACTACTTAC 3008
        421 ATTTATTGGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGAGTCACTACTTAC 480
        3009 GCAGGGAGATGCGAGGCTCTCTAAACGATGATGATGATGATGATGATGATGATGATGATGATG 3068
        481 GCAGGGAGATGCGAGGCTCTCTAAACGATGATGATGATGATGATGATGATGATGATGATGATG 540
        3069 AGTGTATATATGCTCCACACTAGTCTGTGATAACACAAACCTCAGTATTCAGTTATTAGG 3128
        541 AGTGTATATATGCTCCACACTAGTCTGTGATAACACAAACCTCAGTATTCAGTTATTAGG 600
        3129 CACACTAGTTTATPACGCAACTACTGCTTACAT 3161
        601 CACACTAGTTTATATAGCAACTACTGCTTACAT 633

RESULT 8
BM695987
LOCUS      626 bp mRNA linear EST 15-JUL-2002
DEFINITION hd33d04.v1 Human Retina cDNA (Un-normalized, unamplified): hd/ne
ACCESSION  BM695987
VERSION     BM695987.1 GI:21763724
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 626)
AUTHORS   Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
            Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE     Expressed sequence tag analysis of human retina for the NEIBank
            Project: Retbindin, an abundant, novel retinal cDNA and alternative
            splicing of other retina-preferred gene transcripts
JOURNAL    Mol. Vis. 8 (4), 196-204 (2002)
MEDLINE    2103461
PUBMED     12107411
COMMENT    Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: Graeme@helix.nih.gov
            Plate: 33 row: d column: 04
            Seq primer: M13RP1 reverse primer (ABI).
```

FEATURES  
source

Location/Qualifiers  
1. .626  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="hd33d04"  
/tissue\_type="Retina"  
/dev\_stage="Adult"  
/lab\_hosts="EMDH10B"  
/clone\_lib="Human Retina cDNA (Un-normalized,  
unamplified): hd/he"  
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
Bioserve Biotechnology (Laurel MD) essentially following  
the protocols of the SuperScript Plasmid System full  
details of which are contained in the manufacturer's  
instruction manual (<http://www.lifetech.com/>). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-pGACTAGTTCTAGATCGAGCGCGCC(T)15-3']. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 18.8%; Score 626; DB 13; Length 626;  
Best Local Similarity 100.0%; Pred. No. 1.5e-128; Indels 0; Gaps 0;  
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 968 ACCAGGAGCTAGCAGGAAGTCCCACTTCAGATGCAAAAGATATTAAAGAACTTCCAG 1027  
DB 1 ACCAGGAGCTAGCAGGAAGTCCCACTTCAGATGCAAAAGATATTAAAGAACTTCCAG 60  
QY 1028 GATTCAAAATAATCATGTGTAGATTAGACCAAGAGAAAGATGGCTCAAGCT 1087  
DB 61 GATTCAAAATAATCATGTGTAGATTAGACCAAGAGAAAGATGGCTCAAGCT 120  
QY 1088 CCACAGAGATCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAAAGCCCTG 1147  
DB 121 CCACAGAGATCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAAAGCCCTG 180  
QY 1148 CAAGTGACCTCCTGTTTGAATTCACAAATGAAAGTGAAGAGTCTATCATGGAA 1207  
DB 181 CAAGTGACCTCCTGTTTGAATTCACAAATGAAAGTGAAGAGTCTATCATGGAA 240  
QY 1208 CCATGGAGGAGCAGCAACCAAGATCTATCTCAGAGCTACAGACTCAAAAGGCTGA 1267  
DB 241 CCATGGAGGAGCAGCAACCAAGATCTATCTCAGAGCTACAGACTCAAAAGGCTGA 300  
QY 1268 TCAGCAAGACCTAGAGGAAGCAATCTTTGGATGTGGGACAAATTCAGTTCACATGATG 1327  
DB 301 TCAGCAAGACCTAGAGGAAGCAATCTTTGGATGTGGGACAAATTCAGTTCACATGATG 360  
QY 1328 AAATTCCTGGATCACTGCGCCCTTGTGCTGACCCATCAGAGCTGCCACATCTT 1387  
DB 361 AAATTCCTGGATCACTGCGCCCTTGTGCTGACCCATCAGAGCTGCCACATCTT 420  
QY 1388 TTGCTGTTTATAACAGAGATGCTACTTTGAGTCCAGAACTTCTCTCTGTTGAACCCGACG 1447  
DB 421 TTGCTGTTTATAACAGAGATGCTACTTTGAGTCCAGAACTTCTCTCTGTTGAACCCGACG 480  
QY 1448 TTGAGACAGTGGACGGAGCAGAGATGGTCTACCTGACACTTTTGGTCTCCACCTGCTA 1507  
DB 481 TTGAGACAGTGGACGGAGCAGAGATGGTCTACCTGACACTTTTGGTCTCCACCTGCTA 540  
QY 1508 TGGCCTCTACCTCCCTGTGAGAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTC 1567  
DB 541 TGGCCTCTACCTCCCTGTGAGAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTC 600  
QY 1568 TGACTGATCAAGGCAACCAAGATCA 1593

Db

601 TGACTGATCAAGGCACCCACAGATACA 626  
RESULT 9  
BQ638902  
LOCUS  
DEFINITION  
hd29a06.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he  
Homo sapiens cDNA clone hd29a06 5', mRNA sequence.  
ACCESSION  
BQ638902  
VERSION  
BQ638902.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 622)  
AUTHORS  
Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,  
Touchman,J.W., Soufard,G., Smith,D. and Peterson,K.  
TITLE  
Expressed sequence tag analysis of human retina for the NEIBank  
Project: Retbindin, an abundant, novel retinal cDNA and alternative  
splicing of other retina-preferred gene transcripts  
JOURNAL  
Mol. Vis. 8 (4), 196-204 (2002)  
MEDLINE  
22103461  
PubMed  
12107411  
COMMENT  
Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 29 row: a column: 06  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1. .622  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="hd29a06"  
/tissue\_type="Retina"  
/dev\_stage="Adult"  
/lab\_hosts="EMDH10B"  
/clone\_lib="Human Retina cDNA (Un-normalized,  
unamplified): hd/he"  
/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
Bioserve Biotechnology (Laurel MD) essentially following  
the protocols of the SuperScript Plasmid System full  
details of which are contained in the manufacturer's  
instruction manual (<http://www.lifetech.com/>). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-pGACTAGTTCTAGATCGAGCGCGCC(T)15-3']. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."

FEATURES  
source

ORIGIN

Query Match 18.5%; Score 617.2; DB 13; Length 622;  
Best Local Similarity 99.5%; Pred. No. 1.3e-126;  
Matches 619; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2480 AAAAGTTCCTCAATCAACAAATACAGGTAATCAGTAAAGAAATCTCAATTACTGA 2539  
DB 1 AAAAGTTCCTCAATCAACAAATACAGGTAATCAGTAAAGAAATCTCAATTACTGA 60  
QY 2540 CGGTAGAATATGAAGAAATTTACCATCAAGATGGGAGGAAATTAATAAATCTGAATGT 2599  
DB 61 CGGTAGAATATGAAGAAATTTACCATCAAGATGGGAGGAAATTAATAAATCTGAATGT 120  
QY 2600 ACAATATCACTTAGGCTATCTCAAGAGATGATTTCCCTTCTCAAGGAAATGAGAC 2659



```
Db 121 ACAATTATCAATTAGGCTATCTCAGAGAGATGATTTGCCTTCTCAGGAAATGGAGAC 180
Qy 2660 AGGCATATTCATGGGTGATCAAAATCCAGACATACAGTCAACACTGAGATCAGACACA 2719
Db 181 AGGCATATTCATGGGTGATCAAAATCCAGACATACAGTCAACACTGAGATCAGACACA 240
Qy 2720 CCATATTTCAATATAGAGAGTCTATGTTGGCAACCACTAAATCTGAAAAAAGA 2779
Db 241 CCATATTTCAATATAGAGAGTCTATGTTGGCAACCACTAAATCTGAAAAAAGA 300
Qy 2780 CACTTACTTATTTAAACCCCAATCAATCAGCGAAACATATTTTACTATCTTGG 2839
Db 301 CACTTACTTATTTAAACCCCAATCAATCAGCGAAACATATTTTACTATCTTGG 360
Qy 2840 ATGATAGTCAAAATGATCATAGCCAGGTTTGCTTCCACCTTCCCTGAAATTTTACTCA 2899
Db 361 ATGATAGTCAAAATGATCATAGCCAGGTTTGCTTCCACCTTCCCTGAAATTTTACTCA 420
Qy 2900 CAGATCAATTTGCAACAGCATAGCTTACTTATTTGTTAGGCACTCAACAATTTATGGGA 2959
Db 421 CAGATCAATTTGCAACAGCATAGCTTACTTATTTGTTAGGCACTCAACAATTTATGGGA 480
Qy 2960 AGCAAACTCTTATATGCTAGAGATACATTTAAAGATGACTTACTACGCGGAGATG 3019
Db 481 AGCAAACTCTTATATGCTAGAGATACATTTAAAGATGACTTACTACGCGGAGATG 540
Qy 3020 CAGGTCTCTTAAACCGCATGATGTATGTAGTGTGTTAGGCACTGTAGTGTATATAT 3079
Db 541 CAGGTCTCTTAAACCGCATGATGTATGTAGTGTGTTAGGCACTGTAGTGTATATAT 600
Qy 3080 GCTCCACACTAGCTGTGATAAA 3101
Db 601 GCTCCACACTAGCTGTGATAAA 622

RESULT 10
BM685921 525 bp mRNA linear EST 27-FEB-2002
LOCUS UI-E-CKO-aas-h-07-0-UI.r1 UI-E-CKO Homo sapiens cDNA clone
DEFINITION UI-E-CKO-aas-h-07-0-UI 5', mRNA sequence.
ACCESSION BM685921
VERSION BM685921.1 GI:18995817
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLES Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1..653
/organism="Homo sapiens"
/mol_type="mRNA"
```

```
/db xref="taxon:9606"
/clone="UI-E-CKO-aas-h-07-0-UI"
/tissue_type="Retina Foveal and Macular"
/dev_stage="adult"
/lab_host="DH103 (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CKO"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-CKO is a cDNA library containing the following
tissue(s): Retina Foveal and Macular. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is GFFC.
This library was created for the program, Gene Discovery
in the Visual System, supported by National Eye Institute
(NEI)."
```

ORIGIN

Query Match 18.5%; Score 615.6; DB 12; Length 653;  
Best Local Similarity 99.4%; Pred. No. 3.1e-126;  
Matches 618; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2709 ATCAGCACACACATATTTCAATATAGAGAGTCTATGTTGGCAACCACTAAATCTT 2768  
Db 10 ACAGCACACACATATTTCAATATAGAGAGTCTATGTTGGCAACCACTAAATCTT 69

Qy 2769 GAAAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCGAAACATATTTT 2828  
Db 70 GAAGAAAAAGACACTTACTTATTTAAACCCCAATGCAATCAGCGAAACATATTTT 129

Qy 2829 ACTATTTCTGGATGATGCAAAATGATCAAGCCAGGTTTGCCTCCACCTTCCCTGAA 2888  
Db 130 ACTATTTCTGGATGATGCAAAATGATCAAGCCAGGTTTGCCTCCACCTTCCCTGAA 189

Qy 2889 AATTTTACTCACAGATCATTTTGCACCAAGCATAGCTTACTTATTTGTTAGGCACTGAACA 2948  
Db 190 AATTTTACTCACAGATCATTTTGCACCAAGCATAGCTTACTTATTTGTTAGGCACTGAACA 249

Qy 2949 ATTATTTGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGACTTACTTAC 3008  
Db 250 ATTATTTGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGACTTACTTAC 309

Qy 3009 GCAGGAGATGCAAGTCTCTCTAAACGATGATGATGATGATGATGATGATGATGATGATG 3068  
Db 310 GCAGGAGATGCAAGTCTCTCTAAACGATGATGATGATGATGATGATGATGATGATGATG 369

Qy 3069 AGTGTATATATGCTCCACACTAGCTCTGATAAACAACCAACCTCAGTATTTAGTATTAGG 3128  
Db 370 AGTGTATATATGCTCCACACTAGCTCTGATAAACAACCAACCTCAGTATTTAGTATTAGG 429

Qy 3129 CACACTAGTATTTATAGCGCAACTGCTTACATAGTACATGTTGTTGTTGTTGTTGTTGTTGTT 3188  
Db 430 CACACTAGTATTTATAGCGCAACTGCTTACATAGTACATGTTGTTGTTGTTGTTGTTGTTGTT 489

Qy 3189 TTGAATTTGTTCTTTAAAGAAACTGAGGTTTCAGATACACATACCATGGAATAATCTTACT 3248  
Db 490 TTGAATTTGTTCTTTAAAGAAACTGAGGTTTCAGATACACATACCATGGAATAATCTTACT 549

Qy 3249 TTTCTTGTACTACCAAAAGCTATTTTAAAGAGATGCTATGTTGGGAGAGCGGAGT 3308  
Db 550 TTTCTGTTTACTACCAAAAGCTATTTTAAAGAGATGCTATGTTGGGAGAGCGGAGT 609

Qy 3309 TGTACTATATGACATAATCAAT 3330  
Db 610 TGTACTATATGACATAATCAAT 631

```

RESULT 11
BM690735
LOCUS
DEFINITION
  UI-B-CK0-aav-c-12-0-UI.r1 UI-B-CK0 Homo sapiens cDNA clone
  UI-B-CK0-aav-c-12-0-UI 5', mRNA sequence.
ACCESSION
  BM690735
VERSION
  BM690735.1 GI:19003993
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 675)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
JOURNAL
  97044477
MEDLINE
  8889548
PUBMED
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: bento-soares@uiowa.edu
  Tissue Procurement: Dr. Gregg Hageman
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Researchers may obtain clones from Research
  Genetics (www.resgen.com).
  Seq primer: M13 Reverse.
FEATURES
    source
    location/Qualifiers
    1..675
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="UI-B-CK0-aav-c-12-0-UI"
    /tissue_type="Retina Foveal and Macular"
    /dev_stage="adult"
    /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
    /clone_lib="UI-B-CK0"
    /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
    modified polylinker; Site 1: EcoR I; Site 2: Not I;
    UI-B-CK0 is a cDNA library containing the following
    tissue(s): Retina Foveal and Macular. The library was
    constructed according to Bonaldo, Lennon and Soares,
    Genome Research, 6:791-806, 1996. First strand cDNA
    synthesis was primed with an oligo-dT primer containing a
    Not I site. Double stranded cDNA was ligated to an EcoR I
    adaptor, digested with Not I, and cloned directionally
    into pT7T3-Pac vector. The oligonucleotide used to prime
    the synthesis of first-strand cDNA contains a library tag
    sequence that is located between the Not I site and the
    (d)T18 tail. The sequence tag for this library is GTCC.
    This library was created for the program, Gene Discovery
    in the Visual System, supported by National Eye Institute
    (NEI)."
ORIGIN
  Query Match 17.7%; Score 589.4; DB 12; Length 675;
  Best Local Similarity 99.7%; Pred. No. 2.1e-120;
  Matches 601; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
  QY 2728 CAATATAGACAGTCATGCTCTGGCAACAGTAGTAATCTGAAAAAAGACACTTACT 2787
  DB 8 CAATATAGAGA-TCAATGCTCTGGCAACAGTAGTAATCTGAAAAAAGACACTTACT 66
  QY 2788 TATTATTAAACCCCAATGCAATCAGCGAAACATATTTTCTTCTTGATGATAGT 2847
  DB 67 TATTATTAAACCCCAATGCAATCAGCGAAACATATTTTCTTCTTGATGATAGT 126

```

```

QY 2848 CAAATGATCATAGCCAGGTTTGCTTCCACCTTCCCTGAAAAATTTTACTACAGATCAT 2907
DB 127 CAAATGATCATAGCCAGGTTTGCTTCCACCTTCCCTGAAAAATTTTACTACAGATCAT 186
QY 2908 TTGCAACAGCAGTAGCTTACTTATTGTTTGGGAGCTGAACAATTTATTGGGAAGCAACT 2967
DB 187 TTGCAACAGCAGTAGCTTACTTATTGTTTGGGAGCTGAACAATTTATTGGGAAGCAACT 246
QY 2968 CTTTATATGCTAGAAAGTACATTTAAAGATGACTTACGCGAGGAGATCGAGGTCTC 3027
DB 247 CTTTATATGCTAGAAAGTACATTTAAAGATGACTTACGCGAGGAGATCGAGGTCTC 306
QY 3028 TCTTAACGCGATGATGCTAGTGTAGTGCTAGGACACGTAGTGTATATATGCTCCACA 3087
DB 307 TCTTAACGCGATGATGCTAGTGTAGTGCTAGGACACGTAGTGTATATATGCTCCACA 366
QY 3088 CTACGCTCTGATAAACACAAACCTCAGTATTTCAGTTATTAGGCACACTAGTTTATACGCA 3147
DB 367 CTACGCTCTGATAAACACAAACCTCAGTATTTCAGTTATTAGGCACACTAGTTTATACGCA 426
QY 3148 ACTACTGCTTACATAGTAGACTGTTTGTGGCAATATCTTTGAATGTTCTTTTAAAG 3207
DB 427 ACTACTGCTTACATAGTAGACTGTTTGTGGCAATATCTTTGAATGTTCTTTTAAAG 486
QY 3208 AAATGAGGTTTCAGATACACATACCATGAAAAATCTTACTTTCTTGTACTACACAAA 3267
DB 487 AAATGAGGTTTCAGATACACATACCATGAAAAATCTTACTTTCTTGTACTACACAAA 546
QY 3268 GCTATTTTAAAGAGATGCTATGTTGGGAGAGGGCGAAGTTGTACTATATGACATATC 3327
DB 547 GCTATTTTAAAGAGATGCTATGTTGGGAGAGGGCGAAGTTGTACTATATGACATATC 606
QY 3328 AAT 3330
DB 607 AAT 609

```

```

RESULT 12
BM636596
LOCUS
DEFINITION
  hd11h02.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
  Homo sapiens cDNA clone hd11h02 5', mRNA sequence.
ACCESSION
  BM636596
VERSION
  BM636596.1 GI:21761055
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 598)
  Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
  Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
  Expressed sequence tag analysis of human retina for the NEIBank
  Project: Retbindin, an abundant, novel retinal cDNA and alternative
  splicing of other retina-preferred gene transcripts
  Mol. Vis. 8 (4), 196-204 (2002)
JOURNAL
  22103461
MEDLINE
  12107411
PUBMED
  Contact: Wistow G
  Section on Molecular Structure and Function
  National Eye Institute
  6/331 NIH Bethesda, MD 20892-2740, USA
  Tel: 301 402 3452
  Fax: 301 496 0078
  Email: graeme@helix.nih.gov
  Plate: 11 row: h column: 02
  Seq primer: M13RPI reverse primer (ABI).
FEATURES
    source
    location/Qualifiers
    1..598
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="hd11h02"

```



/tissue\_type="Retina"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retina cDNA (Un-normalized,  
unamplified): hd/he"  
/notes="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
was dissected from two 80 year old donors with no observed  
eye disease. 100ug of total RNA was used for library  
construction. A directionally cloned cDNA library in the  
pSPORT1 vector (Life Technologies) was constructed at  
Bioserve Biotechnology (Laurel MD) essentially following  
the protocols of the SuperScript Plasmid System full  
details of which are contained in the manufacturer's  
instruction manual (http://www.lifetech.com/). First  
strand synthesis was carried out using a Not I  
primer-adaptor  
[5'-pACAGTCTAGTACGAGCGCGCC(T)15-3']. EST analysis  
was performed on the unamplified library at the NIH  
Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 17.3%; Score 577.6; DB 13; Length 598;  
Best Local Similarity 99.3%; Pred. No. 8.9e-118;  
Matches 580; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
1490 CTGTGGTCTCCACCTGCTATGGCTCTACCTCCCTGTCAGAGCTCCACCTTTCTTTATGG 1549  
15 CTGTGGTCTCCACCTGCTATGGCTCTACCTCCCTGTCAGAGCTCCACCTTTCTTTATGG 74  
1550 CATCAAGCATCTTCTCTCTGATCTGATCAAGGACCAAGATGATGATGATGATGATGATG 1609  
75 CATCAAGCATCTTCTCTCTGATCTGATCAAGGACCAAGATGATGATGATGATGATGATG 134  
1610 CAATGTCTAGTACAGGCGGCACCATCCACCATGATGATGATGATGATGATGATGATGATG 1669  
135 CAATGTCTAGTACAGGCGGCACCATCCACCATGATGATGATGATGATGATGATGATGATG 194  
1670 CTCTGGGAATTTTCCATCCACCTGCTATCTTCAGATGACAGCGCATCAAGTGCAGTGGCG 1729  
195 CTCTGGGAATTTTCCATCCACCTGCTATCTTCAGATGACAGCGCATCAAGTGCAGTGGCG 254  
1730 AGATATGTCAGACACCTAGATGAATGATGATGATGATGATGATGATGATGATGATGATG 1789  
255 AGATATGTCAGACACCTAGATGAATGATGATGATGATGATGATGATGATGATGATGATG 314  
1790 TACAGAGCTTCAGCAATATGTTTCTGTCCTCCAGATCATTTCTTGGAGGATACCATCTCTG 1849  
315 TACAGAGCTTCAGCAATATGTTTCTGTCCTCCAGATCATTTCTTGGAGGATACCATCTCTG 374  
1850 TCTCAGCTTACAGTATATACCACTAGTCTTATGACATGATGATGATGATGATGATGATGATG 1909  
375 TCTCAGCTTACAGTATATACCACTAGTCTTATGACATGATGATGATGATGATGATGATGATG 434  
1910 TGTGTAGTCTTCTCAGTCTGCGTGTGCTAAAGATGCTTCTCCACGACCTGTTCAACA 1969  
435 TGTGTAGTCTTCTCAGTCTGCGTGTGCTAAAGATGCTTCTCCACGACCTGTTCAACA 494  
1970 AGAGCTCTCTGGAGTACCGAGCTCTGGAGCAAAATTCACAGCTGCTGGTTCATATC 2029  
495 AGAGCTCTCTGGAGTACCGAGCTCTGGAGCAAAATTCACAGCTGCTGGTTCATATC 554  
2030 TAGATCCCAATCTTACAGATTTTAAAGCACTTGAATCTTAAC 2073  
555 TAGATCCCAATCTTACAGATTTTAAAGCACTTGAATCTTAAC 598

RESULT 13

CA393958  
LOCUS CA393958 508 bp mRNA linear EST 06-NOV-2002  
DEFINITION cs44904.y1 Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs44904  
5', mRNA sequence.  
ACCESSION CA393958

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CA393958.1 GI:24728064  
EST. Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 508)  
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
TITLE Expressed sequence tag analysis of human RPE/choroid for the  
NEIBank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
JOURNAL Mol. Vis. 8 (4), 205-220 (2002)  
MEDLINE 22103460  
PUBMED 12107410  
COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 44 row: 9 column: 04  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
1. 508  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="cs44904"  
/tissue\_type="RPE/choroid"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"  
/notes="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the SuperScript  
Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>: The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

FEATURES  
source

1. 508  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="cs44904"  
/tissue\_type="RPE/choroid"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"  
/notes="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the SuperScript  
Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>: The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 15.0%; Score 498.4; DB 14; Length 508;  
Best Local Similarity 98.8%; Pred. No. 3.9e-100;  
Matches 502; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1442 CCCAGCTTGAGACAGTGGAGGACGAGCATGTCTTACCTGACACATCTTGTGCTCCAC 1501  
Db 1 CCCAGCTTGAGACAGTGGAGGACGAGCATGTCTTACCTGACATCTTGTGCTCCAC 60  
QY 1502 CTGCTATGGCTCTTACCTCCCTGTGAGAAGCTCCACTTTCTTTATGGCATCAAGCATCT 1561  
Db 61 CTGCTATGGCTCTTACCTCCCTGTGAGAAGCTCCACTTTCTTTATGGCATCAAGCATCT 120  
QY 1562 TCTCTCTGACTGATCAAGGACCAACAGATCAATGGCCACTGACCAAGCATGCTAGTAC 1621  
Db 121 TCTCTCTGACTGATCAAGGACCAACAGATCAATGGCCACTGACCAAGCATGCTAGTAC 180  
QY 1622 CAGGGCTCACCATCCCCACCAAGTGATTTATCTGCAATTCAGCCAACTGGCTCTGGGAATTT 1681  
Db 181 CAGGGCTCACCATCCCCACCAAGTGATTTATCTGCAATTCAGCCAACTGGCTCTGGGAATTT 240  
QY 1682 CACATCCACTGTGATCTTTCAGATGACAGCCGATCAAGTGCAGTGGCAGAGATATGCTCA 1741  
Db 241 CACATCCACTGTGATCTTTCAGATGACAGCCGATCAAGTGCAGTGGCAGAGATATGCTCA 300

QY 1742 GACACCTAGATGAATGATCTGTCTGACACTCTCTGCCCATCTGAGGTACAGAGCTCA 1801  
 Db 301 GACACCTAGATGAATGATCTGTCTGACACTCTCTGCCCATCTGAGGTACAGAGCTCA 360  
 QY 1802 GCGAATATGTTCTGCTGCCAGATCATTTCTTGAGAGATACCACTCTCTGCTAGCTTTAC 1861  
 Db 361 TCGAATATGTTCTGCTGCCAGATCATTTCTTGAGAGATACCACTCTCTGCTAGCTTTAC 420  
 QY 1862 AGTATATCACCACCTAGTTCTTATGACCATTCGCCCAAGGCCGAGAGCTGGTAGTGTCT 1921  
 Db 421 AGTATATCACCACCTAGTTCTTATGACCATTCGCCCAAGGCCGAGAGCTGGTAGTGTCT 480  
 QY 1922 TCAGTCTGCTGTTGCTTAACATGCGCTT 1949  
 Db 481 TCAGTCTGCTGATGCTTAACATGCGCTT 508  
  
 RESULT 14  
 BX097138 472 bp mRNA linear EST 04-FEB-2003  
 LOCUS BX097138 Soares retina N2b4HR Homo sapiens cDNA clone  
 DEFINITION IMAGp998N11359 ; IMAGE:190666, mRNA sequence.  
 ACCESSION BX097138  
 VERSION  
 KEYWORDS  
 SOURCE EST. GI:27843098  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 472)  
 AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
 Radelof,U., Schneider,D. and Korn,B.  
 TITLE Human UniGeneSet - RZPD3  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGp998N11359.  
 Human UniGeneSet - RZPD3 (RZPDLB No.972)  
 http://www.rzpd.de/Cloncards/cgi-bin/showlib.pl.cgi/?response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, Primer sequence: TTTCACACAGGAACACGATGATGAC.  
 Location/Qualifiers  
 1..472  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGp998N11359 ; IMAGE:190666"  
 /sex="male"  
 /tissue\_type="retina"  
 /dev\_stage="55 year old"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares retina N2b4HR"  
 /note="Organ: eye; Vector: pRT73D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5',  
 TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pRT73 vector  
 (Pharmacia). The retinas were obtained from a 55 year old  
 Caucasian and total cellular poly(A)+ RNA was extracted 6  
 hrs after their removal. The retina RNA was kindly  
 provided by Roderick R. McInnes M.D. Ph.D. from the

University of Toronto. Library constructed by Bento  
 Soares and M.Fatima Bonaldo. "

ORIGIN  
 Query Match 14.2%; Score 472; DB 13; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-94;  
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1307 GGACAAATCAGTTCAGTGAATTTGCTGATCACTGCGAGCCTTTGGTCTGACACCC 1366  
 Db 1 GGACAAATCAGTTCAGTGAATTTGCTGATCACTGCGAGCCTTTGGTCTGACACCC 60  
 QY 1367 AATCAGAGCTGCCACATCTTTGCTGTTAATACAGAGGATGCTTACTTTGAGTCCAGAAC 1426  
 Db 61 AATCAGAGCTGCCACATCTTTGCTGTTAATACAGAGGATGCTTACTTTGAGTCCAGAAC 120  
 QY 1427 TTCTTCTCTGTTGAACCCCAAGCTTCAGACAGTGGAGCGAGAGCATGGTCTACCTGACA 1486  
 Db 121 TTCTTCTCTGTTGAACCCCAAGCTTCAGACAGTGGAGCGAGAGCATGGTCTACCTGACA 180  
 QY 1487 CTCTTTGGTCTCCACCTGCTATGGCTCTACCTCCCTGTCAAGAGCTCCACCTTTCTTTA 1546  
 Db 191 CTCTTTGGTCTCCACCTGCTATGGCTCTACCTCCCTGTCAAGAGCTCCACCTTTCTTTA 240  
 QY 1547 TGGCATCAAGCATCTTCTCTGATCAAGGACCCACAGATACAAATGGCCACTGACC 1606  
 Db 241 TGGCATCAAGCATCTTCTCTGATCAAGGACCCACAGATACAAATGGCCACTGACC 300  
 QY 1607 AGACATGCTAGTACAGGGCTCAACCTCCCAAGAGTATTCTTGCATCAGGCCAAC 1666  
 Db 301 AGACATGCTAGTACAGGGCTCAACCTCCCAAGAGTATTCTTGCATCAGGCCAAC 360  
 QY 1667 TGGCTCTGGGAATTTACATCCACTGCTCATCTTCAGATGACAGCCGATCAAGTGCAGGTG 1726  
 Db 361 TGGCTCTGGGAATTTACATCCACTGCTCATCTTCAGATGACAGCCGATCAAGTGCAGGTG 420  
 QY 1727 GCGAAGATATGTCAGACACCTAGATGAATGGATCTGCTGACACCTCTGCTGC 1778  
 Db 421 GCGAAGATATGTCAGACACCTAGATGAATGGATCTGCTGACACCTCTGCTGC 472

RESULT 15  
 W26960/c  
 LOCUS  
 DEFINITION 16x10 Human retina cDNA randomly primed sublibrary Homo sapiens  
 cDNA, mRNA sequence.  
 ACCESSION W26960  
 VERSION W26960.1 GI:1306188  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 561)  
 AUTHORS Macke,J., Smallwood,P. and Nathans,J.  
 JOURNAL Adult Human Retina cDNA  
 COMMENT Unpublished (1996)  
 Contact: Dr. Jeremy Nathans  
 Johns Hopkins School of Medicine  
 725 North Wolfe Street, Baltimore, MD 21205  
 Tel: 410 955 4678  
 Fax: 410 614 0827  
 Email: jeremy.nathans@gmail.bs.jhu.edu  
 Clones from this library are NOT available.  
 PCR Primers  
 FORWARD: CTTTGTAGCAAGTTCAGCTCGTTAAGT  
 BACKWARD: GAGTGGCTTATGATGATTTCTTCCAGGGTAA  
 Seq primer: GGGTAAAGCAAAAGAAATT.  
 Location/Qualifiers  
 1..561  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

FEATURES  
 source

```
/db_xref="taxon:9606"  
/sex="mixed (males and females)"  
/tissue_type="retina"  
/dev_stage="adult"  
/lab_host="E. coli strain K802"  
/clone_lib="Human retina cDNA randomly primed sublibrary"  
/note="Organ: eye; Vector: lambda gt10, site 1: EcoRI;  
Site 2: EcoRI; The library used for sequencing was a  
sublibrary derived from a human retina cDNA library.  
Inserts from retina cDNA library DNA were isolated,  
randomly primed, PCR amplified, size-selected, and cloned  
into lambda gt10. Individual plaques were arrayed and  
used as templates for PCR amplification, and these PCR  
products were used for sequencing."
```

ORIGIN

```
Query Match      13.8%; Score 459.6; DB 14; Length 561;  
Best Local Similarity 93.4%; Pred. NO. 1.7e-91;  
Matches 493; Conservative 0; Mismatches 33; Indels 2; Gaps 2;  
  
QY 1223 AGCAACCCAGAAATCTATCTCAGAGCTACAGACTCAGAGGCTGATCAGCAAGCACTAG 1282  
Db      |||||  
532  ANCCAACTTGAATCTACNCAGANGNAAAG-CCTCCAGAGGCTGATCANCNAGCACTAG 474  
      |||||  
QY 1283 AGGAGAACAAATCTTTGGATGTGGGACAAATTCAGTTCAGTTCAGTGAATTTGCTGATCAC 1342  
Db      |||||  
473  GGGAGACCAATCTTTGGATGTGGGACAAATTCAGTTCAGTTCAGTGAATTTGCTGATCAC 414  
      |||||  
QY 1343 TGCAGCCTTTGGTCTGTGACACCAATCAGAGCTGCCCAATCTTTTGTGTTATAACAG 1402  
Db      |||||  
413  TGCAGCCTTTGGTCTGTGACACCAATCAGAGCTGCCCAATCTTTTGTGTTATAACAG 354  
      |||||  
QY 1403 AGGATGCTACTTTGAGTCCAGAACTTCCTCCTGTTGAACCCAGCTTGAGACAGTGGACG 1462  
Db      |||||  
353  AGGATGCTACTTTGAGTCCAGAACTTCCTCCTGTTGAACCCAGCTTGAGACAGTGGACG 294  
      |||||  
QY 1463 GAGCAGAGCATGGTCTTACTGACACTTTTGTCTCTCCACCTGCTATGSCCTTACCTCCC 1522  
Db      |||||  
293  GAGCAGAGCATGGTCTTACTGACACTTTTGTCTCTCCACCTGCTATGSCCTTACCTCCC 234  
      |||||  
QY 1523 TGTGAGAGCTCCACTTTTGTGATCAAGCATCTTCTCTGACTGATCAAGGCA 1582  
Db      |||||  
233  TGTGAGAGCTCCACTTTTGTGATCAAGCATCTTCTCTGACTGATCAAGGCA 174  
      |||||  
QY 1583 CCACAGATACAATGGCCACTGACAGACAAATCTAGTACCAGGGCTCACCATCCCCACCA 1642  
Db      |||||  
173  CCACAGANACATGGCCACTGACAGACAAATCTAGTACCAGGGCTCACCATCCCCACCA 114  
      |||||  
QY 1643 GTGATTATTTCTGATCAGCAACTGGCTCTGGGAATTTACATCCACTGCACTTCAG 1702  
Db      |||||  
113  GTGATTATTTCTGATCAGCAACTGGCTCTGGGAATTTACATCCACTGCACTTCAG 54  
      |||||  
QY 1703 ATGACAGCGGATCAAGTG-CAGGTGGCGAAGATATGGTCAGACCTA 1749  
Db      |||||  
53  ATGACAGNCGATCAAGTGAGAGGTGGCGAATAAATGGCGNGNCCANA 6
```

Search completed: March 1, 2004, 20:29:00  
Job time : 8160 secs



QY 121 AAAAGCCAGATGTAATTTGGAACTAGAGAGCTAATTTTTGTTTTTTGGATTTTTCTCCA 180  
DB 121 AAAAGCCAGATGTAATTTGGAACTAGAGAGCTAATTTTTGTTTTTTGGATTTTTCTCCA 180  
QY 181 AGTTCAAGAAACCAAGATATCTCCATTAACATATACATTTCTGAAACTAAAGACATAGA 240  
DB 181 AGTTCAAGAAACCAAGATATCTCCATTAACATATACATTTCTGAACTAAAGACATAGA 240  
QY 241 CAATCCCCCAAGAAATGAACAACTGAAAGTAATGAAAGAAATGTAAGAAATGCAACTAT 300  
DB 241 CAATCCCCCAAGAAATGAACAACTGAAAGTAATGAAAGAAATGTAAGAAATGCAACTAT 300  
QY 301 GAGACGAATATTCGATTTGGCAAGACATCGAAACAAAGATGCGCATTTTTCCCAACGGG 360  
DB 301 GAGACGAATATTCGATTTGGCAAGACATCGAAACAAAGATGCGCATTTTTCCCAACGGG 360  
QY 361 GGTAAAGTCTGTCCACAGGAATCCATGAACACAGATTTTAGACAGTCTTCAAGCTTATTA 420  
DB 361 GGTAAAGTCTGTCCACAGGAATCCATGAACACAGATTTTAGACAGTCTTCAAGCTTATTA 420  
QY 421 TAGATTGAGAGTGTCTAGGAAGCAGTATGGGAAGCATATCGGATCTTTCTGGATCGCAT 480  
DB 421 TAGATTGAGAGTGTCTAGGAAGCAGTATGGGAAGCATATCGGATCTTTCTGGATCGCAT 480  
QY 481 CCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAGGAGACCTTTGCGCT 540  
DB 481 CCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAGGAGACCTTTGCGCT 540  
QY 541 CTTTGAATTTGGAAGAACTTCAGCAATCCAGAGGACCTGGATCTTCCAGAGAG 600  
DB 541 CTTTGAATTTGGAAGAACTTCAGCAATCCAGAGGACCTGGATCTTCCAGAGAG 600  
QY 601 AATAAACAAGAGAGTTTCCCTGACAGAAAGATGAAATATCTCCAGAGAGACATTTGGG 660  
DB 601 AATAAACAAGAGAGTTTCCCTGACAGAAAGATGAAATATCTCCAGAGAGACATTTGGG 660  
QY 661 AGAGCCTGGTGAACCAATTTGCAATTTCAAGCAATCTACATTTCAAGAACTTTGGGCACT 720  
DB 661 AGAGCCTGGTGAACCAATTTGCAATTTCAAGCAATCTACATTTCAAGAACTTTGGGCACT 720  
QY 721 ATTCTAAGAAACCTCTAGAGAGCAATTTCAAGATGTTGCCACGTCCTCAGTTGGGCT 780  
DB 721 ATTCTAAGAAACCTCTAGAGAGCAATTTCAAGATGTTGCCACGTCCTCAGTTGGGCT 780  
QY 781 TTCCCTCTCACTCTCTGATGACACCTCTCAATGAAATTTCTCGATAATACACTCAACGAC 840  
DB 781 TTCCCTCTCACTCTCTGATGACACCTCTCAATGAAATTTCTCGATAATACACTCAACGAC 840  
QY 841 ACCAAGATGCTTACAGAAAGAGAAACAGAAATTCGCTGTTGGAGGAGCAGAGGGTG 900  
DB 841 ACCAAGATGCTTACAGAAAGAGAAACAGAAATTCGCTGTTGGAGGAGCAGAGGGTG 900  
QY 901 GAGCTCAGCGTCTCTCTGTTAAACAGAAAGTTCAAGGACAGCTCGCTGACTCCAGTCC 960  
DB 901 GAGCTCAGCGTCTCTCTGTTAAACAGAAAGTTCAAGGACAGCTCGCTGACTCCAGTCC 960  
QY 961 CCATATTTCCAGGAGCTAGCAGGAAAGTCCAACTTCAGATGCAAAAGATTTAAGAAA 1020  
DB 961 CCATATTTCCAGGAGCTAGCAGGAAAGTCCAACTTCAGATGCAAAAGATTTAAGAAA 1020  
QY 1021 CTTCCAGGATTCAAAAAATCCATGTTTAGATTTAGACCAAGAAAGAAAGATGGC 1080  
DB 1021 CTTCCAGGATTCAAAAAATCCATGTTTAGATTTAGACCAAGAAAGAAAGATGGC 1080  
QY 1081 TCAAGCTCCACAGAGATCAACTACGCGCATCTTTAAGACACAGTGCAGAGCAAAA 1140  
DB 1081 TCAAGCTCCACAGAGATCAACTACGCGCATCTTTAAGACACAGTGCAGAGCAAAA 1140  
QY 1141 AGCCCTGCAAGTACCTCTCTTTGATTTCCAAAGAAATTTGAAGTGAAGAGTCTAT 1200  
DB 1141 AGCCCTGCAAGTACCTCTCTTTGATTTCCAAAGAAATTTGAAGTGAAGAGTCTAT 1200  
QY 1201 CATGGAACCATGGAGGAGCAAGCAACAGAAATCTATCTCACAGCTTACAGACCTCAA 1260

DB 1201 CATGGAACCATGGAGGAGCAAGCAACAGAAATCTATCTCACAGCTTACAGACTCAA 1260  
QY 1261 AGGCTGATCAGCAAGCACTAGAGAGAAACAATCTTTGGATGTGGGACAATTCAGTTC 1320  
DB 1261 AGGCTGATCAGCAAGCACTAGAGAGAAACAATCTTTGGATGTGGGACAATTCAGTTC 1320  
QY 1321 ACTGATGAAATGCTGGATCACTGCCAGCTTTGGTCTGACACCCCAATCAGAGCTGCC 1380  
DB 1321 ACTGATGAAATGCTGGATCACTGCCAGCTTTGGTCTGACACCCCAATCAGAGCTGCC 1380  
QY 1381 ACATCTTTTGTGTTTATAACAGAGATCTACTTTTGTAGTCCAGAACTTCTCTCTGTGAA 1440  
DB 1381 ACATCTTTTGTGTTTATAACAGAGATCTACTTTTGTAGTCCAGAACTTCTCTCTGTGAA 1440  
QY 1441 CCCAGCTTTGAGACAGTGGACGGACAGAGATGGTCTTACCTGACACTTCTTGGTCTCCA 1500  
DB 1441 CCCAGCTTTGAGACAGTGGACGGACAGAGATGGTCTTACCTGACACTTCTTGGTCTCCA 1500  
QY 1501 CTTGCTATGGCTCTTACCTCTGTCAGAAAGCTCCACCTTTCTTATGGCATCAAGCATC 1560  
DB 1501 CTTGCTATGGCTCTTACCTCTGTCAGAAAGCTCCACCTTTCTTATGGCATCAAGCATC 1560  
QY 1561 TTCTCTCTGATGATCAAGGACCAAGATCAATCAATGAGCTTCTGACAGCAATTCGTAGTA 1620  
DB 1561 TTCTCTCTGATGATCAAGGACCAAGATCAATCAATGAGCTTCTGACAGCAATTCGTAGTA 1620  
QY 1621 CCAGGCTCACCATCCCAAGGATGATTTCTGCAATCAGCAACTGGCTCTGGGAAT 1680  
DB 1621 CCAGGCTCACCATCCCAAGGATGATTTCTGCAATCAGCAACTGGCTCTGGGAAT 1680  
QY 1681 TCACATCCACTGATCTTTCAGATGACAGCGCATCAAGTGCAGTGGGGAAGATGTC 1740  
DB 1681 TCACATCCACTGATCTTTCAGATGACAGCGCATCAAGTGCAGTGGGGAAGATGTC 1740  
QY 1741 AGACACCTAGATGAATGGATCTGTCACACTCTCTGCCCATCTGAGGTACCAAGCTC 1800  
DB 1741 AGACACCTAGATGAATGGATCTGTCACACTCTCTGCCCATCTGAGGTACCAAGCTC 1800  
QY 1801 AGGAAATGTTTCTGCTCCAGATCATTTCTTGGAGGATACCACTCTCTCAGCTTTA 1860  
DB 1801 AGGAAATGTTTCTGCTCCAGATCATTTCTTGGAGGATACCACTCTCTCAGCTTTA 1860  
QY 1861 CAGTATATCACAATGTTTCTATGACCAATGCCCCCAAGGGCCGAGAGCTGTGTGTC 1920  
DB 1861 CAGTATATCACAATGTTTCTATGACCAATGCCCCCAAGGGCCGAGAGCTGTGTGTC 1920  
QY 1921 TTTCACTGCTGTTGCTTAAACATGCTTCTCCACGACCTGTTCAAACAGAGCTCTCTG 1980  
DB 1921 TTTCACTGCTGTTGCTTAAACATGCTTCTCCACGACCTGTTCAAACAGAGCTCTCTG 1980  
QY 1981 GAGTACCGAGCTCTGGAGCAAAATTCACAGCTGCTGGTTCATATCTACGATCCAAAT 2040  
DB 1981 GAGTACCGAGCTCTGGAGCAAAATTCACAGCTGCTGGTTCATATCTACGATCCAAAT 2040  
QY 2041 CTTACAGGATTTAAGCACTTGAATTAATTTAACTTACAGAAACGGAGTGTGTGTGAT 2100  
DB 2041 CTTACAGGATTTAAGCACTTGAATTAATTTAACTTACAGAAACGGAGTGTGTGTGAT 2100  
QY 2101 AGCAAAATGAAGTTTGTAAAGTCTCTGCGGTATAA CCTCACAAGCTGTGTGACGGGTC 2160  
DB 2101 AGCAAAATGAAGTTTGTAAAGTCTCTGCGGTATAA CCTCACAAGCTGTGTGACGGGTC 2160  
QY 2161 TTTGAGGATTTTCTGCTGACGCCCAACACTCTGGAATAGACAGCTACTCT 2220  
DB 2161 TTTGAGGATTTTCTGCTGACGCCCAACACTCTGGAATAGACAGCTACTCT 2220  
QY 2221 CTCACATTTGAACACAGCTGATCAACAGATCCCTCAAGTTCTCTGGCTGGCGGAATTT 2280  
DB 2221 CTCACATTTGAACACAGCTGATCAACAGATCCCTCAAGTTCTCTGGCTGGCGGAATTT 2280  
QY 2281 GGCCTATGTTTAAAGAACGAGCTGAGGAGCGGAGTGTGCTGCTCAACACAGGATAT 2340





Db 598 AATATAACAGAGAAAGTTTCCCTGACAGAAAGATGAATAATCTGCAGAGAGACATTGGG 657  
Qy 661 AGAGCCTGGTGAACCAATTTGTCATTTCAACAGCAATCTACATTTCAAAAGACTTGGGCAGT 720  
Db 658 AGAGCCTGGTGAACCAATTTGTCATTTCAAC----- 687  
Qy 721 ATTCTAAGAAAAACCTCTAGAGAGCAAAATTCAGATGTTGCCAAGCTCTCAGTTGGGCCT 780  
Db 688 -----AGATGTTGCCAAGCTCTCAGTTGGGCCT 715  
Qy 781 TTCCCTCTCACTCCTGATGACACCTCTCCTCAATGAATTTCTCGATAATAACATCAACGAC 840  
Db 716 TTCCCTCTCACTCCTGATGACACCTCTCCTCAATGAATTTCTCGATAATAACATCAACGAC 775  
Qy 841 ACCAAGATGCTTACAACAGAAAGAGAAACAGAAATTCGCTGTTGGAGAGACAGAGGTTG 900  
Db 776 ACCAAGATGCTTACAACAGAAAGAGAAACAGAAATTCGCTGTTGGAGAGACAGAGGTTG 835  
Qy 901 GAGCTCAGCGTCTCTCTGGTAAACACAGAGTTCAAGGACAGAGCTCGCTGACTCCAGTCC 960  
Db 836 GAGCTCAGCGTCTCTCTGGTAAACACAGAGTTCAAGGACAGAGCTCGCTGACTCCAGTCC 895  
Qy 961 CCATATTACAGAGGCTAGCAGSAAAGTCCAACTTCAGATGCAAAAGATATTTAAGAAA 1020  
Db 896 CCATATTACAGAGGCTAGCAGSAAAGTCCAACTTCAGATGCAAAAGATATTTAAGAAA 955  
Qy 1021 CTTCCAGGATTCAAAAAATCCATGCTGTAGGATTTAGCCAAAGAAAGATGGC 1080  
Db 956 CTTCCAGGATTCAAAAAATCCATGCTGTAGGATTTAGCCAAAGAAAGATGGC 1015  
Qy 1081 TCAAGCTCCAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTCGAGAGCAAAA 1140  
Db 1016 TCAAGCTCCAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTCGAGAGCAAAA 1075  
Qy 1141 AGCCCTGCAAGTGACCTCCTGCTTTTGAATTCACAAATTTGAAAGTGAGGAGTCTAT 1200  
Db 1076 AGCCCTGCAAGTGACCTCCTGCTTTTGAATTCACAAATTTGAAAGTGAGGAGTCTAT 1135  
Qy 1201 CATGGAACCATGGAGGAGCAAGCAACAGAAATCTATCTCAGCTCAGACCTCAA 1260  
Db 1136 CATGGAACCATGGAGGAGCAAGCAACAGAAATCTATCTCAGCTCAGACCTCAA 1195  
Qy 1261 AGGCTGATCAGAAAGCTATAGAGAGAGAAACAATCTTTGATGTGGGAGCAATTCAGTTC 1320  
Db 1196 AGGCTGATCAGAAAGCTATAGAGAGAGAAACAATCTTTGATGTGGGAGCAATTCAGTTC 1255  
Qy 1321 ACTGATGAATTTGCTGGATCTCCAGCCTTTGGTCTGACACCCCAATCAGAGCTGCC 1380  
Db 1256 ACTGATGAATTTGCTGGATCTCCAGCCTTTGGTCTGACACCCCAATCAGAGCTGCC 1315  
Qy 1381 ACATCTTTTGCTTTATACAGAGGATGCTACTTTGAGTCCAGAACTTCCTCTGTTGAA 1440  
Db 1316 ACATCTTTTGCTTTATACAGAGGATGCTACTTTGAGTCCAGAACTTCCTCTGTTGAA 1375  
Qy 1441 CCCAGCTTGACAGAGTGAGCGGACAGAGATGGTCTACTGACACTTCTTGCTCTCCA 1500  
Db 1376 CCCAGCTTGACAGAGTGAGCGGACAGAGATGGTCTACTGACACTTCTTGCTCTCCA 1435  
Qy 1501 COTGCTATGGCTCTACCTCCTCTGTCAGAGCTCCACTTTCTTTATGGCATCAAGCATC 1560  
Db 1436 COTGCTATGGCTCTACCTCCTCTGTCAGAGCTCCACTTTCTTTATGGCATCAAGCATC 1495  
Qy 1561 TTCTCTGATGATCAAGGACCAACAGATACAATGGCCACTGACCCAGACAAATGCTAGTA 1620  
Db 1496 TTCTCTGATGATCAAGGACCAACAGATACAATGGCCACTGACCCAGACAAATGCTAGTA 1555  
Qy 1621 CCAGGCTCACCATCCACAGTGAATTTCTGCAATCAGCCAACTGGCTCTGGGAATT 1680  
Db 1556 CCAGGCTCACCATCCACAGTGAATTTCTGCAATCAGCCAACTGGCTCTGGGAATT 1615  
Qy 1681 TCACATCCACTGCACTTTCAGATGACAGCCGATCAAGTCAGGTGGGAGATATGGTC 1740  
Db 1616 TCACATCCACTGCACTTTCAGATGACAGCCGATCAAGTCAGGTGGGAGATATGGTC 1675

Qy 1741 AGACACCTAGATGAATGGATCTGTGACACTCTCTGCCCATCTGAGGTACCGAGGCTC 1800  
Db 1676 AGACACCTAGATGAATGGATCTGTGACACTCTCTGCCCATCTGAGGTACCGAGGCTC 1735  
Qy 1801 ACGGAATATGTTCTGTCCTCCAGATCATTTCTTGAGGATACCACTCTCTGTCTCAGCTTTA 1860  
Db 1736 ACGGAATATGTTCTGTCCTCCAGATCATTTCTTGAGGATACCACTCTCTGTCTCAGCTTTA 1795  
Qy 1861 CAGTATATCAACCATAGTTCTATGACATTTGCCCAAGGCGGAGAGCTGGTAGTGTTC 1920  
Db 1796 CAGTATATCAACCATAGTTCTATGACATTTGCCCAAGGCGGAGAGCTGGTAGTGTTC 1855  
Qy 1921 TTCAGTCTGCGTGTGCTAAACATGSCCTTCTCCACAGACCTGTTCAACAAGAGCTCTCTG 1980  
Db 1856 TTCAGTCTGCGTGTGCTAAACATGSCCTTCTCCACAGACCTGTTCAACAAGAGCTCTCTG 1915  
Qy 1981 GAGTACCCAGAGCTCTGGAGCAACAATTCACAGCTGTCTGTTCCATATCTACGATCCAAT 2040  
Db 1916 GAGTACCCAGAGCTCTGGAGCAACAATTCACAGCTGTCTGTTCCATATCTACGATCCAAT 1975  
Qy 2041 CTTACAGATTTAAGCAACTTGAATACTTAATCTCAGAAAAGGAGTGTGTTGTGAAT 2100  
Db 1976 CTTACAGATTTAAGCAACTTGAATACTTAATCTCAGAAAAGGAGTGTGTTGTGAAT 2035  
Qy 2101 AGCAAAATGAAGTTTGTGCTAAGTCTGCGCGTATAACCTCACAAAGGCTGTGCACGGGTC 2160  
Db 2036 AGCAAAATGAAGTTTGTGCTAAGTCTGCGCGTATAACCTCACAAAGGCTGTGCACGGGTC 2095  
Qy 2161 TTGGAGGATTTTGTGTTCTGCTGAGCCCAACAATCTCCATCTGGAAATAGACAGCTACTCT 2220  
Db 2096 TTGGAGGATTTTGTGTTCTGCTGAGCCCAACAATCTCCATCTGGAAATAGACAGCTACTCT 2155  
Qy 2221 CTCACATTTGAACACAGCTGATCAAGCAGATCCCTGCAAGTTCTCTGGCTCGGGCGAAATTT 2280  
Db 2156 CTCACATTTGAACACAGCTGATCAAGCAGATCCCTGCAAGTTCTCTGGCTCGGGCGAAATTT 2215  
Qy 2281 GCCCAATGTGTAAGAACGAAACGGAAGCTGAGGAAGCGGAGTGTGCTGCAAAACAGGATAT 2340  
Db 2216 GCCCAATGTGTAAGAACGAAACGGAAGCTGAGGAAGCGGAGTGTGCTGCAAAACAGGATAT 2275  
Qy 2341 GACAGCCAGGGAGCTGAGCGGTCTGGAACCGAGCTCTGTCGCCCTGGGCACAAAAGAA 2400  
Db 2276 GACAGCCAGGGAGCTGAGCGGTCTGGAACCGAGCTCTGTCGCCCTGGGCACAAAAGAA 2334  
Qy 2401 TCGGAGGCTCTCCAGGAAAGGAGCTCCATGCGAGGTTGCCAGATCACTCTGAAAAATCAA 2460  
Db 2335 TCGGAGGCTCTCCAGGAAAGGAGCTCCATGCG--GGTTCCAGATCACTCTGAAAAATCAA 2392  
Qy 2461 GATACAAAACCTAGTGTGTTAAAGTTCCAAAATCAAAATTAACAAGGTAATCAGTAAA 2520  
Db 2393 GATACAAAACCTAGTGTGTT--AAAAGTTCCAAAATCAAAATTAACAAGGTAATCAGTAAA 2451  
Qy 2521 AGAAATCTGAATTAAGTGAAGTATGAAAGATTTAAACCAAGATTGGAAGGA 2580  
Db 2452 AGAAATCTGAATTAAGTGAAGTATGAAAGATTTAAACCAAGATTGGAAGGA 2511  
Qy 2581 AATTAATAAATCTGAATGTACAAATTAATCACTTAGGCTATCTCAAGAGAGATGATTTGCT 2640  
Db 2512 AATTAATAAATCTGAATGTACAAATTAATCACTTAGGCTATCTCAAGAGAGATGATTTGCT 2571  
Qy 2641 TCTCAAGGAAATGAGGACAGGATTTCTAGGCTATCTCAAGAGAGATGATTTGCT 2700  
Db 2572 TCTCAAGGAAATGAGGACAGGATTTCTAGGCTATCTCAAGAGAGATGATTTGCT 2631  
Qy 2701 CACTGAGATCAGCACACCAATTTCAAAATATAGAGAGTCAATGTTGGCAACCAAG 2760  
Db 2632 CACTGAGATCAGCACACCAATTTCAAAATATAGAGAGTCAATGTTGGCAACCAAG 2691  
Qy 2761 TAAATCTGAAAAAAGACACTTACTTATTTAAABCCCAATGCAATCAGCGAAAC 2820  
Db 2692 TAAATCTGAAAAAAGACACTTACTTATTTAAABCCCAATGCAATCAGCGAAAC 2751



QY 1596 GGCACCTGACGACACAAATGCTAGTACACAGGGCTCACCATCCACACAGTGAATTAATCTGCG 1655  
DB 1153 GGCACCTGACGACACAAATGCTAGTACACAGGGCTCACCATCCACACAGTGAATTAATCTGCG 1212  
QY 1656 AATCAGGCAACTGGCTCTCGGGAATTTTCCACATCCACCTGCACTCTTCAGATCACAGCCGATC 1715  
DB 1213 AATCAGGCAACTGGCTCTCGGGAATTTTCCACATCCACCTGCACTCTTCAGATCACAGCCGATC 1272  
QY 1716 AAGTGCAGGTGGGGAAGATATGCTGACACACCTAGATGAATGGATCTGCTGACACTCC 1775  
DB 1273 AAGTGCAGGTGGGGAAGATATGCTGACACACCTAGATGAATGGATCTGCTGACACTCC 1332  
QY 1776 TGCCCCATCTCAGGTACGAGCTCAGCAATATGTTTCTGTCGCCAGATCATTTCTTGA 1835  
DB 1333 TGCCCCATCTCAGGTACGAGCTCAGCAATATGTTTCTGTCGCCAGATCATTTCTTGA 1392  
QY 1836 GGATACCACTCTCTCAGCTTACAGTATATCACCACTAGTCTTATGACCAATGCC 1895  
DB 1393 GGATACCACTCTCTCAGCTTACAGTATATCACCACTAGTCTTATGACCAATGCC 1452  
QY 1896 CAAGGCGGAGAGCTGCTGAGTCTTTCAGTCTGCGGTGTTGCTAAATGCGCTTCTCCAA 1955  
DB 1453 CAAGGCGGAGAGCTGCTGAGTCTTTCAGTCTGCGGTGTTGCTAAATGCGCTTCTCCAA 1512  
QY 1956 CGACCTGTTCACCAAGAGCTCTCTGAGTACCGAGCTCTGAGCAACAATTCACAGCT 2015  
DB 1513 CGACCTGTTCACCAAGAGCTCTCTGAGTACCGAGCTCTGAGCAACAATTCACAGCT 1572  
QY 2016 GCTGGTTCATATCTAGATCCATCTTACAGATTTTAAAGCACTTGAATCTTAACT 2075  
DB 1573 GCTGGTTCATATCTAGATCCATCTTACAGATTTTAAAGCACTTGAATCTTAACT 1632  
QY 2076 CAGAAACGGAGTGTGATGTGAATAGCAAAATGAAGTTTGTAAAGTCTGCGGTATAA 2135  
DB 1633 CAGAAACGGAGTGTGATGTGAATAGCAAAATGAAGTTTGTAAAGTCTGCGGTATAA 1692  
QY 2136 CCTCACAAGCTGTGACAGGGGTCTTGAGGATTTTCGTCTGCTGAGCCCAACA 2195  
DB 1693 CCTCACAAGCTGTGACAGGGGTCTTGAGGATTTTCGTCTGCTGAGCCCAACA 1752  
QY 2196 CCATCTGGAATAGACAGTACTCTCTCAATTTGAACCACTGATCAAGCAGATCCCTG 2255  
DB 1753 CCATCTGGAATAGACAGTACTCTCTCAATTTGAACCACTGATCAAGCAGATCCCTG 1812  
QY 2256 CAAGTTCCTGCTGCGGCGAATTTGCCAATGTGTAAAGAACGAACTGAGGAAGC 2315  
DB 1813 CAAGTTCCTGCTGCGGCGAATTTGCCAATGTGTAAAGAACGAACTGAGGAAGC 1872  
QY 2316 GGAGTGTGCTGCAACCCAGATATGACAGGAGGAGCTGACGGTCTGGAACGAG 2375  
DB 1873 GGAGTGTGCTGCAACCCAGATATGACAGGAGGAGCTGACGGTCTGGAACGAG 1932  
QY 2376 CCTCTGGCCCTGGCAAGGAATGCGAGTCTCTCCAGGAAAGGAGCTCCATGCGAG 2435  
DB 1933 CCTCTGGCCCTGGCAAGGAATGCGAGTCTCTCCAGGAAAGGAGCTCCATGCGAG 1992  
QY 2436 GTTCCAGATCACTCTGAAATCAAGCATACCAAACTAGTGTAAAGTTCCAAATCA 2495  
DB 1993 GTTCCAGATCACTCTGAAATCAAGCATACCAAACTAGTGTAAAGTTCCAAATCA 2052  
QY 2496 ACAAATTAACAGGTAATCAGTAAAGAAATTTCTGAATTTACTGACCTAGATATGAAGA 2555  
DB 2053 ACAAATTAACAGGTAATCAGTAAAGAAATTTCTGAATTTACTGACCTAGATATGAAGA 2112  
QY 2556 ATTTAAACATCAAGATTTGGGAAGAAATTTAAAACTGAAATGTACAAATATCACTTAGG 2615  
DB 2113 ATTTAAACATCAAGATTTGGGAAGAAATTTAAAACTGAAATGTACAAATATCACTTAGG 2172  
QY 2616 CTATCTCAAGAGATGATTTTGCCTTCTCAAGGAAATGGAGCAGGCATATTCATGGGT 2675  
DB 2173 CTATCTCAAGAGATGATTTTGCCTTCTCAAGGAAATGGAGCAGGCATATTCATGGGT 2232

QY 2676 CATCAAAATCCAGACATACAGTCAACCTGAGAAATCAGCACACCATATTTTCAATATA 2735  
DB 2233 CATCAAAATCCAGACATACAGTCAACCTGAGAAATCAGCACACCATATTTTCAATATA 2292  
QY 2736 GAAAGAGTCACTGCTAGTCTGGCAACCAAGTAAATTTCTGAAAGAAAGACACTTACTTATTA 2795  
DB 2293 GAAAGAGTCACTGCTAGTCTGGCAACCAAGTAAATTTCTGAAAGAAAGACACTTACTTATTA 2352  
QY 2796 AAACCCCAATGCAATCAGCGAAACATATTTTCTTACTATTTCTTGGATGATGATCAAAATGA 2855  
DB 2353 AAACCCCAATGCAATCAGCGAAACATATTTTCTTACTATTTCTTGGATGATGATCAAAATGA 2412  
QY 2856 TCATAAGCCAGGTTTGTCTTCCACCTTCCCTGAAATTTTACTCACAGATCAATTTGCAACA 2915  
DB 2413 TCATAAGCCAGGTTTGTCTTCCACCTTCCCTGAAATTTTACTCACAGATCAATTTGCAACA 2472  
QY 2916 AGCATAGCTTACTTATTTGTTAGGACCTGAACAATTTTATTTGGGAAGCAACTCTTTATAT 2975  
DB 2473 AGCATAGCTTACTTATTTGTTAGGACCTGAACAATTTTATTTGGGAAGCAACTCTTTATAT 2532  
QY 2976 GCTAGAAAGTACATTTAAAGATGACTTACCGAGGAGATGAGGTCTCTCTAAACG 3035  
DB 2533 GCTAGAAAGTACATTTAAAGATGACTTACCGAGGAGATGAGGTCTCTCTAAACG 2592  
QY 3036 CATGAATGTATGTAGTGTGTAGGCACTGTAGTGTATATATGCTCCACACTACGTCT 3095  
DB 2593 CATGAATGTATGTAGTGTGTAGGCACTGTAGTGTATATATGCTCCACACTACGTCT 2652  
QY 3096 GATTAACCAACAACCTCAGTATTCAGTTATTAGGCACACTAGTTTATACGCAACTACTGC 3155  
DB 2653 GATTAACCAACAACCTCAGTATTCAGTTATTAGGCACACTAGTTTATACGCAACTACTGC 2712  
QY 3156 TTACATAGTACAGTGTTTTGTGCAATAATCTTTGAATGTTCTTTTAAAGAACTAGAG 3215  
DB 2713 TTACATAGTACAGTGTTTTGTGCAATAATCTTTGAATGTTCTTTTAAAGAACTAGAG 2772  
QY 3216 GTTCAGATACATACATACATGGAAGAAATCTTACTTCTTGTGTACTACAAAGCTATTT 3275  
DB 2773 GTTCAGATACATACATACATGGAAGAAATCTTACTTCTTGTGTACTACAAAGCTATTT 2832  
QY 3276 AAAGAAGATGCTATGTTGGGAGAGGGCGAAGTTGTACTATATGACATAATCAAT 3330  
DB 2833 AAAGAAGATGCTATGTTGGGAGAGGGCGAAGTTGTACTATATGACATAATCAAT 2887

## RESULT 4

US-10-007-270-5  
; Sequence 5, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 2244  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform C  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(2244)  
; OTHER INFORMATION: n is a, c, g, or t.

US-10-007-270-5

Query Match 65.6%; Score 2184.2; DB 13; Length 2244;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 2211; Conservative 0; Mismatches 10; Indels 2; 0

	Matches	221L; Conservative	0; Mismatches	10; Indels	2; Gaps	2;
QY	1	TAAACCAAGAGGTTATCTCCTCAATCATCTCGTATCAATATATAATTAATTTTTTCACATTTC	60			
Db	22	TAAACCAAGAGGTTATCTCCTCAATCATCTCGTATCAATATATAATTAATTTTTTCACATTTC	81			
QY	61	TGTACTCTTTTAATCAGATTTCAGGTTGTCTGTGATGGTTATFCAGAATTACCAATGCAC	120			
Db	82	TGTACTCTTTTAATCAGATTTCAGGTTG-CTGTGATTTGTTATCAGANTTACCAATGCAC	140			
QY	121	AAAAGCCGAATGTAATTTGGAAAACTAGAAGAGCTATTTTTTGTTTTTGGATTTTTCTCCA	180			
Db	141	AAAAGCCGAATGTAATTTGGAAAACTAGAAGAGCTATTTTTTGTTTTTGGATTTTTCTCCA	200			
QY	181	AGTTCAAGGAACCAAAGATATCTCCATTAAACATATACCATTCTGAAACTTAAAGACATAGA	240			
Db	201	AGTTCAAGGAACCAAAGATATCTCCATTAACTATACATATACCATTCTGAAACTTAAAGACATAGA	260			
QY	241	CATCTCCCACAAGAATGAAAACAACTGAAGAGTACTGAAAAAATGTCAAAATGTCACATAT	300			
Db	261	CAATNCCCCAAGAAATGAAAACAATGAAAGTACTGAAAAAATGTCAAAATGTCACATAT	320			
QY	301	GAGACGAATATTTGCATTTGGCAAGAGCATCGAACAAAAAGATCCGATTTTTTCCCRAACGG	360			
Db	321	GAGACGAATATTTGCATTTGGCAAGNATCGAACAAAAAGATCCGATTTTTTCCCRAACGG	380			
QY	361	GTTTAAAGTCTGTGCCACAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTA	420			
Db	381	GTTTAAAGTCTGTGCCACAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTA	440			
QY	421	TAGATTGAGAGTGTGTGAGGAAGCAGTATCGGAAGCAGATATCGATCTTTTCTGGATCGCAT	480			
Db	441	TAGATTGAGAGTGTGTGAGNAGCAGCATCGGAAGCAGTATCGATCTTTTCTGGATCGCAT	500			
QY	481	CCCTGACACAGGGGAATATCAGGACTGGGTACGATCTGCCAGCAGGAGACCTTTCGCCT	540			
Db	501	CCCTGACACAGGGGAATATCAGGACTGGGTACGATCTGCCAGCAGGAGACCTTTCGCCT	560			
QY	541	CTTTGACATTCGAAAAAATTTACAGCAATCCCAGGAGCACCTGGATCTTCTCCAGCAGAG	600			
Db	561	CTTTGACATTCGAAAAAATTTACAGCAATCCCAGGAGCACCTGGATCTTCTCCAGCAGAG	620			
QY	601	AATAAAAACAGAGAAGTTTCCTCTGACAGAAAAGATGAANAATATCTGACAGAGAAACATTGGG	660			
Db	621	AATAAAAACAGAGAAGTTTCCTCTGACAGAAAAGATGAANAATATCTGACAGAGAAACATTGGG	680			
QY	661	AGAGCCTGGTCAAAACCATTTGTCATTTCAACAGACAAATCTACATTTCAAAAGACTTGGGAGT	720			
Db	681	AGAGCCTGGTGBAAACCATTTGTCATTTCAACAGCAATCTACATTTCAAAAGACTTGGGAGT	740			
QY	721	ATTTCTAGAAAAACCTCTCAGAAAGACAAATTCAGATGTGTGCCAAGCTCTCATCTTGGGCGCT	780			
Db	741	ATTTCTAGAAAAACCTCTCAGAAAGACAAATTCAGATGTGTGCCAAGCTCTCATCTTGGGCGCT	800			
QY	781	TTCCCTCTCACTCTGTGATGACCCCTCCTCAATGAAATTTCTGATTAATACACTCAAGCAG	840			
Db	801	TTCCCTCTCACTCTGTGATGACCCCTCCTCAATGGAATTTCTGATTAATACACTCAAGCAG	860			
QY	841	ACCAAGATGCCTTACAAACAGAAAAGAGAAACAGAAATTCGCTGTGTTGGAGGACAGAGGTTG	900			
Db	861	ACCAAGATGCCTTACAAACAGAAAAGAGAAACAGAAATTCGCTGTGTTGGAGGACAGAGGTTG	920			
QY	901	GAGCTCAGCGTCTCTCTGTGTAAACACAGAAAGTTCAAGGACAGAGCTCGCTGACTCCCAAGTCC	960			
Db	921	GAGCTCAGCGTCTCTCTGTGTAAACACAGAAAGTTCAAGGACAGAGCTCGCTGACTCCCAAGTCC	980			
QY	961	CCATATTTACAGGAGCTAGCAGGAAAGTCCCAACTTTCAGATCCAAAAAGATATTTAAGAAA	1020			
Db	981	CCATATTTACAGGAGCTAGCAGGAAAGTCCCAACTTTCAGATCCAAAAAGATATTTAAGAAA	1040			

Qy	1021	CTTCCAGGATCAAAAATTCATGTGTTAGGATTTAGACCAAAAGAAAAGATGGC	1087
Db	1041	CTTCCAGGATCAAAAATTCATGTGTTAGGATTTAGACCAAAAGAAAAGATGGC	1100
Qy	1081	TCAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTCAGAGAACA	1140
Db	1101	TCAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTCAGAGAACA	1160
Qy	1141	AGCCCTGCAAGTGAACCTCTGTCTTTTGATTCACAACAAATTCGAAAAGTGGAGTCTAT	1200
Db	1161	AGCCCTGCAAGTGAACCTCTGTCTTTTGATTCACAACAAATTCGAAAAGTGGAGTCTAT	1220
Qy	1201	CATGGAACCATGAGGAGGACAAACACAGAAATCTATCTCACAGCTACAGACCTCAAA	1260
Db	1221	CATGGAACCATGAGGAGGACAAACACAGAAATCTATCTCACAGCTACAGACCTCAAA	1280
Qy	1261	AGCGTGNATCAGCAAGCACTAGAGGAAGACAATCTTTGGATGTGGGACAATTCAGTTC	1320
Db	1281	AGCGTGNATCAGCAAGCACTAGAGGAAGACAATCTTTGGATGTGGGACAATTCAGTTC	1340
Qy	1321	ACTGATGAAATTCCTGGATCACTGCCAGCGCTTTGGTCTCTGACACCCAAATCAGAGCTGCC	1380
Db	1341	ACTGATGAAATTCCTGGATCACTGCCAGCGCTTTGGTCTCTGACACCCAAATCAGAGCTGCC	1400
Qy	1381	ACATCTTTTGCTGTTTATAACAGAGATGCTACTTTTGAGTCCAGAACTTCCTCTGTGAA	1440
Db	1401	ACATCTTTTGCTGTTTATAACAGAGATGCTACTTTTGAGTCCAGAACTTCCTCTGTGAA	1460
Qy	1441	CCCAGCTTTGAGACAGTGGACGGAGCAGAGCATGCTCTACCTGACACTTCTTGGTCTCCA	1500
Db	1461	CCCAGCTTTGAGACAGTGGACGGAGCAGAGCATGCTCTACCTGACACTTCTTGGTCTCCA	1520
Qy	1501	CTGTCTATGSCCTACCTCCCTGTGCAGAGCTCCACCTTTCTTTATGGCATCAGCATC	1560
Db	1521	CTGTCTATGSCC-CTACCTCCCTGTGCAGAGCTCCACCTTTCTTTATGGCATCAGCATC	1579
Qy	1561	TTCTCTCTGACTGATCAAGGCACCAAGATACAATGGCCACTGACACAGACAATGCTAGTA	1620
Db	1580	TTCTCTCTGACTGATCAAGGCACCAAGATACAATGGCCACTGACACAGACAATGCTAGTA	1639
Qy	1621	CCAGGCTCACCATCCCACCAAGTGAATTTCTGCAATCAGGCCAACTGGCTCTCGGAAAT	1680
Db	1640	CCAGGCTCACCATCCCACCAAGTGAATTTCTGCAATCAGGCCAACTGGCTCTCGGAAAT	1699
Qy	1681	TCACATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGGAGATATGGTC	1740
Db	1700	TCACATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGGAGATATGGAC	1759
Qy	1741	AGACACTAGATGAATGATCTGTCTGACATCTCTGCCCCATCTGAGGTACACAGCTC	1800
Db	1760	AGACACTAGATGAATGATCTGTCTGACATCTCTGCCCCATCTGAGGTACACAGCTC	1819
Qy	1801	AGCGAATATGTTCTGTCACAGATCAATTTCTGGAGGATACCACTCTGTCTCAGCTTTA	1860
Db	1820	AGCGAATATGTTCTGTCACAGATCAATTTCTGGAGGATACCACTCTGTCTCAGCTTTA	1879
Qy	1861	CAGTATATCACCACATGTTCTATGACCATTGTGCCCCCAGGGCCGAGAGCTGTGTGTTCT	1920
Db	1880	CAGTATATCACCACATGTTCTATGACCATTGTGCCCCCAGGGCCGAGAGCTGTGTGTTCT	1939
Qy	1921	TTCAGTCTGGTGTGCTTAACATGGCCTTCTCCAAAGAGCTGTTCTCAAGAGCTCTCTG	1980
Db	1940	TTCAGTCTGGTGTGCTTAACATGGCCTTCTCCAAAGAGCTGTTCTCAAGAGCTCTCTG	1999
Qy	1981	GAGTACCGAGCTCTGGAGCAACAAATTCACAGAGCTGTGGTTCATATCTACGATCCAA	2040
Db	2000	GAGTACCGAGCTCTGGAGCAACAAATTCACAGAGCTGTGGTTCATATCTACGATCCAA	2059
Qy	2041	CTTACAGGATTTAAGCACTTGAAATPACTTAATCTTCAGAAACGGAGGTGTGATTTGTGA	2100
Db	2060	CTTACAGGATTTAAGCACTTGAAATPACTTAATCTTCAGAAACGGAGGTGTGATTTGTGA	2119





QY 1482 T-----GACACTTCTGGTCTCCACCTGCTATGCGCTCTACCTCCCTGTC 1526  
DB 1485 TGGATGCTCTCAAGACAGTGTCTTGGTCTCCACCTGTATCAGCCTCAATTTCCCGATC 1544  
QY 1527 AGAAGCTCCACCTTTCTTTATGGCATCAAGCATCTCTCTCTGACTGATCAAGGCACAC 1586  
DB 1545 AGAAATCTACCTTCGTTTA--CACCTAGCATCTCTCTCTAGATGCTCAAGCCCCC 1601  
QY 1587 AGATACATGGCCACTGACACAGCAATGTAGTACAGGGCTCACCATCCCAACAGTGA 1646  
DB 1602 TCCTTGATGACCACTGGCCCAACAGCACTCAATCCCAAGCCCACTCTCCCACTATCGA 1661  
QY 1647 TTATCTGCAATCAGCCAACTGGCTCTGGGAAATTTCACATCCACCTGCACTTTCAGATGA 1706  
DB 1662 TTATCTACCATCCGCCAATGGCTCTGGAAATGTCATGTCGCTGTGATCTCTCCAGTGA 1721  
QY 1707 CAGCCGATCAAGTGCAGGTGGGAAATATGGTCAACACCTAGATGAATGATCTGTC 1766  
DB 1722 CAGAGAGCTGATCACAAGCAGCCATGACAAATCCGAGACCTAGATGGCATGGATGTC 1781  
QY 1767 TGACACTCTCCCTCCCATCTGAGTACAGAGCTCAGGATATGTTTCTGTCCTCCAGATCA 1826  
DB 1782 TGACACCCAGCCTTGTGCAAAATATCAGAACTGAGTGGATGATTTGCTCGGGTCA 1841  
QY 1827 TTTCTTGGAGATACCACTCCTGTCTCAGCTTTACAGATATATCACCACCTAGTTCTATGAC 1886  
DB 1842 GTTCTTGGAGATGACACACCCATCCCAACAGTACGTTTCATCACCACCACTCCGAGAC 1901  
QY 1887 CATGCCCCCAAGGCGGAGAGCTGTGATGTTCTTCAGTCTGCGTGGTGGCTAACTGGC 1946  
DB 1902 CATTGGCCCAAGGCGGAGAGCTGTGATGTTCTTCAGCCTGCGTGGTGGCTAACTGGC 1961  
QY 1947 CTTCTCCCAAGCACTGTTTCAACAGAGCTCTCGGAGTACCGAGCTCTGAGCAACAAT 2006  
DB 1962 GTTCTCTGATGACTGTTTCAACAGAGTCTCTGGAGTATCAGCCCTGGAAACAGATT 2021  
QY 2007 CACACAGCTCTGGTTCATATACGATCCAACTTTACAGAGTTTAAACACTTGAAT 2066  
DB 2022 CACAGACCTCTGGTTCCTTATCAGATCGAATCTTACGGGATTTAAGCAACTGGAAT 2081  
QY 2067 ACTTAAGTTCAGAAACGGAGTGTGATGTAATGCAAAATGAAGTTGCTTAAGTCTGT 2126  
DB 2082 ACTCAGCTTCAGAAACGGAGTGTGATGTAATGCAAAATGAAGTTGCTTAAGTCTGT 2141  
QY 2127 GCGGTAACTCACCAGGCTGTGACGCGGTCTTGGAGGATTTTCTGCTGCGAGC 2186  
DB 2142 ACCCTACACCTCACCAGGCGGTGCGGGGTCTTGGAGGATCTCGTCCACCGCAGC 2201  
QY 2187 CCAACAACTCCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACAGCTGATCAAGC 2246  
DB 2202 TCAAGGCTCAATCTGGAATCGAAAGCTACTCCCTCGAATGAAACCAAGCTGATCAGC 2261  
QY 2247 AGATCCCTCAAGTCTCTGCGCTCGCGCAATTTGCCAATGTGTAAGAAACGAACGAGC 2306  
DB 2262 GGATCCCTGCAACTCTAGACTGTGGCAATTTGCCAGTGTGTAAGAAATGATGGAC 2321  
QY 2307 TGAGGAAGCGAGTGTGCTGCAAAACAGGATATGACCCAGGGAGCCTCGAAGCTT 2366  
DB 2322 AGAGGAAGCAGAGTGTGCTGCAAGAGGACATGAGAGCCAGGGACCTCGAATACCA 2381  
QY 2367 GGAAACGAGGCTCTGTGGCCTGGCAAGAGGATGCGAGTCTCTCAGGGAAGGGAGC 2426  
DB 2382 GACCTTGAACTCTGTGCCCCCTGG---AAGACTTGTGTGGCGCGCGGAGAACAGCAAC 2438  
QY 2427 TCCATGAGGTTGCCAGATCACTCTGAAATCAAGCATACAAACTAGTGTGTTAAAGTT 2486  
DB 2439 TCCATGAGGCCACAGATCACTCTCAAAACCAAGCTCAGGAACCTGTGGTGTAAAGCT 2498  
QY 2487 CCAAAATCAACAAATTAACAGTATTCAGTAAAGAAATTTGAAATTTACTGACCGTGA 2546  
DB 2499 ACCTCAGCAA-----AATAGGCTAGTCAAGAAAGAAATTTCTAAATCTATCAGCTATAGG 2552

QY 2547 ATATCAGAAATTTAACCATCAAGATTGGAGGAAATTTAAAACTGAA----- 2595  
DB 2553 ATTTGAAGATTTGAAGACCCAGGACTGGGGGAAATTTAAAGCTGGAATCATATGCAATT 2612  
QY 2596 -----ATGTACAATTTATCACTTAGCTATCTCAAGAGAGATGATTTGCT 2640  
DB 2613 ATGTTGCAAACTCTGTTGAAAGGAACTTTTATTTCTTTAAAGAAAGTGTATCTGTTCTGT 2672  
QY 2641 TCTCAGGAAATGGAGACAGGCATATTCATGGGTCAATCAAAATCCAGACATACAGTCAA 2700  
DB 2673 TAACTTCTGAAAAAACAAGAGAGATTCAGTGTGCTATTTGGAATACAGGCATGTAATCAA 2732  
QY 2701 CACTGAGAAATCAGCACACACCATATTTCAAAATATAGAGAGTCAATGACTTGGCAACAG 2760  
DB 2733 CTTTGAGACTCAG-----CATGCTTGAACAAGACAGCAGGCGTGTATTTGTATGA-CAG 2784  
QY 2761 TAAATCTGAAAAAAGACACTTATTTATTTA--AAACCCCAATGCAATCAGCGAA 2818  
DB 2785 TTAAGCCTGGTGGGGGGGGGACATATTTTAGTCAAAACTCAAGCAATCATTTGA 2844  
QY 2819 ACATATTTTACTATCTTGGATGATAGTCAAAATGATCATAGCCAGGTTTGGTTCAC 2878  
DB 2845 ACACA-TTGTACTATTTTGGACAGTACTC--AAGTAGCAAGATAAGTTAGCTTTTT 2901  
QY 2879 CTTCCCTGAAATTTTACTCAGATCATTTTGCACCAAGCATAGCTTACTTATTTGTTAG 2938  
DB 2902 CTTTCTTTAAATTTATCATATAAATCTTATTTCAAAATAAATACAC-----TTGTTTAG 2954  
QY 2939 GGACTGCAACATTTTGGGAGCAAACTCTTATATGCTAGAAAGTACATTTAAAGAT 2998  
DB 2955 TGGGTGTACAATATGAGGATCTGATCTTTTATATGTTAGAAATATACAGTTAAAGAT 3014  
QY 2999 CACTACTTACGC 3010  
DB 3015 TATCATTTGGGC 3026

## RESULT 6

US-10-007-270-10  
; Sequence 10, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 1726  
; TYPE: DNA  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform D  
US-10-007-270-10

Query Match 16.0%; Score 534; DB 13; Length 1726;  
Best Local Similarity 72.0%; Pred. No. 1.4e-133;  
Matches 792; Conservative 0; Mismatches 225; Indels 83; Gaps 4;  
QY 396 TTTTAGACAGTCTTCAAGCTTATATAGATGAGGTGTCAGGAGCAGTATGGGAAG 455  
DB 171 TTTTGGGATTTTCTCCAAAGTTCAGGAATCAAGATGTCAGAAAGTCTGTGGGAAG 230  
QY 456 CATATCGGATCTTTCTGGATCGCATCCCTGACACAGGGGAATATCAGGATCGGCTCAGCA 515



Db 231 CATATCGTATCTTTCTGGACCGAATTCCTGACACAGAGGAATATCAAGACTGGGTGAGCC 290  
Qy 516 TCTGCCAGCAGGAGACCTCTGCTCTTTGACATTTGAAAAAATTTTTCAGCAATTCCTGAG 575  
Db 291 TCTGCCAGAAAGAACCTTCTGCTCTTTGACATTTGGGAATTTTTCAGCAATTCCTGAG 350  
Qy 576 AGCACTGGATCTTCTCCAGAGAGATATAAAGAGAGATTTTCTCTGACAGAAAGATG 635  
Db 351 AGCACTGATCTTCTTTCAGAGAGATATAAAGAGAGATTTTCTCTGAGAGAAAGATG 410  
Qy 636 AATATCTGAGAGAGACATTTGGAGAGCTGGTGAACCATTTGTCATTTCAACAGCAA 695  
Db 411 AGACAGCTCCATGAGAGACATTTGAGAGACCTTACTGAGCCCTTGTGTACCCAC 465  
Qy 696 TCTACATTTCAAAGACTTTGGGAGATTTCTAAGAAACCTTCAGAAAGAGCAATTTCAA 755  
Db 466 -----AGG 468  
Qy 756 TGTTCGCAACGCTCTCACTTGGGCTTTCCCTCTCACTCTCTGATGACACCTCTCAATGA 815  
Db 469 TGTTCGAGAGATGCTCTGAGGCTTCCCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 528  
Qy 816 AATCTCGATTAATCACTCAACGACCAACAGATGCTTACACAGAAAGAGAAACGAA 873  
Db 529 GATTTCTGATGCTCACTCAAGGACATTTCAAAGCCCAACAGAAAGATATAACAGAAC 588  
Qy 874 -----TTCTGCTGTGTGGAGGACAGAGGCTGAGCTCAGGCTCTCTCTGTTAA 923  
Db 589 TATTCAGTGTCTGAATTTCTCATCAGAGGAGAGGTTGAGTTGAGCATCTCTCTGCAA 648  
Qy 924 CCAGAGTTTCAAGCAGAGCTCGTGTCTCCAGTCCCTCTATTTACAGAGAGTAGCAGG 983  
Db 649 CCAGAGTTTCAAGCAGAGCTCACCACCTCTGGGTCACTACTACAGGAACTGGTGG 708  
Qy 984 AAGTCTCACTCAGATGCAAGAGATATTTAAGAACTTTCCAGGATTTCAAAATTC 1043  
Db 709 ACAGTCTCACTGAGTTGCAAGAGATATTTAAGAACTTTCCAGGATTTCCGGAATCC 768  
Qy 1044 TGTGTAGGATTTAGCAAGAAAGAAAGATGGCTCAAGCTCCACAGAGTGCAACT 1103  
Db 769 TGTATTAGATTTAGCAAGAAAGAGAGATGGTTCAAGTCTCCACAGAAATACAGCT 828  
Qy 1104 TACGGCCATTTAAGAGACACAGTGAGAGCAAGAAAGCCCTGCAAGTCACTCTGTC 1163  
Db 829 TATGGCCATCTTAAGAGGACCATGCAAGAGCAAAAGCCCTGATAGTCTATCTGTC 888  
Qy 1164 TTTTGAATTCGAACAAATTTGAAGTGAAGATTTTGAAGTGAAGATTTTGAAGTGAAG 945  
Db 889 TCTTGAATTCGAACAAATTTGAAGTGAAGATTTTGAAGTGAAGATTTTGAAGTGAAG 1223  
Qy 1224 GCAACAGAAATCTATCTCAGAGCTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGA 1283  
Db 946 ACAACAGAAATCTATCTCAGAGCTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGA 1005  
Qy 1284 GGAAGAAATCTTTGGATTTGGGAGATTTCACTGATGATGAATTTCTGATCACT 1343  
Db 1006 TGAAGACCTGTCTTTGGTAGAAGGAAATTTCCATTTGGTGTATGAAGTACTTGGGAC 1065  
Qy 1344 GCCAGCTTTGCTCTGACACCCATCAGAGCTGCCACATCTTTTGTGTTATAACAGA 1403  
Db 1066 -----CTTCAGACCTGTCTGACACAGATCTGCCAGGCTTGTGATGTACAGA 1119  
Qy 1404 GATGCTATTTTGAAGTCAAGAACTTTCTCTCTGTTGAAACCCAGCTTTGAGACAGTGGAC 1463  
Db 1120 GATGCTATTTTGAAGTCAAGAACTTTCTCTCTGTTGAGCTTAGGCTTAGGCGAGTGGAC 1179  
Qy 1464 AGCAGAGATGCTGTACCTG 1483  
Db 1180 AGAGATCTGAGCTGCTG 1199

RESULT 7

US-10-007-270-12

; Sequence 12, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; PRIOR FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 1321  
; TYPE: DNA  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform E  
; US-10-007-270-12

Query Match 14.8%; Score 491.6; DB 13; Length 1321;  
Best Local Similarity 76.0%; Pred. No. 3.8e-122;  
Matches 634; Conservative 1; Mismatches 190; Indels 9; Gaps 2;  
Qy 1767 TCACACTCTGCCCCATCTGAGGTACAGAGCTCAGCGAATATCTTCTGTCGCCAGATCA 1826  
Db 319 TGAACCGCGCCCTGTTCAGAAATATCAGAACTCAGTGTGATACGATTTCTGCTGGGTCA 378  
Qy 1827 TTTCTTGAGGATACCACTCTCTCAGCTTTTACAGTATATCACCACTAGTTCTTATGAC 1886  
Db 379 GTTCTTGAGATGACCAACCCATCCCAACAGTACGGTTTCATCACCAGCTCCGAGAC 438  
Qy 1887 CATTGCCCCCAAGGCGGAGAGCTGTAGTGTCTTCTCAGTCTGGGTGTGTGTAACATGCC 1946  
Db 439 CATTGCCCAAGGCGGAGAGCTAGTGTATTTCTTACGCTGCGTGTGTGTAACATGCC 498  
Qy 1947 CTTCTCCCAACGACCTGTTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAT 2005  
Db 499 GTTCTCTATGACCTGTTTCAACAGAGTCTCTGGAGTATCAAGCCCTTGAACACGAT 558  
Qy 2007 CACAGAGCTGTGTTCCATATCTACGATCCAAATCTTACAGATTTAAGCAACTTGAAT 2065  
Db 559 CACAGACCTGTGTTCCCTATCAGATCCGAATCTTACGGGATTTAAGCAACTTGAAT 618  
Qy 2067 ACTTAACCTCAGAAACGGAGTGTGATTTGTAATAGCAAAATGAAGTTTGTAACTGT 2126  
Db 619 ACTCAGCTTCAAGAAACGGAGTGTGATTTGTAATAGCAAAAGTGGGTTTGAAGGCGGT 678  
Qy 2127 GCGGTATAACCTCACCAAGGCTGTGCAGGGGTCTTGGAGGATTTTGTGTCGACG 2186  
Db 679 ACCCTACACCTCACCCAGGCGGTGCGGGGTCTTGGAGGATCTTCGGTCCACGCGAC 738  
Qy 2187 CCAACAACTCCATCTGGAATATAGACAGCTACTCTCTCAACATTTGAACAGCTGATCAAGC 2246  
Db 739 TCAGGGCTCAATCTGGAATTCGAAAGCTACTCCCTCCGACATTTGAACAGCTGATCAGC 798  
Qy 2247 AGATCCCTGCAAGTTCTCTGGCCCTGCGGGGAAATTTGCCCAATGTGTAAAGAACGAG 2306  
Db 799 GGATCCCTGCAACCTCTAGACTGTGGCAATTTTCCCGAGTGTGTAAAGAAATGAGTGGAC 858  
Qy 2307 TGAAGAGCGGAGTGTGCTGTGAAACAGGATATGACAGCCAGGGAGCTTGGAGGCT 2366  
Db 859 AGAGGAAGCAGAGTGTGCTGTGAGACAGGACATGAGAGCCACGCGGACCTTGGACTACCA 918  
Qy 2367 GGAACCCAGGCTCTGTGGCCCTGGGCAAAAGGAATGCGAGGTCTCTCCAGGGAAGGGAGC 2426  
Db 919 GACCTTGAACCTCTGTCCCTCTGG---AAAGACTTGTGTGGCCGCGGACAGACGAC 975  
Qy 2427 TCCATGACGTTGCCAGATCACTCTGAAAAATCAGCATACAAAACTAGTTTAAAAAGTT 2486

Db 976 TCCATGAGGCCACAGATCCTCTACAAACCAAGCTCAGAACCTGGTGTAAAAGCT 1035  
QY 2487 CCAAAATCAACAAATACAGGTAATCAAGTAAGAAATTTCTGAATTAATCTGACCTAGTA 2546  
Db 1036 ACGTCAGCAA-----AATAAGGTAGTCAAGAAACGAAATCTTAAACTATCAGCTATAGG 1089  
QY 2547 ATATGAAGATTTTAAACCATCAAGATTCGGAGGAAATTTAAAACTGAAATGTA 2600  
Db 1090 ATTGAAATTTTGAAGACCAAGGACTGGAGGAAATTTAAAGCTGAATCATA 1143  
RESULT 8  
US-10-007-270-14  
; Sequence 14, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 555  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Monkey IPM 150 cDNA (partial)  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Monkey species  
US-10-007-270-14  
Query Match 13.2%; Score 439; DB 13; Length 555;  
Best Local Similarity 85.8%; Pred. No. 3,8e-108;  
Matches 526; Conservative 0; Mismatches 25; Indels 62; Gaps 1;  
QY 347 TTTTCCCAACGGGGTTAAAGTCTCTCCACAGGAATCCATGAACAGATTTTAGACAGT 406  
Db 4 TTCTTTCCGAACGGGGTTAAAGTCTCTCCACAGGAATCCATGAACAGATTTTAGCAGT 63  
QY 407 CTTCAAGCTTATTATAGATTGAGTGTGTCCAGGAAGCAGTATGGGAAGCATATCGGATC 466  
Db 64 CTTCAAGCTTATTATAGATTGAGTGTGTCCAGGAAGCAGTATGGGAAGCATATCGGATC 123  
QY 467 TTTCTGGATCGCATCCCTGCACACAGGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAG 526  
Db 124 TTCTCGATCGCATCCCTGCACACAGGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAG 183  
QY 527 GAGACCTTCGCTCTTTGACATTTGAAAATCTTCAGCAATTCAGGAGCACTTCCAGGACCTTGGAT 586  
Db 184 GAGACCTTCGCTCTTTGACATTTGAAAATCTTCAGCAATTCAGGAGCACTTCCAGGAGCACTTGGAT 243  
QY 587 CTTCTCCAGCAGAGATAAAACAGAGAAGTTTCCCTGCAGAGAAAGATGAATATCTGCA 646  
Db 244 CTTCTCCAGCAGAGATAAAACAGAGAAGTTTCCCTGCAGAGAAAGATGAATATCTGCA 303  
QY 647 GAGAAGACATTTGGAGAGCTGGTGAACCATTTGTCATTTCAACAGCAATCTPACATTTCA 706  
Db 304 GAGAAGACATTTGGAGAGCTGGTGAACCATTTGTCATTTCAACAGCAATCTPACATTTCA 347  
QY 707 AAGACTTGGGCAGTATCTCTAAGAAACCCCTCAGAGAGCAATTTCAAGATGTTGCCAAGC 766  
Db 348 -----AGATGTTGCCAGC 361  
QY 767 TCTCACTTGGGCGCTTCCCTCTCACTCTCTGATGACACCCCTCTCAATGAAATTTCTCGATA 826

Db 362 TCTCACTTGGGCGCTTCCCTCTGATGACACCCCTCTCAATGAAATTTCTCGATA 421  
QY 827 ATACACTCAAGACACCAAGATGCTTCAACAGAAAGAGAAACAGAAATTCGCTGTGTGG 886  
Db 422 ATGCACTCAAGACACCAAGATGCTTCAACAGAAAGAGAAACAGAAATTCGCTGTGTGG 481  
QY 887 AGGAGCAGAGGGTGGAGCTCAGCGTCTCTCTGTTAAACCAAGATTTCAAGGACAGGCTCG 946  
Db 482 AGGAGCAGAGGGTGGAGCTCAGCGTCTCTCTGTTAAACCAAGATTTCAAGGACAGGCTCG 541  
QY 947 CTGACTCCCGAGTC 959  
Db 542 CTGACTCTCAGTC 554  
RESULT 9  
US-10-027-632-286848/c  
; Sequence 286848, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; POLYMORPHISMS IN THE HUMAN GENOME  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 286848  
; LENGTH: 596  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-286848

Query Match 6.1%; Score 204.6; DB 15; Length 596;  
Best Local Similarity 86.9%; Pred. No. 1.7e-44;  
Matches 225; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
QY 1 TAAACCAAGAGGTTATCCCTCAATCATCTCGTATCAATATATATATTTTTCACATTC 60  
Db 525 TAAACCAAGAGGTTATCCCTCAATCATCTCGTATCAATATATATATTTTTCACATTC 466  
QY 61 TGTACTTTTAAATGAGATTTGAGGTTGTTCTGTGATTTGTTATCAGAAATACCAATGCAC 120  
Db 465 TGTACTTTTAAATGAGATTTGAGGTTGTTCTGTGATTTGTTATCAGAAATACCAATGCAC 406  
QY 121 AAAGCCAGATGTAATTTGAAACTAGAGAGCTATTTTGTGTTTGGATTTTCTCCA 180  
Db 405 AAAGCCAGATGTAATTTGAAACTAGAGAGCTATTTTGTGTTTGGATTTTCTCCA 346  
QY 181 AGTTCAAGGAACCAAGATATCTCCATTAACATATACCATTTCTGAAACTAAAGACATAGA 240  
Db 345 AGTTCAAGGAACCAAGATATCTTAATCTTTTACITTTTAAATGCTTATCTATAA 286  
QY 241 CAATCCCCCAAGAAATGAA 259  
Db 285 ATCTACCGATAGAAGTGA 267



OTHER INFORMATION: Mouse IPW 200 cDNA sequence (partial)

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)..(4204)

OTHER INFORMATION: n is a, c, g, or t.

US-10-007-270-23

Query Match 5.9%; Score 197.8; DB 13; Length 4204;

Best Local Similarity 62.8%; Pred. No. 4.7e-42;

Matches 307; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 1877 GTTCTATGACATGTCCTCCCAAGCGGCGAGAGCTGTGGAGTCTCTTTCAGTCTCGGTG 1936

DB 2152 GTGTTCTGAGTCACACCGAGCTGCGAGCAATGGTGGTTCCTTCAGCCTCGCGTGA 2211

QY 1937 CTAACTGGGCTCTCCCAAGCTGTTCACAGAGCTCTCTGGAGTACCGAGCTCTGG 1996

DB 2212 CAACATGTTGTTTCAGAGACTGTTCACAAAACCTCTTTGGAATATAAAGCCCTGG 2271

QY 1997 AGCAACAATTACACAGCTGCTGTTCCATATCTACGATCCAACTCTTACAGGATTTAAGC 2056

DB 2272 AACAAAGATCTTAGAACTGCTGCTCCCTATCTCCAGTCAAACTCTCAGGCTCCAGA 2331

QY 2057 AACTGGAATACCTTAACCTCAGAAACGGGAGTGTGATGTGAATAGCAAAATGAAGTTG 2116

DB 2332 ACCTAGAAATCCCTGAGTTTCAGAAACGGCAGCATTTGTGTGAACCGAGTGGGTTGC 2391

QY 2117 CTAAGTCTGGCCGTATTAACCTCACCAGGCTGTGCACGGGGCTTGGAGGATTTTCGTT 2176

DB 2392 CCGAGTCTGCCCTCCTTAAGTGTACAAAGGCCATGTATAGGATCTTGGAGACTTTTGA 2451

QY 2177 CTGCTGAGGCCCAACAACTCCATCTGGAATAGACAGTACTCTCTCAACATTTGAACCG 2236

DB 2452 CCACTGCTACCAAAACCATGAATCTGATATCGAATAGTACTCCCTGGAGCTGGAATCAG 2511

QY 2237 CTGATCAAGCAGATCCCTGCAAGTCTCTGCGCTGGCGGATTTGCCAATGTGAAGA 2296

DB 2512 GTGATGAGGCCAACCCCTTGAAGTTTCAGGCTGTGAATGAATTTCTGAGTGTTCGTA 2571

QY 2297 ACGAACGGACTGAGGAAGCGAGTGTGCTGCAACCCAGGATATGACAGCCGGGAGGC 2356

DB 2572 ATCCATGGAGTGAGAGCAAGATGCAAAATGCTACCTGGGTACCTGAGTGTGGATGAC 2631

QY 2357 TGGACGCTC 2365

DB 2632 TGCCTTCTC 2640

RESULT 13

US-10-007-270-18

Sequence 18, Application US/10007270

Publication No. US20020160954A1

GENERAL INFORMATION:

APPLICANT: Hageman, Gregory S.

APPLICANT: Kuehn, Markus H.

APPLICANT: University of Iowa Research Foundation

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES

FILE REFERENCE: 020618-00012005

CURRENT APPLICATION NUMBER: US/10/007,270

CURRENT FILING DATE: 2001-11-08

PRIOR APPLICATION NUMBER: US 09/430,195

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 09/183,972

PRIOR FILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 18

LENGTH: 2964

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Human IPW 200 cDNA sequence, isoform C

US-10-007-270-18

Query Match 5.5%; Score 184.8; DB 13; Length 2964;

Best Local Similarity 66.1%; Pred. No. 1.2e-38;

Matches 267; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 1883 TGACCAATTGCCCCCAAGGCGGAGAGCTGGTAGTGTCTTCAGTCTCGGTGTGCTAACA 1942

DB 2520 TGAGTTATACCAGACTTCAGAGCTTTGGTGGTTCCTTCAGCTCCGAGTGACTAACA 2579

QY 1943 TGGCCCTCTCCAAAGACCTGTTCACAAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAAC 2002

DB 2580 TGATGTTTTTCAAGAGATCTGTTTAAATAAAACTCTCTGGAGTATAAAGCCCTGGAGCAA 2639

QY 2003 AATTCCACAGCTGCTGCTTCCATATCTACGATCCAACTCTTACAGGATTTTAAGCAACTTG 2062

DB 2640 GATTTTGAATGCTGTTCCCTATCTCCAGTCAAACTCTCAGGGTTCAGAACTTAG 2699

QY 2063 AAATATCTTAATCTCAGAAACGGGAGTGTGATTTGAAATAGCAAAATGAAGTTTCTAAGT 2122

DB 2700 AAATCTCTCAACTTCAGAAATGGCAGCAATTTGGTGAACAGTCAATGAAGTTTGCCTAAT 2759

QY 2123 CTGTGCGGTATATACCTCACCAGGCTGTGCACGGGGTCTTGGAGGATTTTCTGCTGCTG 2182

DB 2760 CTGTCCCTCTTAAAGTCAACCAATGCGGTGTACATGATTTCTGGAAGACTTTTGTACCCTG 2819

QY 2183 CAGCCCAACAACTCCATCTCGAAATAGACAGCTACTCTCTCAACATTTGAACCCAGCTGATC 2242

DB 2820 CCTACAAATACCACTTGGCTATTGATAAATACTCTCTTGATGTGAATCAGGTGATG 2879

QY 2243 AAGCAGATCCCTGCAAGTTCCTGCGCTCGCGGCAATTTGGCCAA 2286

DB 2880 AAGCAACCCCTTGAAGTTTCAGGCTGTATGAATTTTCAGAA 2923

RESULT 14

US-10-311-455-2147/c

Sequence 2147, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: PIERPNER, Kurt

APPLICANT: BERLIN, Kurt

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining

FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR APPLICATION NUMBER: PCT/EP01/07537

PRIOR FILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 2424

SEQ ID NO 2147

LENGTH: 113515

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-311-455-2147

Query Match

Best Local Similarity

Matches 193; Conservative

0; Mismatches 220; Indels

0; Gaps

0;

QY 2444 ATCACTCTGAAATCAAGCATACAAAACCTAGTGTAAAGTTCCAAAATCAACAAATA 2503

DB 51718 ATTAACAAAAA

QY 2504 ACAAGGTAATCAGTAAAGAAATTTCTGAATCTACGACCGTAGAATATGAAGAATTTAAC 2563

DB 51658 AAAAAA

QY 2504 ACAAGGTAATCAGTAAAGAAATTTCTGAATCTACGACCGTAGAATATGAAGAATTTAAC 2563

DB 51658 AAAAAA

QY 2504 ACAAGGTAATCAGTAAAGAAATTTCTGAATCTACGACCGTAGAATATGAAGAATTTAAC 2563

DB 51658 AAAAAA



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 14:09:16 ; Search time 230 seconds  
(without alignments)  
8034.724 Million cell updates/sec

Title: US-10-007-270-1  
Perfect score: 3330  
Sequence: 1 taaaccaagaaggttatcct.....tactatatgacataatcaat 3330

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	57.4	1.7	7218	1	US-08-232-463-14
C 2	44.8	1.3	5562	4	US-10-204-708-63
C 3	44.6	1.3	5852	1	US-07-867-106-2
C 4	43.6	1.3	6243	2	US-09-056-075-1
C 5	43.2	1.3	8607	4	US-10-204-708-72
C 6	43	1.3	1035	4	US-09-134-001C-687
C 7	42.6	1.3	1664976	4	US-08-916-421B-1
C 8	42	1.3	832	4	US-09-621-976-2813
C 9	41.6	1.2	7304	4	US-10-204-708-43
C 10	41.2	1.2	2244	4	US-10-204-708-2
C 11	41.2	1.2	10457	4	US-08-356-171B-270
C 12	40.8	1.2	640681	4	US-09-790-988-1
C 13	40.6	1.2	832	4	US-09-621-976-2813
C 14	40.2	1.2	4970	1	US-08-764-100-14
C 15	40.2	1.2	4970	1	US-08-764-100-20
C 16	40.2	1.2	63588	4	US-09-873-404-3
C 17	40	1.2	6306	4	US-10-204-708-50
C 18	39.8	1.2	580073	4	US-08-545-528D-1
C 19	39.6	1.2	6113	4	US-10-204-708-14
C 20	39.6	1.2	7218	1	US-08-232-463-14
C 21	39.6	1.2	19513	4	US-10-204-708-39
C 22	39.4	1.2	2429	3	US-09-386-493-3
C 23	39.2	1.2	2733	4	US-09-134-000C-1272
C 24	38.8	1.2	5152	4	US-10-204-708-74
C 25	38.8	1.2	8537	4	US-10-204-708-41
C 26	38.6	1.2	1310	4	US-09-721-870-110
C 27	38.6	1.2	5360	4	US-10-204-708-65

C 28	38.2	1.1	16550	4	US-08-916-421B-3
C 29	38.2	1.1	19124	2	US-08-487-826B-13
C 30	38.2	1.1	1664976	4	US-08-916-421B-1
C 31	37.8	1.1	1318	4	US-09-719-108-5
C 32	37.8	1.1	1696	4	US-09-835-811-1
C 33	37.8	1.1	2555	2	US-08-960-022-15
C 34	37.6	1.1	399	4	US-09-621-976-8976
C 35	37.6	1.1	5152	4	US-10-204-708-47
C 36	37.6	1.1	5610	4	US-10-204-708-54
C 37	37.6	1.1	6368	4	US-10-204-708-68
C 38	37.4	1.1	5455	4	US-10-204-708-34
C 39	37.4	1.1	5501	4	US-10-204-708-38
C 40	37.2	1.1	658	3	US-08-998-416-595
C 41	37.2	1.1	2223	1	US-08-257-073-4
C 42	37.2	1.1	6306	4	US-10-204-708-50
C 43	37.2	1.1	43360	4	US-09-453-702B-206
C 44	37.2	1.1	45325	4	US-09-453-702B-261
C 45	37	1.1	505	4	US-09-621-976-15639

## ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)693-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZgpt-F18  
; US-08-232-463-14

Query Match 1.7%; Score 57.4; DB 1; Length 7218;



[illegible]

```

RESULT 2
US-10-204-708-63/c
; Sequence 63, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 63
; LENGTH: 5562
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-63

```

[illegible]

RESULT 3  
 US-07-867-106-2/c  
 Sequence 2, Application US/07867106  
 Patent No. 5389526  
 GENERAL INFORMATION:  
 APPLICANT: Slade, Martin B  
 APPLICANT: Chang, Andy C M  
 APPLICANT: Williams, Keith L  
 TITLE OF INVENTION: Improved Plasmid Vectors for Cellular  
 TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526aris  
 STREET: One liberty Place 46th Floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/867,106  
 FILING DATE: 19920625  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: AU PJ 7187  
 APPLICATION NUMBER: PCT/AU90/00530  
 FILING DATE: 02-NOV-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Feeney, Joanne Longo  
 REGISTRATION NUMBER: 35,134  
 REFERENCE/POCKET NUMBER: RICE-0002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-568-3100  
 TELEFAX: 215-568-3439  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5852 base pairs  
 TYPE: NUCLEIC ACID

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2378..5038  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2378..5038  
US-07-867-106-2

Query Match 1.3%; Score 44.6; DB 1; Length 5852;  
Best Local Similarity 51.1%; Pred. No. 0.033;  
Matches 158; Conservative 0; Mismatches 144; Indels 7; Gaps 2;  
QY 42 TAATTATTTTCACATTCGTTACTTTTAAAGAGATTGAGTTGCTGTGATGTT 101  
Db 2065 TAATTATATTTATAATGAGGGTTTTTTTTTTTTTTTTTTTTTTTTCAAAGTA 2006  
QY 102 ATCAGAAATACCAATGCACAAAGCCAGAAATGTTTGGAACTAGAGAGCTATTTTG 161  
Db 2005 AAAAAAAGAAAAAAG 1951  
QY 162 TTTTGGATTTTTCRAAGTTCAAGGACCAAGATATCTCCATTAACATATACCAT 221  
Db 1950 TTTTATATATTTTGCATATTTTAAAGATAAATCTTTTAAATTTGATTTTAA 1893  
QY 222 CTGAATAAGACATAGACAAATCCCAAGAAATGAAACCACTGAAAGTCTGAAAAA 281  
Db 1892 ATGAGATCTATTAATAAAGAAAAAATTTTAAATTTAAAGAAAAAAGAAAAA 1833  
QY 282 TGTCAAAATGTCACATGAGACGAAATATTCGATTTGGCAAGCATCGAACAAAAAGAT 341  
Db 1832 AGTAAATTTTAAAGAAATTAATAATTTTCAATCTTAATAATTAAGTATATATCGAT 1773  
QY 342 CGCATTTT 350  
Db 1772 AGCAATTT 1764

RESULT 4  
US-09-056-075-1  
; Sequence 1, Application US/09056075  
; Patent No. 595368  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Eric A.  
; APPLICANT: Bradshaw, Marite  
; APPLICANT: Rood, Julian  
; TITLE OF INVENTION: Expression System for Clostridium  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles & Brady  
; STREET: 1 South Pinckney Street  
; CITY: Madison  
; STATE: WI  
; COUNTRY: US  
; ZIP: 53701-2113  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056,075  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seay, Nicholas J.  
; REGISTRATION NUMBER: 27386  
; REFERENCE/DOCKET NUMBER: 960296.95238  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6243 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 3770..4013  
; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from  
; plasmid RP4"  
US-09-056-075-1

Query Match 1.3%; Score 43.6; DB 2; Length 6243;  
Best Local Similarity 55.2%; Pred. No. 0.069;  
Matches 85; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
QY 2453 AAATCAAGCATACAAACTAGTGTAAAAAGTTCCAAATCAACAAATACCAAGTAA 2512  
Db 1229 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAA 1288  
QY 2513 TCAGTAAAGAAATTCGAATTTACTGACCGTAGAATATGAAGATTTTAAACCATCAAGATT 2572  
Db 1289 AAATATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA 1348  
QY 2573 GGAAGAAATTAATAAACTGAAATGTACAAATTA 2606  
Db 1349 TATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATA 1382

RESULT 5  
US-10-204-708-72/c  
; Sequence 72, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication  
; TITLE OF INVENTION: by Assessing DNA Methylation  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/204,708  
; CURRENT FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 72  
; LENGTH: 8607  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-72

Query Match 1.3%; Score 43.2; DB 4; Length 8607;  
Best Local Similarity 50.4%; Pred. No. 0.11;  
Matches 131; Conservative 0; Mismatches 128; Indels 1; Gaps 1;  
QY 2454 AAATCAAGCATACAAACTAGTGTAAAAAGTTCCAAATCAACAAATACCAAGTAA 2513  
Db 7055 AAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAA 6996

QY 2514 CAGTAAAGAAATCTGAATTACTGACGCTAGATATGAAGAATTTAAACCATCAAGATTG 2573  
DB |||||  
6995 AAAAAAAAAAAAAAAAAAATAAACAATATACAAATAAATAAACAATATAACATA 6936  
QY 2574 GGAAGGAAATTAATAAATGTAACAATTA-TCATTAGGCTATCTCAAGAGAGATG 2632  
DB |||||  
6935 CAAATTTCTTCACTATATACTCAATCTCAATCTCTTTTACCAATCTTATTAAAAATA 6876  
QY 2633 ATTTCCTTCAAGGAAATGAGACAGCATATTCATGGGTCATCAAAATCCAGACAT 2692  
DB |||||  
6875 TTTTAACTTAACGGATTAATACATCTATATCCCACTTTTAAAAAACTAAAT 6816  
QY 2693 ACATCAACATGGAATCA 2712  
DB |||||  
6815 AAAGCAATCACCTAAATCA 6796

## RESULT 6

US-09-134-001C-687  
; Sequence 687, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134.001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 687  
; LENGTH: 1035  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-687

Query Match 1.3%; Score 43; DB 4; Length 1035;

Best Local Similarity 48.9%; Pred. No. 0.031;

Matches 115; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 94 TGATTGTATCAGAAATACCAATCCACAAAGCCAGATCTATTGGAACTAGAGAGC 153  
DB |||||  
738 TGAACGCTATCTTTGACAAAGGCGATTGAAATATGAATCGGGAAGAACCAAGCCA 797  
QY 154 TATTTTGTGTTTGTGATTTTCTCCAAAGTTCAAGGACCAAGATATCTCCATTAAACAT 213  
DB |||||  
798 AAAGATTTTAAACAATATTGTTAAGCAATTAAGAGATATAAGTGAATAATTTTAAAT 857  
QY 214 ATACATCTGAAACTAAAGACATAGACATCCCCGAAAGAAATGAACAACACTGAAAGTAC 273  
DB |||||  
858 AGAAGAAATGATCTCTATAAGTAGCAGATACGGTAAAGAAAGAGACAAATCTTAAAC 917  
QY 274 TGAAGAAATGTACAAATGTCAACTATGAGACGAATATTCGATTGGCAAGCAT 328  
DB |||||  
918 AATTAATTTTACATATGCGATACACACAAACAAAGATGATGACACCAAT 972

## RESULT 7

US-08-916-421B-1/c  
; Sequence 1, Application US/08916421B  
; Patent No. 6503729  
; GENERAL INFORMATION:  
; APPLICANT: Bulc et al.  
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco  
; TITLE OF INVENTION: jannaschii  
; FILE REFERENCE: PB275  
; CURRENT APPLICATION NUMBER: US/08/916.421B  
; CURRENT FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: US 60/024,428

; PRIOR FILING DATE: 1996-08-22  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 1664976  
; TYPE: DNA  
; ORGANISM: Methanococcus jannaschii  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (28222)..(28222)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (28257)..(28258)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (84773)..(84773)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (84808)..(84808)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (84812)..(84812)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (98120)..(98120)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (98159)..(98159)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (98239)..(98239)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (98266)..(98266)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (98343)..(98343)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (103998)..(103998)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (163385)..(163385)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (191989)..(191989)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (191995)..(191995)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (231980)..(231980)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (234187)..(234187)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (234220)..(234220)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (234814)..(234814)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (309398)..(309398)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (309418)..(309418)  
; OTHER INFORMATION: n equals a, t, c, or g  
; NAME/KEY: misc feature  
; LOCATION: (312837)..(312837)

```

; NAME/KEY: misc_feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

Query Match      1.3%; Score 42.6; DB 4; Length 1664976;
Best Local Similarity 44.9%; Pred. No. 6;
Matches 162; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 2928 TTATTGTTTAGGGACTGAACAATTATTGGGAAGCAAACTCTTTATATGCTAGAAAGTAC 2987
DB 710981 TTATTTCCATGGTATTCCACACTTTAGATTATTGCTAACTTCATCAACATTAAACTATA 710982

QY 2988 ATTTAAAGATGACACTATTAGCGAGGAGATGCAAGTCTCTCTAAAGCGCATGAATGTATG 3047
DB 710921 ACATAACCAATGACAAACAAACGGAACAAATGGGTAGGTTTTTATATACATTTAGTTGTCA 710862

QY 3048 TAGTGTGTAGGCACGTGAGTGAGTGATATATGCTCCACACTACGCTGTGATAACACAAA 3107
DB 710861 GGAATTTTCCCTCCATATAGAGTTTTTATTTTTCGAATGCTTCATTGGATAACCCCT 710802

QY 3108 CTTCAAGTATTCAAGTTATTAGGCACACTAGTTTTTATACGCAACTACTGCTTACATAGTAGA 3167
DB 710801 TCTCCATCGGTTAATATTATTTCCTTTTCATTTCTTTGATTTTCATGTTCTATAGAAAT 710742

QY 3168 CTGTTTCTTGCCCAATACTTTGAATGTCTTTAAAGAAACTAGGTTCAAGATACAC 3227
DB 710741 TTTATCTTTTCATTTATATTATTTAAGTTTTTTTACCTCAACACCATCTTTGTCTATTATATA 710692

QY 3228 ATACCATGGAAAAATCTTACTTTTCTTGTTTACTACACAAAGCTATTTTAAAGAAAGATGCT 3287
DB 710681 ACATCCCTCAAAATATCTCCTTCTTTTAACTTCATATGTTTTTTCAGAGAGTTCT 710622

QY 3288 A 3288
DB 710621 A 710621

RESULT 8
US-09-621-976-2813/c
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

```



```
;
;
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 270:
US-08-956-171E-270

Query Match      1.2%; Score 41.2; DB 4; Length 2244;
Best Local Similarity 54.7%; Pred. No. 0.18;
Matches 82; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 2447 ACTCTGAAATCAAGCATACAAACTAGTCTTAAAGATTCCAAATCAACAAATAACA 2506
Db 518 ATTATATAATAGATCAATGACGACAGTATTTATATGATGGATTAATAAAGAAACTA 577

QY 2507 AGTAAATCAGTAAAGAAATCTGAATCTAGCCGTAGAAATGAAGAAATTTAACATC 2566
Db 578 AGTAAACGAAACAAAGAAATTTTGTGTTTTTAAATACGTGAATAAAGATTATTGATATA 637

QY 2567 AAGATTCGGAGGAAATTTAAAACTGAAA 2596
Db 638 AAGTTTTCAAAGTTATACAAAGATAA 667

RESULT 11
US-10-204-708-2/c
; Sequence 2, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 2
; LENGTH: 10467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-2

Query Match      1.2%; Score 41.2; DB 4; Length 10467;
Best Local Similarity 45.4%; Pred. No. 0.5;
Matches 186; Conservative 0; Mismatches 223; Indels 1; Gaps 1;

QY 2447 ACTCTGAAATCAAGCATACAAACTAGTCTTAAAGATTCCAAATCAACAAATAACA 2506
Db 8253 ACTAATAAAATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8194

QY 2507 AGGTAATCAGTAAAGAAATCTGAATCTAGCCGTAGAAATGAAGAAATTTAACATC 2566
Db 8193 AAAAACAACGTAAATAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8134

QY 2567 ARGATTGGGAAGAAATTTAAATACTGAAATGTAATATATCACTTAGGCTATCTCAAG 2626
Db 8133 TATTTCGATTAATCGCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8075

QY 2627 GAGATGATTTGGCTTCTCAAGGAATGAGACAGCATATTCATGGGTATCAAAATCC 2686
Db 8074 CAAATATTTTAAATTTATTCAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8015
```

```
QY 2687 AGACATACAGTCAACACTGAGAATCAGCACACACCATATTTTCATATATAGAGAGTCATG 2746
Db 8014 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 7955

QY 2747 TACTTGGCAACAGTAAATCTGAAAAAAGACACACTTACTTATTTAAACCCCAAT 2806
Db 7954 ATAAATATAACTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 7895

QY 2807 GCATCAGCGAAACATATTTTACTATTTCTTGGATGATAGTCAAAATCAT 2856
Db 7894 TTCTCCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 7845

RESULT 12
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match      1.2%; Score 40.8; DB 4; Length 640681;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 130; Conservative 0; Mismatches 127; Indels 3; Gaps 1;

QY 45 TTATTTTTCACATTTCTGTTACTTTTAAATGAGATTTGAGTCTGTTGTTGTTATC 104
Db 29756 TTCTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 297815

QY 105 AGAATTACCAATGCACAAAGCCAGAAATGTATTTGGAACTAGAGAGCTATTTTGT 164
Db 297816 AGAATTTCTAAGAAACATTTCTCGTGAATGTACACGAGTGTACGAATATTAGAA 297875

QY 165 TTTGATTTTCTCCAGTTCAAGAACCAAGATATCTCCATTAACATATACCATTTCTG 224
Db 297876 TTTAGTATTTCTCATTCATCATCATGTTCTCAT---TATATCCGTTCAAGGTAA 297932

QY 225 AAATCAAGACATAGACAAATCCCAAGAAATGAAACAACTGAAAGTACTGAAAAATGT 284
Db 297933 TTACTTAAATAATTAATATCAAAATGAGAAATTAATATTTTATATATTAAAGAA 297992

QY 285 ACAAAATGTCAACTATGAGA 304
Db 297993 GATTATTAAACATATAAAA 298012
```

```
RESULT 13
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
```



```
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match
Best Local Similarity 12.5%; Score 40.6; DB 4; Length 832;
Matches 47; Conservative 176; Mismatches 150; Indels 2; Gaps 2;

QY 2920 TAGCTTACTTATTTAGGACCTGGAACAATTTATGCGAAGCAAACTCTTTATATGCTA 2979
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
5 WKKYTTWYAKWTWKWSWSYMMYKWKYKWTYWRWRKKKWKWKYKWTWTWYWRYYAM 64
QY 2980 GAAAGTACATTTAAAGATGACTTACGACGAGATGAGTCTCTCTAAACGCA-T 3038
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65 WGTYYKKAMCKTKKKKKGGYMMWMTGWGWSRSMAMWTWTGYAYYSMMYKWTWYRCW 124
QY 3039 GAATGTATGTAGTGTAGGACCTGTAGTGTAGTGTATATGCTCCACACTACGCTGTAT 3098
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
125 KKKAYYRKTTCYSSKGTWKKWKKAWTTWKKTYWAAATRYMMWCMWTKRWASWNYC 184
QY 3099 AAACACAACTCAGTATCA-GTTATTAGGCACACTAGTATTTATACGCACTACTGCTT 3157
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
185 WWMGKARKSTWRKRSYASARSAXRCCYSCSGWMSWKYMWWRWWRWGTAGWKAMR 244
QY 3158 ACATAGTAGACTGTTTGTGCGCAATTAATCTTTGAATGTTCTTTAAAGAAACTGAGGT 3217
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
245 ASCWRRKYAGKSKTSYKSMWYCWTRSKYCYTKARWTGYCYRKGMMGKRGRWYASKK 304
QY 3218 TCAGATACATACCATGGGAAAATCTTCTTCTTCTTACTACACAAAGCTATTTTAA 3277
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
305 YMKRWKWCWARMYRYSTGTGRASMMRRWYTYWMMKWKYAWARAAMWMMWAWERAC 364
QY 3278 AGAAGATGCTATGTT 3292
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
365 AAAATATAATATTT 379

RESULT 14
US-08-764-100-14
; Sequence 14, Application US/08764100
; Patent No. 5773700
; GENERAL INFORMATION:
; APPLICANT: van Grinsven J., Martinus Q.
; APPLICANT: De Haan, Petrus T.
; APPLICANT: Gielen L., Johannes J.
; APPLICANT: Peters, Dirk
; APPLICANT: Goldbach, Robert W.
; TITLE OF INVENTION: Improvements in or Relating to Organic
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sandoz Agro, Inc
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,100
; FILING DATE: 06-DEC-1996

; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US/08/214,064
; FILING DATE:
; APPLICATION NUMBER: US 08/032,235
; FILING DATE: 17-MAR-1993
; APPLICATION NUMBER: GB 9206016.9
; FILING DATE: 19-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5773700ris, Allen E.
; REGISTRATION NUMBER: 34,490
; REFERENCE/DOCKET NUMBER: 137-1061
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 354-3592
; TELEFAX: (415) 857-1125
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-764-100-14

Query Match
Best Local Similarity 1.2%; Score 40.2; DB 1; Length 4970;
Matches 155; Conservative 0; Mismatches 173; Indels 1; Gaps 1;

QY 23 ATCATCTCGTATCAATATATATATTTTTCACATTTCTGTACTTTTAAATGAGATTG 82
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
976 ATCATTTGATTAATGAATCTAAATATGTTTCATTTTAAATAATAATATATATATAT 1035
QY 83 AGGTTGTTCTGTGATGTATCAGAAATACCAATGCGACAAAGCCAGAAATGTTTGGAA 142
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1036 ATAATATTTTG-AATGTTTAAGTAAAAATAAAGCAAGATAAAAAAACTATATATAT 1094
QY 143 ACTAGAAGAGCTATTTTGTGTTTGGATTTTCTCCAGTTTCAAGGAACCAAGATATC 202
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1095 ATATATGAAGTATAAATATATATATGTTTGTGTTTAAATAACAAATCAAAACCAA 1154
QY 203 TCCATTATACATATACCAATCTTGAACCTAAAGACATAGACATCCCAAGAAATGAAACA 262
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1155 AGAAAAAGAAAAAATAAACAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAA 1214
QY 263 ACTGAAAGTACTGAAAAATGTACAAATGTCAACTATGAGACGAAATATTCGATTGCA 322
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1215 AATGAAAAAGTTGAAAAAACCAAAAAACAAAAAAATTTTTTGTAAATAATAAAGGCTCCGGC 1274
QY 323 AAGCATCGAACAAAAAGATCCGCAATTTT 351
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1275 CAGATTTCGTCTAGACCTTTTATTGT 1303

RESULT 15
US-08-764-100-20/c
; Sequence 20, Application US/08764100
; Patent No. 5773700
; GENERAL INFORMATION:
; APPLICANT: van Grinsven J., Martinus Q.
; APPLICANT: De Haan, Petrus T.
; APPLICANT: Gielen L., Johannes J.
; APPLICANT: Peters, Dirk
; APPLICANT: Goldbach, Robert W.
; TITLE OF INVENTION: Improvements in or Relating to Organic
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sandoz Agro, Inc
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,100  
FILING DATE: 06-DEC-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/214,064  
FILING DATE:  
APPLICATION NUMBER: US 08/032,235  
FILING DATE: 17-MAR-1993  
APPLICATION NUMBER: GB 9206016.9  
FILING DATE: 19-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5773700ris, Allen E.  
REGISTRATION NUMBER: 34,490  
REFERENCE/DOCKET NUMBER: 137-1061  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 354-3592  
TELEFAX: (415) 857-1125  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4970 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-764-100-20

Query Match 1.2%; Score 40.2; DB 1; Length 4970;  
Best Local Similarity 47.1%; Pred. No. 0.6;  
Matches 155; Conservative 0; Mismatches 173; Indels 1; Gaps 1;

QY	23	ATCATCTGGTATCAATATATATATTTTTCACATTTCTGTTACTTTTAAATGAGATTG	82
Db	3995	ATCATTTGATTAAGCAATCTAAATATGTTTTCATTTAAATAATAATATATATATGTTTC	3936
QY	83	AGGTTGTTCTGCGATTGTTTATCAGAAATACCAATGCACAAAGCCAGAAATGTTTGGAA	142
Db	3935	ATAATATTTTG-AATGTTTAAAGTAAATAATAAGCAAGATAAAAACTATATATATAT	3877
QY	143	ACTAGAGAGCTATTTTGTGTTTTCAGATTTCCTCAGTTTCAGGACCAAGATATC	202
Db	3876	ATATAGAGGTATAAAATATATATATGTTTGTGTTTAAAAACAAATCAAAACCAAAA	3817
QY	203	TCCATTAAACATATACCATCTGAAACTGAAACATAGACAAATCCCCAGAAATGAACA	262
Db	3816	AGAAAAAGAAAAATAACAAAAACAAAAACAAAAACAAAAACAAAAACAAAA	3757
QY	263	ACTGAAAGTACTGAAAAATGTACAAAATGTCAACTATGAGACGAATATTCGATTGGCA	322
Db	3756	AATGAAAAAAGTTGAAAAAACCAAAAAAATTTTTTTGTAATAATAAAGGCTCCGGC	3697
QY	323	AGCATCGAACAAAAAGATCCGCATTTT	351
Db	3696	CAGATTGGTCTAAGACCTTTTATTGT	3668

Search completed: March 1, 2004, 20:33:06  
Job time : 241 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 12:39:45 ; Search time 1245 Seconds  
(without alignments)  
11362.650 Million cell updates/sec

Title: US-10-007-270-1

Perfect score: 3330

Sequence: 1 taaacaagaaggttatctct.....tactatatgacataatcaat 3330

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373963 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*

1: Geneseq\_1980s:\*

2: Geneseq\_1990s:\*

3: Geneseq\_2000s:\*

4: Geneseq\_2001as:\*

5: Geneseq\_2001bs:\*

6: Geneseq\_2002s:\*

7: Geneseq\_2003as:\*

8: Geneseq\_2003bs:\*

9: Geneseq\_2003cs:\*

10: Geneseq\_2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3330	100.0	3330	7	ADAL4840 Human int
2	3330	100.0	3330	8	ACC57946 Human int
3	3125.6	93.9	3263	3	AAA46205 CDNA enco
4	3124.6	93.8	3261	7	ADAL4866 Human cdn
5	3124.6	93.8	3261	8	ACC57960 Human int
6	2765.8	83.1	2887	7	ADAL4842 Human int
7	2765.8	83.1	2887	8	ACC57947 Human int
8	2724.6	81.8	2966	3	AAA46328 Interphot
9	2184.2	65.6	2244	3	AAA46329 Interphot
10	2184.2	65.6	2244	7	ADAL4844 Human int
11	2184.2	65.6	2244	8	ACC57948 Human int
12	1375.6	41.3	3668	7	ADAL4847 Mouse int
13	1375.6	41.3	3668	8	ACC57950 Mouse int
14	1127.2	33.8	3206	3	AAA46309 CDNA enco
15	534	16.0	1726	7	ADAL4849 Mouse int
16	534	16.0	1726	8	ACC57951 Mouse int
17	491.6	14.8	1321	7	ADAL4851 Mouse int
18	491.6	14.8	1321	8	ACC57952 Mouse int
19	439	13.2	555	3	AAA46204 CDNA enco
20	439	13.2	555	7	ADAL4853 Monkey in
21	439	13.2	555	8	ACC57953 Monkey in
22	204.6	6.1	1858	3	AAA46327 Exon 1 an
23	204.6	6.1	1858	7	ADAL4846 Human int

24	204.6	6.1	1858	8	ACC57949 Human int
25	203.4	6.1	4165	3	AAA46206 CDNA enco
26	203.4	6.1	4166	7	ADAL4855 Human int
27	203.4	6.1	4166	8	ACC57954 Human int
28	197.8	5.9	4204	3	AAA46310 CDNA enco
29	197.8	5.9	4204	7	ADAL4862 Mouse int
30	197.8	5.9	4204	8	ACC57958 Mouse int
31	184.8	5.5	2964	7	ADAL4857 Human int
32	184.8	5.5	2964	8	ACC57955 Human int
33	103	3.1	1094	3	AAA46321 Exon 13 o
34	61.8	1.9	1088	3	AAA46312 Exon 3 of
c	61	1.8	113515	6	ABL34174 Human imm
36	60	1.8	60	6	ABN43651 Human spl
37	57.6	1.7	1817	3	AAA46320 Exon 12 o
38	56.4	1.7	434	5	ABV58531 Human pro
c	54.6	1.6	3683	7	ABZ10199 Haematopo
c	54	1.6	16633	6	ABN79984 Human che
c	53.2	1.6	6255	6	ABL32960 Human imm
c	52.6	1.6	516	7	ABX40620 Bovine ES
c	52.6	1.6	6775	6	ABQ67159 Human ang
c	52.2	1.6	2000	7	ADA71938 Rice gene
c	52.2	1.6	5586	6	ABK40004 Human che

## ALIGNMENTS

### RESULT 1

ADAL4840

ID ADAL4840 standard; cdna; 3330 BP.

XX

AC ADAL4840;

XX

DT 06-NOV-2003 (first entry)

XX

DE Human interphotoreceptor matrix component, IPMC, 150 isoform A cdna.

XX

KW ss; gene; human; IPMC 150 isoform A; gene therapy;

KW interphotoreceptor matrix component; IPMC; ocular disorder;

KW macular degeneration; photoreceptor death; retinal detachment.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS

FT 131..2586

FT /\*tag= b

FT /product= "IPMC 150 isoform A"

FT /transl\_except= (pos:689..756,aa:Thr-Asp)

FT sig\_peptide

FT 131..190

FT /\*tag= a

FT mat\_peptide

FT /label= Signal\_sequence

FT 191..2583

FT /\*tag= c

FT /label= Mature\_IPMC\_150\_isoform\_A

FT misc\_feature

FT 692..753

FT /\*tag= d

FT /note= "This region could represent intronic sequence not removed from the cdna sequence"

US2002160954-A1

31-OCT-2002.

08-NOV-2001; 2001US-00007270.

29-OCT-1998; 98US-00183972.

29-OCT-1999; 99US-00430195.

(IOWA ) UNIV IOWA RES FOUND.

Hageman GS, Kuehn MH;

WPI; 2003-238235/23.

DR P-PSDB; ADA14841.  
XX New isolated or recombinant interphotoreceptor matrix component  
PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
PT treating or prognosticating ocular disorders, e.g. macular degeneration  
PT or retinal detachment.  
XX  
XX  
PS Claim 3; Page 29-30; 76pp; English.  
XX  
CC The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
CC gene operatively linked to the IPMC polynucleotide. The IPMC  
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
CC preventing, treating or prognosticating ocular disorders, e.g. macular  
CC degeneration, photoreceptor death or retinal detachment. They are also  
CC useful for identifying a compound capable of modulating IPMC gene  
CC expression in a cell. The present sequence represents cDNA encoding human  
CC interphotoreceptor matrix component, IPMC, 150 isoform A.  
XX  
SQ Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 3330; DB 7; Length 3330;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TAAACCAAGAGGTATCTCTCAATCATCTGGTATCATATATATATATTTTTCACATTTTC 60  
DB 1 TAAACCAAGAGGTATCTCTCAATCATCTGGTATCATATATATATATTTTTCACATTTTC 60  
  
QY 61 TGTACTTTTAAATGAGATTGAGTTGTTCTCTGATGTTGTTATCAGAAATACCAATGAC 120  
DB 61 TGTACTTTTAAATGAGATTGAGTTGTTCTCTGATGTTGTTATCAGAAATACCAATGAC 120  
  
QY 121 AAAAGCCAGATGTTTGAAGTACTAGAGAGCTATTTTGTGTTTGTGATTTTCTCCA 180  
DB 121 AAAAGCCAGATGTTTGAAGTACTAGAGAGCTATTTTGTGTTTGTGATTTTCTCCA 180  
  
QY 181 AGTTCAAGGAACCAAGATATCTCCATTAACATATACCATCTTGAACCTAAAGACATAGA 240  
DB 181 AGTTCAAGGAACCAAGATATCTCCATTAACATATACCATCTTGAACCTAAAGACATAGA 240  
  
QY 241 CAATCCCCCAAGAAATGAACCAATGAAGTACTGAAATAATGTACAAAATGTCAACTAT 300  
DB 241 CAATCCCCCAAGAAATGAACCAATGAAGTACTGAAATAATGTACAAAATGTCAACTAT 300  
  
QY 301 GAGACGAATATTCGATTGGCAAGCATCGAACAAAGATCCGCAATTTTCCCAACGGG 360  
DB 301 GAGACGAATATTCGATTGGCAAGCATCGAACAAAGATCCGCAATTTTCCCAACGGG 360  
  
QY 361 GGTTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTATAGACAGTCTTCAAGCTTATTA 420  
DB 361 GGTTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTTATAGACAGTCTTCAAGCTTATTA 420  
  
QY 421 TAGATTGAGAGTGTGTCAGAGAGCATATGGGAAGCATATCGGATCTTTCTGGATCGCAT 480  
DB 421 TAGATTGAGAGTGTGTCAGAGAGCATATGGGAAGCATATCGGATCTTTCTGGATCGCAT 480  
  
QY 481 CCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCGACAGAGACCTTCTGCCT 540  
DB 481 CCCTGACACAGGGGAATATCAGGACTGGGTGAGCATCTGCGACAGAGACCTTCTGCCT 540  
  
QY 541 CTTTGGACATTGGAAAAAATTTAGCAATTTCCAGAGAGCACTTGGATCTTCTCAGCAGAG 600  
DB 541 CTTTGGACATTGGAAAAAATTTAGCAATTTCCAGAGAGCACTTGGATCTTCTCAGCAGAG 600  
  
QY 601 AATTAACACAGAGAGTTTCCCTGACAGAAAGATGAAATATCTGACAGAGACATTTGGG 660  
DB 601 AATTAACACAGAGAGTTTCCCTGACAGAAAGATGAAATATCTGACAGAGACATTTGGG 660  
  
QY 661 AGAGCCTGGTGAACCAATGTCTATTTCAACAGCAATCTTACATTTCAAGACTTTGGGCAGT 720  
DB 661 AGAGCCTGGTGAACCAATGTCTATTTCAACAGCAATCTTACATTTCAAGACTTTGGGCAGT 720

QY 721 ATTCTAAGAAAAACCTCTCAGAAGAGCAAAATTCAGATGTTGCCAACGTTCTCACTTGGGCCT 780  
DB 721 ATTCTAAGAAAAACCTCTCAGAAGAGCAAAATTCAGATGTTGCCAACGTTCTCACTTGGGCCT 780  
  
QY 781 TTCCCTCTCACTCTGATGACACCCCTCCTCAATGAAATTTCTCGATAATACACTCAACGAC 840  
DB 781 TTCCCTCTCACTCTGATGACACCCCTCCTCAATGAAATTTCTCGATAATACACTCAACGAC 840  
  
QY 841 ACCAAGATGCTCAACACAGAAAGAAACAGAAATTCGCTGTGTTGGAGGAGAGAGGTG 900  
DB 841 ACCAAGATGCTCAACACAGAAAGAAACAGAAATTCGCTGTGTTGGAGGAGAGAGGTG 900  
  
QY 901 GAGTCAGCTCTCTCTGTTAAACCAAGATTCAGGACAGAGCTCGTGTGCTCCAGTCC 960  
DB 901 GAGTCAGCTCTCTCTGTTAAACCAAGATTCAGGACAGAGCTCGTGTGCTCCAGTCC 960  
  
QY 961 CCATATTACCAAGAGAGCTAGCAGAGAAAGTCCCACTTCAGATGCAAAAAGATATTTAAGAAA 1020  
DB 961 CCATATTACCAAGAGAGCTAGCAGAGAAAGTCCCACTTCAGATGCAAAAAGATATTTAAGAAA 1020  
  
QY 1021 CTTCCAGATTCAAAAAATTCATGTTAGGATTTAGACCAAAAGAAAGAAAGATGGC 1080  
DB 1021 CTTCCAGATTCAAAAAATTCATGTTAGGATTTAGACCAAAAGAAAGAAAGATGGC 1080  
  
QY 1081 TCAAGCTCCACAGAGATGCAACTTTACGGCCATCTTTAAGAGACACAGCTGCAGAGCAAAA 1140  
DB 1081 TCAAGCTCCACAGAGATGCAACTTTACGGCCATCTTTAAGAGACACAGCTGCAGAGCAAAA 1140  
  
QY 1141 AGCCTCGAAGTACCTCTGTTTGAATTCACAAATAATGAAAGTGAAGAGTCTAT 1200  
DB 1141 AGCCTCGAAGTACCTCTGTTTGAATTCACAAATAATGAAAGTGAAGAGTCTAT 1200  
  
QY 1201 CATCGAACCTGGAGGAGGACAGCAACAGAAATCTATCTCAGCTACAGACCTCAA 1260  
DB 1201 CATCGAACCTGGAGGAGGACAGCAACAGAAATCTATCTCAGCTACAGACCTCAA 1260  
  
QY 1261 AGGCTGATCAGCAAGCACTAGAGGAGAAACAATCTTTGGATGTGGGACAATTCAGTTTC 1320  
DB 1261 AGGCTGATCAGCAAGCACTAGAGGAGAAACAATCTTTGGATGTGGGACAATTCAGTTTC 1320  
  
QY 1321 ACTGATGAATTCGTGATCACTGCGAGCCTTTGGTCTCAGACCCCAATCAGAGCTGCC 1380  
DB 1321 ACTGATGAATTCGTGATCACTGCGAGCCTTTGGTCTCAGACCCCAATCAGAGCTGCC 1380  
  
QY 1381 ACATCTTTTGTGTTATAACAGAGGATGTACTTTGAGTCCAGAACTTCTCTCTGTTGAA 1440  
DB 1381 ACATCTTTTGTGTTATAACAGAGGATGTACTTTGAGTCCAGAACTTCTCTCTGTTGAA 1440  
  
QY 1441 CCCAGCTTGAGACAGTGGACGAGAGAGATGTTCTACCTGACACTTCTGTTCTCCA 1500  
DB 1441 CCCAGCTTGAGACAGTGGACGAGAGAGATGTTCTACCTGACACTTCTGTTCTCCA 1500  
  
QY 1501 CCTGCTATGGCCTCTACCTCCCTGTCAGAGAGCTCCACTTTTATGGCATCAAGCATC 1560  
DB 1501 CCTGCTATGGCCTCTACCTCCCTGTCAGAGAGCTCCACTTTTATGGCATCAAGCATC 1560  
  
QY 1561 TTCTCTCTGATGATCAAGGACCAACAGATACAATGGCCACTGACCAACAATGCTAGTA 1620  
DB 1561 TTCTCTCTGATGATCAAGGACCAACAGATACAATGGCCACTGACCAACAATGCTAGTA 1620  
  
QY 1621 CCAGGCTCACCATCCCAACAGTATTTCTGCAATCAGCCAACTGGCTCTGGGAAT 1680  
DB 1621 CCAGGCTCACCATCCCAACAGTATTTCTGCAATCAGCCAACTGGCTCTGGGAAT 1680  
  
QY 1681 TCACATCCACCTGATCTTCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGATATGGTC 1740  
DB 1681 TCACATCCACCTGATCTTCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGATATGGTC 1740  
  
QY 1741 AGACACCTAGATGAATGGATCTGTCTGACACTCTGTCGCCCATCTGAGGTACAGAGCTC 1800  
DB 1741 AGACACCTAGATGAATGGATCTGTCTGACACTCTGTCGCCCATCTGAGGTACAGAGCTC 1800

```
QY 1801 AGCGAATATGTTTCTGTCGCCGATCATTTCTTGGAGGATACCACTCCTGTCTCAGCTTTA 1860
Db 1801 AGCGAATATGTTTCTGTCGCCGATCATTTCTTGGAGGATACCACTCCTGTCTCAGCTTTA 1860
QY 1861 CAGTATATCACCACATAGTTCTATGACCACTTGCCCCCAAGGGCCGAGAGCTGTTAGTGTTC 1920
Db 1861 CAGTATATCACCACATAGTTCTATGACCACTTGCCCCCAAGGGCCGAGAGCTGTTAGTGTTC 1920
QY 1921 TTCAGTCTGCGTGTCTTAAACATGAGCTTCTTCAAGACCTGTTTCAACAAGAGCTCTCTG 1980
Db 1921 TTCAGTCTGCGTGTCTTAAACATGAGCTTCTTCAAGACCTGTTTCAACAAGAGCTCTCTG 1980
QY 1981 GAGTACCGAGCTCTCGAGCAACAATTCACAGCTGCTGCTTCCATATCTACGATCCAAAT 2040
Db 1981 GAGTACCGAGCTCTCGAGCAACAATTCACAGCTGCTGCTTCCATATCTACGATCCAAAT 2040
QY 2041 CTTACAGGATTTAAGCAACTTGAATACTTAACCTTCAGAAACGGGAGTGATGTGAAT 2100
Db 2041 CTTACAGGATTTAAGCAACTTGAATACTTAACCTTCAGAAACGGGAGTGATGTGAAT 2100
QY 2101 AGCAAAATGAAGTTTGTCTGCTGCGGATACAGCTGCTGCTTCCATATCTACGATCCAAAT 2160
Db 2101 AGCAAAATGAAGTTTGTCTGCTGCGGATACAGCTGCTGCTTCCATATCTACGATCCAAAT 2160
QY 2161 TTGGAGGATTTTGTCTGCTGCGGATACAGCTGCTGCTTCCATATCTACGATCCAAAT 2220
Db 2161 TTGGAGGATTTTGTCTGCTGCGGATACAGCTGCTGCTTCCATATCTACGATCCAAAT 2220
QY 2221 CTCACATTTGAACAGCTGATCAGCAGATCCCTGCAAGTTTCTTGGGCTGGGGCAATTT 2280
Db 2221 CTCACATTTGAACAGCTGATCAGCAGATCCCTGCAAGTTTCTTGGGCTGGGGCAATTT 2280
QY 2281 GCCCAATGTGAAGAACGAGCTGAGGAGCGGAGTGTCTGCTGCAAAACAGGATAT 2340
Db 2281 GCCCAATGTGAAGAACGAGCTGAGGAGCGGAGTGTCTGCTGCAAAACAGGATAT 2340
QY 2341 GACAGCCAGGGAGCTGGAAGCTGTGGAACAGGCTCTGTGGCCCTGGGCACAAAGAA 2400
Db 2341 GACAGCCAGGGAGCTGGAAGCTGTGGAACAGGCTCTGTGGCCCTGGGCACAAAGAA 2400
QY 2401 TGGAGGTCCTCCAGGAAAGGAGCTCCATGCAAGTTGCGAGTATCACTCTGAAATCAA 2460
Db 2401 TGGAGGTCCTCCAGGAAAGGAGCTCCATGCAAGTTGCGAGTATCACTCTGAAATCAA 2460
QY 2461 GCATACAAACTAGTGTGTTAAAGTTCCAAATCAACAAATACAAAGGTAATCAGTAA 2520
Db 2461 GCATACAAACTAGTGTGTTAAAGTTCCAAATCAACAAATACAAAGGTAATCAGTAA 2520
QY 2521 AGAAATCTGAATTTACTGACCGTGAATATGAAGAAATTAACCAATCAAGATTGGGAAGA 2580
Db 2521 AGAAATCTGAATTTACTGACCGTGAATATGAAGAAATTAACCAATCAAGATTGGGAAGA 2580
QY 2581 AATTAAAACTGAAATGTCAATATCACTTAGGCTATCTCAAGAGAGATGATTTGCTT 2640
Db 2581 AATTAAAACTGAAATGTCAATATCACTTAGGCTATCTCAAGAGAGATGATTTGCTT 2640
QY 2641 TCTCAAGAAATCGAGACAGGATATTCATGGTTCATCAAAATCCAGACATACAGTCAA 2700
Db 2641 TCTCAAGAAATCGAGACAGGATATTCATGGTTCATCAAAATCCAGACATACAGTCAA 2700
QY 2701 CACTGAGAAATCAGACACACATATTTCAATATAGAGAGTCTGCTGCTGCAACCCAG 2760
Db 2701 CACTGAGAAATCAGACACACATATTTCAATATAGAGAGTCTGCTGCTGCAACCCAG 2760
QY 2761 TAAATCTGAAAAAAGACACTTACTTATTTAAACCCCAATATCAATCAGCGAAAC 2820
Db 2761 TAAATCTGAAAAAAGACACTTACTTATTTAAACCCCAATATCAATCAGCGAAAC 2820
QY 2821 ATATTTTACTATTTCTGGATGATGATCAAAATGATCAATAGCAGGTTTGTCTCCACCT 2880
Db 2821 ATATTTTACTATTTCTGGATGATGATCAAAATGATCAATAGCAGGTTTGTCTCCACCT 2880
QY 2881 TCCCTGAAAAATTTTACTCAGAGATCATTTGCAACAGCATAGCTTACTTATTGTTAGGG 2940
```

## RESULT 2

```
ACC57946
ID ACC57946 standard; cDNA; 3330 BP.
XX ACC57946;
XX DT 11-AUG-2003 (first entry)
XX Human interphotoreceptor matrix IPM 150, isoform A, cDNA.
DE Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
KW receptor; ophthalmological; gene therapy; gene; ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT CDS 131..2586
FT FT /*tag= a
FT FT /product= "IPM 150"
FT FT /transl_except= (pos:668..756,aa:Thr-Asp)
FT FT sig_peptide 131..150
FT FT /*tag= b
XX FN WO2003039346-A2.
XX PD 15-MAY-2003.
XX PF 08-NOV-2002; 2002WO-US036090.
XX PR 08-NOV-2001; 2001US-00077270.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI Hageman GS, Kuehn MH;
XX DR WPI: 2003-441440/41.
XX DR P-PSDB; ABR42342.
XX PT New interphotoreceptor matrix proteins and polynucleotides, useful for
treating or preventing photoreceptor death or retinal detachment, or for
treating ocular disorders.
```

XX Claim 1; Page 77; 105pp; English.

XX The present sequence is that of cDNA encoding isoform A of novel human

CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified

CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene

CC is located on chromosome 6q13-q15, a region that also contains loci for

CC progressive bifocal choriorretinal atrophy, autosomal dominant Stargardt's

CC-like macular dystrophy, North Carolina macular dystrophy, and Salla

CC disease. Members of the IPMC gene family have been identified in humans,

CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2

CC Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The

CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,

CC antibodies that specifically bind the polypeptides, and vectors

CC comprising the polynucleotides. A claimed method of treating or

CC preventing photoreceptor death or retinal detachment involves

CC administering an IPMC polynucleotide, polypeptide or antibody. Also

CC claimed is a method for identifying a compound capable of modulating IPMC

CC gene expression

XX

SQ Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;

Query Match 100.0%; Score 3330; DB 8; Length 3330;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACCAAGAGGTTATCTCAATCATCTGGTATCAATATATATATATTTTTCACATTTC 60

DB 1 TAAACCAAGAGGTTATCTCAATCATCTGGTATCAATATATATATTTTTCACATTTC 60

QY 61 TGTACTTTTAAATGAGATTTGAGTGTCTCTGTGATTTGATCAGAAATACCAATGCAC 120

DB 61 TGTACTTTTAAATGAGATTTGAGTGTCTCTGTGATTTGATCAGAAATACCAATGCAC 120

QY 121 AAAAGCCAGAGATGTATTTGGAACTAGAAAGAGCTATTTTCTTTTGGATTTTCTCCA 180

DB 121 AAAAGCCAGAGATGTATTTGGAACTAGAAAGAGCTATTTTCTTTTGGATTTTCTCCA 180

QY 181 AGTTCAAGAAACCAAGATATCTCCATTAACATATACCATTTCTGAAACTAAAGACATAGA 240

DB 181 AGTTCAAGAAACCAAGATATCTCCATTAACATATACCATTTCTGAAACTAAAGACATAGA 240

QY 241 CAATCCCCCAAGAAATGAACCACTGAAAGTACTGAAAGATGACAAATGTCAAAAT 300

DB 241 CAATCCCCCAAGAAATGAACCACTGAAAGTACTGAAAGATGACAAATGTCAAAAT 300

QY 301 GAGACGAATATTCGATTTGGCAAGCATCGAACCAAAAGATCCGCAATTTTCCCAACGGG 360

DB 301 GAGACGAATATTCGATTTGGCAAGCATCGAACCAAAAGATCCGCAATTTTCCCAACGGG 360

QY 361 GGTAAAGTCTGTCCACAGGAATCCATGAACAGATTTTGAACAGTCTTCAAGCTTATTA 420

DB 361 GGTAAAGTCTGTCCACAGGAATCCATGAACAGATTTTGAACAGTCTTCAAGCTTATTA 420

QY 421 TAGATTGAGAGTGTCTCAGGAAGCAGATGGAAGCAGATATCGGATCTTTCTGGATCGCAT 480

DB 421 TAGATTGAGAGTGTCTCAGGAAGCAGATGGAAGCAGATATCGGATCTTTCTGGATCGCAT 480

QY 481 CCTGACACAGGGGAATATCAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 540

DB 481 CCTGACACAGGGGAATATCAGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 540

QY 541 CTTTTCACATTTGGAAAAAATTTCCAGCAATTTCCAGGAGCAGCTGATCTTCTCCAGCAGAG 600

DB 541 CTTTTCACATTTGGAAAAAATTTCCAGCAATTTCCAGGAGCAGCTGATCTTCTCCAGCAGAG 600

QY 601 AATAAAACAGAGAGTTTCCCTGACAGAAAGATGAATATTTCTCAGAGAGACATTTGGG 660

DB 601 AATAAAACAGAGAGTTTCCCTGACAGAAAGATGAATATTTCTCAGAGAGACATTTGGG 660

QY 661 AGAGCCTGGTGAACCATTTGATTTCAACAGCATCTTCAATTTTCAAGACTTTGGGCAGT 720

DB 661 AGAGCCTGGTGAACCATTTGATTTCAACAGCATCTTCAATTTTCAAGACTTTGGGCAGT 720

QY 721 ATTCTAAGAAAAACCTCTCAGAGAGCAAAATTCAGATGTTTGGCAACGTCTCTCACTTGGGCCT 780

DB 721 ATTCTAAGAAAAACCTCTCAGAGAGCAAAATTCAGATGTTTGGCAACGTCTCTCACTTGGGCCT 780

QY 781 TTCCCTCTCACTCTCATGATCAGACCCCTCTCAATGAATTTCTCGAATAATACACTCAACGAC 840

DB 781 TTCCCTCTCACTCTCATGATCAGACCCCTCTCAATGAATTTCTCGAATAATACACTCAACGAC 840

QY 841 ACCAAGATGCTTACAAAGAGAGAAAAAGATTCGCTGTGTTGGAGGAGCAGAGGGTG 900

DB 841 ACCAAGATGCTTACAAAGAGAGAAAAAGATTCGCTGTGTTGGAGGAGCAGAGGGTG 900

QY 901 GAGCTCAGAGTCTCTCTGTGTAACAGAGATTCAGAGCAGAGCTCGCTGACTCCGAGTCC 960

DB 901 GAGCTCAGAGTCTCTCTGTGTAACAGAGATTCAGAGCAGAGCTCGCTGACTCCGAGTCC 960

QY 961 CCATATTACAGAGCTAGCAGGAAAGTCCCAACTTTCAGATGCAAAAGATATTTAAGAAA 1020

DB 961 CCATATTACAGAGCTAGCAGGAAAGTCCCAACTTTCAGATGCAAAAGATATTTAAGAAA 1020

QY 1021 CTTTCCAGGATTCAAAAAATCCATGTTAGATTTAGACCAAAAGAAAAAGATGTC 1080

DB 1021 CTTTCCAGGATTCAAAAAATCCATGTTAGATTTAGACCAAAAGAAAAAGATGTC 1080

QY 1081 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAACAAAA 1140

DB 1081 TCAAGCTCCACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAACAAAA 1140

QY 1141 AGCCCTGAAAGTGAACCTCTCTGTTTGTATTCGACAAAAATTTGAAAGTGAGGAAGTCTAT 1200

DB 1141 AGCCCTGAAAGTGAACCTCTCTGTTTGTATTCGACAAAAATTTGAAAGTGAGGAAGTCTAT 1200

QY 1201 CATGGAACCATCGAGGAGGACAAAGCAACCCAGAAATCTATCTCACAGCTACACACCTCAAA 1260

DB 1201 CATGGAACCATCGAGGAGGACAAAGCAACCCAGAAATCTATCTCACAGCTACACACCTCAAA 1260

QY 1261 AGCTGATCAGAAAGCACTAGAGAAAGAAACAAATTTTGGATGTGGGAGCAATTCAGTTC 1320

DB 1261 AGCTGATCAGAAAGCACTAGAGAAAGAAACAAATTTTGGATGTGGGAGCAATTCAGTTC 1320

QY 1321 ACTGATGAATTTGCTGGATCACTGCGAGCTTTTGTCTTGACACCCCAATTCAGAGTGGCC 1380

DB 1321 ACTGATGAATTTGCTGGATCACTGCGAGCTTTTGTCTTGACACCCCAATTCAGAGTGGCC 1380

QY 1381 ACATCTTTTGTCTTATTAACAGAGGATGCTACTTTTGGTCCAGAACTCTCTCTGTGAA 1440

DB 1381 ACATCTTTTGTCTTATTAACAGAGGATGCTACTTTTGGTCCAGAACTCTCTCTGTGAA 1440

QY 1441 CCCCAGCTTGAGACAGTGGACGGAGCAGAGATGCTACCTGACACTTCTTGGTCTCCA 1500

DB 1441 CCCCAGCTTGAGACAGTGGACGGAGCAGAGATGCTACCTGACACTTCTTGGTCTCCA 1500

QY 1501 CTTGCTATGGCCCTCACTCCCTCTCAGAAAGTCCACCTTTCTTTATGGCATCAAGCATC 1560

DB 1501 CTTGCTATGGCCCTCACTCCCTCTCAGAAAGTCCACCTTTCTTTATGGCATCAAGCATC 1560

QY 1561 TTCTCTCTGATGATCAAGGACCAACAGATACATGAGGCACTGACCAAGCAATTCAGTA 1620

DB 1561 TTCTCTCTGATGATCAAGGACCAACAGATACATGAGGCACTGACCAAGCAATTCAGTA 1620

QY 1621 CCAGGGCTCACCATCCCAACAGTGAATTTCTGCAATTCAGCAACTGGCTCTGGGAATT 1680

DB 1621 CCAGGGCTCACCATCCCAACAGTGAATTTCTGCAATTCAGCAACTGGCTCTGGGAATT 1680

QY 1681 TCACATCCACCTGCACTCTCAGATCAGAGCGGATCAAGTGCAGGTTGGGAGATATGTC 1740

DB 1681 TCACATCCACCTGCACTCTCAGATCAGAGCGGATCAAGTGCAGGTTGGGAGATATGTC 1740

QY 1741 AGACACCTAGATGAATGATCTGACACTCTGCCCCCATCTGCTGAGCTTCCAGAGCTC 1800

DB 1741 AGACACCTAGATGAATGATCTGCTGACACTCTGCCCCCATCTGCTGAGCTTCCAGAGCTC 1800



QY 1801 AGCGAATATGTTCTCTGCCAGATCAATTTCTTGGAGATACCACTCTCTCTCAGCTTTA 1860  
 DB 1801 AGCGAATATGTTCTCTGCCAGATCAATTTCTTGGAGATACCACTCTCTCTCAGCTTTA 1860  
 QY 1861 CAGTATATCACCACCTAGTTCTATGACCAATGCCCCCAAGGCCGAGAGCTGTAGTGTTC 1920  
 DB 1861 CAGTATATCACCACCTAGTTCTATGACCAATGCCCCCAAGGCCGAGAGCTGTAGTGTTC 1920  
 QY 1921 TTCAAGTCTGGTCTGCTAACTAGCTGCTCTCAACGACCTCTTCAACAAGAGCTCTCTG 1980  
 DB 1921 TTCAAGTCTGGTCTGCTAACTAGCTGCTCTCAACGACCTCTTCAACAAGAGCTCTCTG 1980  
 QY 1981 GAGTACCGAGCTCTGGAGCAACAATTCACACAGCTGCTGTTCCATATCTACGATCCAA 2040  
 DB 1981 GAGTACCGAGCTCTGGAGCAACAATTCACACAGCTGCTGTTCCATATCTACGATCCAA 2040  
 QY 2041 CTTACAGGATTTAAGCAACTTGAATACCTTCAAGAGCTGCTGTTCCATATCTACGATCCAA 2100  
 DB 2041 CTTACAGGATTTAAGCAACTTGAATACCTTCAAGAGCTGCTGTTCCATATCTACGATCCAA 2100  
 QY 2101 AGCAAAATGAAGTTTCTAAGTCTGTGCGTATACCTCACCAAGCTGTGCAAGGCTC 2160  
 DB 2101 AGCAAAATGAAGTTTCTAAGTCTGTGCGTATACCTCACCAAGCTGTGCAAGGCTC 2160  
 QY 2161 TTGGAGGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220  
 DB 2161 TTGGAGGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220  
 QY 2221 CTCACATTTGAACCACTGATCAACGAGATCCCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCT 2280  
 DB 2221 CTCACATTTGAACCACTGATCAACGAGATCCCTGCAAGTCTGCTGCTGCTGCTGCTGCTGCT 2280  
 QY 2281 GCCCAATGTGTAAGAAAGCAAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340  
 DB 2281 GCCCAATGTGTAAGAAAGCAAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340  
 QY 2341 GACAGCCAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400  
 DB 2341 GACAGCCAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400  
 QY 2401 TCGGAGGCTCTCCAGGAAAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460  
 DB 2401 TCGGAGGCTCTCCAGGAAAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460  
 QY 2461 GCATACAACTAGTGTGTAAGTTCACAAATCAACAAATCAACAAATCAACAAATCAACAAATCAAC 2520  
 DB 2461 GCATACAACTAGTGTGTAAGTTCACAAATCAACAAATCAACAAATCAACAAATCAACAAATCAAC 2520  
 QY 2521 AGAAATCTGAATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580  
 DB 2521 AGAAATCTGAATTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580  
 QY 2581 AATTAAATCTGAAATGTAACAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAAT 2640  
 DB 2581 AATTAAATCTGAAATGTAACAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAAT 2640  
 QY 2641 TCTCAAGAAATGAGACAGGATTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
 DB 2641 TCTCAAGAAATGAGACAGGATTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
 QY 2701 CACTGAGATCAGACACACCATATTTCAATATAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760  
 DB 2701 CACTGAGATCAGACACACCATATTTCAATATAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760  
 QY 2761 TAAATCTGAAATGAGACAGGATTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820  
 DB 2761 TAAATCTGAAATGAGACAGGATTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820  
 QY 2821 ATATTTTACTATTTCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880  
 DB 2821 ATATTTTACTATTTCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880  
 QY 2881 TCCCTGAAATTTTACTCAGATCAATTTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940

DB 2881 TCCCTGAAATTTTACTCAGATCAATTTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940  
 QY 2941 ACTGAACAATTTTATGGAAGCAAACTCTTATATGCTAGAAAAGTACATTTAAAGATGA 3000  
 DB 2941 ACTGAACAATTTTATGGAAGCAAACTCTTATATGCTAGAAAAGTACATTTAAAGATGA 3000  
 QY 3001 CTACTTACGAGGAGGAGTGTCTCTCTTAAACGATGAATGTATGTAGTGTAGGCA 3060  
 DB 3001 CTACTTACGAGGAGGAGTGTCTCTCTTAAACGATGAATGTATGTAGTGTAGGCA 3060  
 QY 3061 CTGTAGTGTAGTGTATATGCTCCACATGCTGTGATAAACAACCAACCTCAGTATTCAG 3120  
 DB 3061 CTGTAGTGTAGTGTATATGCTCCACATGCTGTGATAAACAACCAACCTCAGTATTCAG 3120  
 QY 3121 TTATTAGGCACTAGTGTATATGCTTAAACGATGAATGTATGTAGTGTAGGCA 3180  
 DB 3121 TTATTAGGCACTAGTGTATATGCTTAAACGATGAATGTATGTAGTGTAGGCA 3180  
 QY 3181 AATAATCTTTGAATTTCTTAAAGAACTGAGGTTGAGATACATACCATGGAAGA 3240  
 DB 3181 AATAATCTTTGAATTTCTTAAAGAACTGAGGTTGAGATACATACCATGGAAGA 3240  
 QY 3241 ATCTTACTTTTCTTGTACTACACAAAGCTATTTAAAGAGATGCTATGTTGGGAGAG 3300  
 DB 3241 ATCTTACTTTTCTTGTACTACACAAAGCTATTTAAAGAGATGCTATGTTGGGAGAG 3300  
 QY 3301 GCGAGTGTACTATATGACATATCAAT 3330  
 DB 3301 GCGAGTGTACTATATGACATATCAAT 3330

## RESULT 3

AAAA6205  
ID AAA46205 standard; cDNA; 3263 BP.

XX AAA46205;

XX 04-SBP-2000 (first entry)

XX cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).

XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 XX chromosome 6q13-q15; ocular disease; retinal detachment;  
 XX choriorretinal degeneration; retinal degeneration; cone degeneration;  
 XX age related macular degeneration; photoreceptor degeneration;  
 XX retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 XX rod- cone dystrophy; cone-rod dystrophy; ms.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 128..2444

XX /tag= a

XX /transl\_except= (pos: 2411..2414, aa: Lys)

XX /product= "interphotoreceptor matrix proteoglycan IPM150"

XX W0200026367-A2.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US025440.

XX 29-OCT-1998; 98US-00183972.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;

XX WPI; 2000-365616/31.

XX P-PSDB; AAY93336.

XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for

PT preventing, diagnosing and treating ocular disorders such as retinal  
 XX detachment and chorioretinal degeneration.  
 XX Claim 2; Fig 3; 183pp; English.  
 XX  
 CC The present sequence encodes an interphotoreceptor matrix (IPM)  
 CC proteoglycan, designated IPM150. The protein is an IPM component (IPMC).  
 CC Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene  
 CC is located on chromosome 6q13-q15, between markers CHLC.GAT11P10 and  
 CC D6S284. The IPM proteins may be used to supplement a patient's own  
 CC production of the protein or to rectify alterations in their nucleic  
 CC acids that result in expression of an inactive protein. The IPM nucleic  
 CC acids may be used in this way to treat ocular diseases such as retinal  
 CC detachment, chorioretinal degeneration, retinal degeneration, age related  
 CC macular degeneration, photoreceptor degeneration, RPE (retinal pigment  
 CC epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-  
 CC cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may  
 CC also be used to assay for other modulators of IPM proteoglycan expression  
 CC and activity that may be used to treat ocular diseases. The nucleic acids  
 CC and proteins may also be used as diagnostic reagents to detect the  
 CC presence of IPM nucleic acids and their products in samples from patients  
 CC according to standard methodologies  
 XX  
 SQ Sequence 3263 BP; 1040 A; 721 C; 663 G; 938 T; 0 U; 1 Other;

Query Match 93.9%; Score 3125.6; DB 3; Length 3263;  
 Best Local Similarity 97.8%; Pred. No. 0;  
 Matches 3257; Conservative 0; Mismatches 5; Indels 69; Gaps 6;  
 1 TAAACCAAGAGGTTATCTCTCAATCATCTGGTATCATATATATATATTTTTCACATTTC 60  
 1 TAAACCAAGAGGTTATCTCTCAATCATCTGGTATCATATATATATATTTTTCACATTTC 58  
 61 TGTTACTTTTAAAGAGATTGAGTTGGTGTCTGTGATTTATCAGAAATACCAATGCAC 120  
 59 TGTTACTTTTAAAGAGATTGAGTTGGTGTCTGTGATTTATCAGAAATACCAATGCAC 117  
 121 AAAAGCCAGATCTATTTCGAACTAGAGAGCTATTTTGGTATTTTGGATTTTCTCCA 180  
 118 AAAAGCCAGATCTATTTCGAACTAGAGAGCTATTTTGGTATTTTGGATTTTCTCCA 177  
 181 AGTTCAAGGAACCAAGATATCTTCAATTAACATATACCAATCTGAACTTAAAGACATAGA 240  
 178 AGTTCAAGGAACCAAGATATCTTCAATTAACATATACCAATCTGAACTTAAAGACATAGA 237  
 241 CAATCCCCAGAAATGAAACCACTGAAAGTACTGAAAGATGTAACAAATGTAACATAT 300  
 238 CAATCCCCAGAAATGAAACCACTGAAAGTACTGAAAGATGTAACAAATGTAACATAT 297  
 301 GAGACGAATATTCGATTTGGCAAGCATCGAAACAAAGATCCGATTTTCCCAACGGG 360  
 298 GAGACGAATATTCGATTTGGCAAGCATCGAAACAAAGATCCGATTTTCCCAACGGG 357  
 361 GGTTAAAGTCTGTGCCACAGAAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTTA 420  
 358 GGTTAAAGTCTGTGCCACAGAAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTTA 417  
 421 TAGATTGAGAGTGTGTCAGAGAGCATATGGGAAGCATATCGGATCTTCTGGATCGCAT 480  
 418 TAGATTGAGAGTGTGTCAGAGAGCATATGGGAAGCATATCGGATCTTCTGGATCGCAT 477  
 481 CCCTGACACAGGGGAATATCAGAGTCTGGGTTCAGCATCTGCCAGCAGGAGACCTTCTGGCT 540  
 478 CCCTGACACAGGGGAATATCAGAGTCTGGGTTCAGCATCTGCCAGCAGGAGACCTTCTGGCT 537  
 541 CTTTGGATCTGGAAATCTCAGGAATTTCCAGAGGACCTTGGATCTTCTCCAGCAGAG 600  
 538 CTTTGGATCTGGAAATCTCAGGAATTTCCAGAGGACCTTGGATCTTCTCCAGCAGAG 597  
 601 AATAAACACAGAGAGTTTCCCTGACAGAAAGATGAAATATCTGACAGAGACATTTGGG 660  
 598 AATAAACACAGAGAGTTTCCCTGACAGAAAGATGAAATATCTGACAGAGACATTTGGG 657

QY 661 AGAGCCGTGGTGAACACCATTTGTCAATTTTCAACAGCAATCTCATATTTCAAGAGACTTTGGGCAGT 720  
 DB 658 AGAGCCGTGGTGAACACCATTTGTCAATTTTCAAC----- 687  
 QY 721 ATTTCAAGAAACACCTCAGAGAGCAAAATTTCAAGATGTTTCCCAACGCTTCTCACTTGGGCCT 780  
 DB 688 -----AGATGTTGCCAACGCTTCTCACTTGGGCCT 715  
 QY 781 TTCCCTCTCACTCTGATGACACCCCTCCTCAATGAAATTTCTCGATATATACACTCAACGAC 840  
 DB 716 TTCCCTCTCACTCTGATGACACCCCTCCTCAATGAAATTTCTCGATATATACACTCAACGAC 775  
 QY 841 ACCAAGATGCTCTCAACAGAGAAAGAGAAACAGAAATTCGCTGTGTTGGAGGACGAGGGTG 900  
 DB 776 ACCAAGATGCTCTCAACAGAGAAAGAGAAACAGAAATTCGCTGTGTTGGAGGACGAGGGTG 835  
 QY 901 GAGCTCAGCTCTCTCTGTTAAACAGAGATTTCAAGCAGAGCTCGCTGACTCCAGTCC 960  
 DB 836 GAGCTCAGCTCTCTCTGTTAAACAGAGATTTCAAGCAGAGCTCGCTGACTCCAGTCC 895  
 QY 961 CCATATTACCAGGAGCTAGCAGGAAAGTCCCAACTTTCAGATGCAAAAGATATTTAAAGAA 1020  
 DB 896 CCATATTACCAGGAGCTAGCAGGAAAGTCCCAACTTTCAGATGCAAAAGATATTTAAAGAA 955  
 QY 1021 CTTCCAGGATTTCAAAATAATTCATGTTAGGATTTTAGACCAAGAAAGAAAGATGTC 1080  
 DB 956 CTTCCAGGATTTCAAAATAATTCATGTTAGGATTTTAGACCAAGAAAGAAAGATGTC 1015  
 QY 1081 TCAAGCTCCACAGAGATGCAACTTTCAGGCCATCTTTAAAGAGACACAGTGCAGAGCAAA 1140  
 DB 1016 TCAAGCTCCACAGAGATGCAACTTTCAGGCCATCTTTAAAGAGACACAGTGCAGAGCAAA 1075  
 QY 1141 AGCCCTCAAGTACCTCTCTGTTTGAATTCACAAATAATGAAAGTGAAGGAGTCTAT 1200  
 DB 1076 AGCCCTCAAGTACCTCTCTGTTTGAATTCACAAATAATGAAAGTGAAGGAGTCTAT 1135  
 QY 1201 CATGGAACCATGAGGAGGACAGCAACAGAAATCTATCTCAGCTACAGACCTCAAA 1260  
 DB 1136 CATGGAACCATGAGGAGGACAGCAACAGAAATCTATCTCAGCTACAGACCTCAAA 1195  
 QY 1261 AGGCTGATCAGCAAAACACCTAGAGGAGCAACATCTTTGGATGTTGGGCAATTCAGTTC 1320  
 DB 1196 AGGCTGATCAGCAAAACACCTAGAGGAGCAACATCTTTGGATGTTGGGCAATTCAGTTC 1255  
 QY 1321 ACTGATGAATTTGCTGATCAGCTGCGAGCCCTTTGGTCTTGACACCAATCAGAGCTGCC 1380  
 DB 1256 ACTGATGAATTTGCTGATCAGCTGCGAGCCCTTTGGTCTTGACACCAATCAGAGCTGCC 1315  
 QY 1381 ACATCTTTTCTGTTTAAACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTCTGTTGAA 1440  
 DB 1316 ACATCTTTTCTGTTTAAACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTCTGTTGAA 1375  
 QY 1441 CCCAGCTTGAGACAGTGGACGAGCAGAGCATGGTCTTACCTGACACTTCTTGGTCTCCA 1500  
 DB 1376 CCCAGCTTGAGACAGTGGACGAGCAGAGCATGGTCTTACCTGACACTTCTTGGTCTCCA 1435  
 QY 1501 CTTGCTATGCTCTACCTCCCTGTCAGAGGCTCCACCTTTCTTTATGGCATCAAGCATC 1560  
 DB 1436 CTTGCTATGCTCTACCTCCCTGTCAGAGGCTCCACCTTTCTTTATGGCATCAAGCATC 1495  
 QY 1561 TTCTCTGATCTGATCAAGGACCAACAGATACAAATGCCCACTGACCAAGCAATGCTAGTA 1620  
 DB 1496 TTCTCTGATCTGATCAAGGACCAACAGATACAAATGCCCACTGACCAAGCAATGCTAGTA 1555  
 QY 1621 CCAGGCTCAGATCTCCCAAGGATGATTTCTGCAATCAGCCACTGCTGCTGGAAAT 1680  
 DB 1556 CCAGGCTCAGATCTCCCAAGGATGATTTCTGCAATCAGCCACTGCTGCTGGAAAT 1615  
 QY 1681 TCATATCCACTGCTCTTTCAGATGACAGCCGATCAAGTGCAGGTCGCGAAGATATGGTC 1740  
 DB 1616 TCATATCCACTGCTCTTTCAGATGACAGCCGATCAAGTGCAGGTCGCGAAGATATGGTC 1675  
 QY 1741 AGACACCTAGATGAATGGATCTGCTGACACTCTGCTGCCCTCTGAGGTACAGAGCTC 1800





QY	1861	CAGTATATCACCACTAGTTCTATGACCAATGSCCCCGAGGCGAGAGCTGGTAGTGTTC	1920
DB	1796	CAGTATATCACCACTAGTTCTATGACCAATTTGCCCCCAGGCGCGAGAGCTGGTAGTGTTC	1855
QY	1921	TTCACTCTGCGTGTTCCTAACATCGGCTTCTCCAAACGACCTGTTTCAAACAAGAGCTCTCTG	1980
DB	1856	TTCACTCTGCGTGTTCCTAACATCGGCTTCTCCAAACGACCTGTTTCAAACAAGAGCTCTCTG	1915
QY	1981	GAGTACCGAGCTCTGGAGCAACAATTACACACAGCTGCTGTTCCATATCTACAGATCCAAT	2040
DB	1916	GAGTACCGAGCTCTGGAGCAACAATTACACACAGCTGCTGTTCCATATCTACAGATCCAAT	1975
QY	2041	CTTACAGGATTTAAGCAACTGTAAATACTTAACTTACAGAAACGGGAGTGTAATGTGAAT	2100
DB	1976	CTTACAGGATTTAAGCAACTGTAAATACTTAACTTACAGAAACGGGAGTGTAATGTGAAT	2035
QY	2101	AGCAAAATGAAGTTTGCTTAAGTCTGTGCCGTATAACCTTACCAAGGCTGTGCACGGGTTC	2160
DB	2036	AGCAAAATGAAGTTTGCTTAAGTCTGTGCCGTATAACCTTACCAAGGCTGTGCACGGGTTC	2095
QY	2161	TTGGAGGATTTTGGTCTGCTGAGCGCCAAACAACCTCCATCTCGAAATAGACAGCTACTCT	2220
DB	2096	TTGGAGGATTTTGGTCTGCTGAGCGCCAAACAACCTCCATCTCGAAATAGACAGCTACTCT	2155
QY	2221	CTCAACAATTGAAACGAGCTGATCAAGCAGATCCCTTGCAGTTCCTGGCCTCGGCGAATTT	2280
DB	2156	CTCAACAATTGAAACGAGCTGATCAAGCAGATCCCTTGCAGTTCCTGGCCTCGGCGAATTT	2215
QY	2281	GCCCAATGTGTAAGAAGCAACGGAATGAGGAAACGGAGTGTGCTGTCAAACGAGGATAT	2340
DB	2216	GCCCAATGTGTAAGAAGCAACGGAATGAGGAAACGGAGTGTGCTGTCAAACGAGGATAT	2275
QY	2341	GACAGCCAGGGAGCCTGAGCGTCTGGAAACGAGGCTCTGTGGCCCTGGCAAAAGGAA	2400
DB	2276	GACAGCCAGGGAGCCTGAGCGTCTGGAAACGAGGCTCTGTGGCCCTGGCAAAAGGAA	2334
QY	2401	TGCGAGGTCCTCCAGGGAAGGGAGGCTCCATGTCAGGTTGCGCAGATCACTCTGAAATCAA	2460
DB	2335	TGCGAGGTCCTCCAGGGAAGGGAGGCTCCATGTCAGGTTGCGCAGATCACTCTGAAATCAA	2392
QY	2461	GCATACAAACTAGTGTAAAAGTTCCAAAATCAAACAAAATAACAGGTAATCAGTAAA	2520
DB	2393	GCATACAAACTAGTGT-AAAAGTTCCAAAATCAAACAAAATAACAGGTAATCAGTAAA	2451
QY	2521	AGAAATCTGAAATTACTGACCGTAGAATATGAAGATTTAAACATCAAGATTGGGAAGA	2580
DB	2452	AGAAATCTGAAATTACTGACCGTAGAATATGAAGATTTAAACATCAAGATTGGGAAGA	2511
QY	2581	AAATTAATACTGAAAAATGTACAATTATCACTTAGGCTATCTCAAGAGAGATGATTTGCT	2640
DB	2512	AAATTAATACTGAAAAATGTACAATTATCACTTAGGCTATCTCAAGAGAGATGATTTGCT	2571
QY	2641	TCTCAGGAAATGAGAGAGCATATTCATGGTTCATCAAAAATCCAGACATACAGTCAA	2700
DB	2572	TCTCAGGAAATGAGAGAGCATATTCATGGTTCATCAAAAATCCAGACATACAGTCAA	2631
QY	2701	CACGTGAAATCAGCACACACCATATTTCAAATATAGAAGATCATGTACTTGGCAACAG	2760
DB	2632	CACGTGAAATCAGCACACACCATATTTCAAATATAGAAGATCATGTACTTGGCAACAG	2691
QY	2761	TAAATTCGAAAAAAGAAGACATTACTTATTTAAACCCCAAAATGCAATCAGCGAAAC	2820
DB	2692	TAAATTCGAAAAAAGAAGACATTACTTATTTAAACCCCAAAATGCAATCAGCGAAAC	2751
QY	2821	ATATTTTTACTATTTCTTGATGATAGTCAAAATGATCATAAAGGCTTTGCTCCACCT	2880
DB	2752	ATATTTTTACTATTTCTTGATGATAGTCAAAATGATCATAAAGGCTTTGCTCCACCT	2811
QY	2881	TCCTGAAAAATTTACTCAAGATCATTTGCAACCAAGATAGCTTACTTATTTGTTAGGG	2940
DB	2812	TCCTGAAAAATTTACTCAAGATCATTTGCAACCAAGATAGCTTACTTATTTGTTAGGG	2871

QY	2941	ACTGACAAATTATTGGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTTAAAGATGA	3000
DB	2872	ACTGACAAATTATTGGGAAGCAAACTCTTTATATGCTAGAAAGTACATTTTAAAGATGA	2931
QY	3001	CTACTTACGACGAGGAGATGCAGGTCTCTCTFAAACGCATGAATCTATGTAGTGTGTAGGCA	3060
DB	2932	CTACTTACGACGAGGAGATGCAGGTCTCTCTFAAACGCATGAATCTATGTAGTGTGTAGGCA	2991
QY	3061	CTGTAGTAGTGATATATATGCTCCACACTACGCTCTGATAAAACAAACCTTCAGTATTCAG	3120
DB	2992	CTGTAGTAGTGATATATATGCTCCACACTACGCTCTGATAAAACAAACCTTCAGTATTCAG	3051
QY	3121	TTATTAGGCACACTAGTTTTTATACGCAACTACTGCTTTACATAGTAGACCTGTTTGTGTC	3180
DB	3052	TTATTAGGCACACTAGTTTTTATACGCAACTACTGCTTTACATAGTAGACCTGTTTGTGTC	3111
QY	3181	AATAAATCTTTGAAATGTCTTTTAAAGAAACTGAGGTTTCAGATACACATACCATTGAAAA	3240
DB	3112	AATAAATCTTTGAAATGTCTTTTAAAGAAACTGAGGTTTCAGATACACATACCATTGAAAA	3171
QY	3241	ATCTTACTTCTTCTGTACTACACAAAGCTATTTTAAAGAAAGATGCTATGTTGGGAGAAG	3300
DB	3172	ATCTTACTTCTTCTGTACTACACAAAGCTATTTTAAAGAAAGATGCTATGTTGGGAGAAG	3231
QY	3301	GGCGAAGTTGCTACTATATGACATAATCAAT	3330
DB	3232	GGCGAAGTTGCTACTATATGACATAATCAAT	3261
RESULT 5			
ACCS7960			
ID	ACCS7960 standard; cDNA; 3261 BP.		
XX			
AC	ACCS7960;		
XX			
DT	11-AUG-2003 (first entry)		
XX			
DE	Human interphotoreceptor matrix IPM 150, isoform A variant, cDNA.		
XX			
KW	Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;		
KW	receptor; ophthalmological; gene therapy; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key		
FT	CDS		
FT	Location/Qualifiers		
FT	128..2443		
FT	/*tag= a		
FT	/*product= "IPM 150"		
XX			
PN	WO2003039346-A2.		
XX			
PD	15-MAY-2003.		
XX			
PF	08-NOV-2002; 2002WO-US036090.		
XX			
PR	08-NOV-2001; 2001US-00077270.		
XX			
PA	(IOWA ) UNIV IOWA RES FOUND.		
XX			
PI	Hageman GS, Kuehn MH;		
XX			
PI	WPI; 2003-441440/41.		
DR	P-PSDB; ABR42354.		
XX			
PT	New interphotoreceptor matrix proteins and polynucleotides, useful for		
PT	treating or preventing photoreceptor death or retinal detachment, or for		
PT	treating ocular disorders.		
XX			
PS	Claim 1; Page 91-94; 105pp; English.		
XX			
CC	The present sequence is that of cDNA encoding a variant of isoform A of		
CC	novel human interphotoreceptor matrix 150 (IPM 150), a member of the		
CC	newly identified interphotoreceptor matrix component (IPMC) gene family.		







Db 1796 CAGTATATCACCACCTAGTCTTATGACCATTTGCCCCCAAGGCCGAGAGCTGTAGTGTTC 1855  
Qy 1921 TTCACTCTGGGTGTCTTAACATGGCCCTTCTCCAAAGACCTGTTCACAAAGAGCTCTCTG 1980  
Db 1856 TTCACTCTGGGTGTCTTAACATGGCCCTTCTCCAAAGACCTGTTCACAAAGAGCTCTCTG 1915  
Qy 1981 GAGTACCGAGCTCTGGAGCAACAACTTCAACAGCTGTCTGTTCATATCTACCATCCAAT 2040  
Db 1916 GAGTACCGAGCTCTGGAGCAACAACTTCAACAGCTGTCTGTTCATATCTACCATCCAAT 1975  
Qy 2041 CTTACAGGATTTAAGCACTTGAATCTTAACTTCAAGAAACCGGAGTGTGATTTGAAT 2100  
Db 1976 CTTACAGGATTTAAGCACTTGAATCTTAACTTCAAGAAACCGGAGTGTGATTTGAAT 2035  
Qy 2101 AGCAAAATGAAGTTTGTCTAGTCTGTCCGTATTAACCTCACCAGGCTGTGACGGGTC 2160  
Db 2036 AGCAAAATGAAGTTTGTCTAGTCTGTCCGTATTAACCTCACCAGGCTGTGACGGGTC 2095  
Qy 2161 TTGAGGATTTTGTCTGTCTGAGCCCAACAACTTCCATCTGGAATAGACAGCTACTCT 2220  
Db 2096 TTGAGGATTTTGTCTGTCTGAGCCCAACAACTTCCATCTGGAATAGACAGCTACTCT 2155  
Qy 2221 CTCAACATTCGACAGCTGTATCAGCAGATCCCTGCMAGTTCTGGCCTGCGCGCAATTT 2280  
Db 2156 CTCAACATTCGACAGCTGTATCAGCAGATCCCTGCMAGTTCTGGCCTGCGCGCAATTT 2215  
Qy 2281 GCCCAATGTGTAAAGAACGACGAGTGTGAGGAGCGAGTGTCTGCGCAACCCAGGATAT 2340  
Db 2216 GCCCAATGTGTAAAGAACGACGAGTGTGAGGAGCGAGTGTCTGCGCAACCCAGGATAT 2275  
Qy 2341 GACAGCCAGGGAGCTGAGCGGTCTGGAACCAAGGCTCTGTGGCCCTGGCAAAAGGAA 2400  
Db 2276 GACAGCCAGGGAGCTGAGCGGTCTGGAACCAAGGCTCTGTGG--CCTGGCAAAAGGAA 2334  
Qy 2401 TGGGAGTCTCTCAGGAAAGGAGCTTCCATGACAGTTCAGATCAGTCTGGAATCAA 2460  
Db 2335 TGGGAGTCTCTCAGGAAAGGAGCTTCCATG--GGTTCAGATCAGTCTGGAATCAA 2392  
Qy 2461 GCATACAAACTAGTGTAAAGAGTTTCCAAATTCACAAATTAACAAAGGTATCAGTAAA 2520  
Db 2393 GCATACAAACTAGTGT--AAAAGTTTCCAAATTCACAAATTAACAAAGGTATCAGTAAA 2451  
Qy 2521 AGAAATCTGAATCTGACCGTAGAATATGAAGATTTAACATCAAGATTTGGGAGGA 2580  
Db 2452 AGAAATCTGAATCTGACCGTAGAATATGAAGATTTAACATCAAGATTTGGGAGGA 2511  
Qy 2581 AATTAAAACTGAAAATGTACAAATATCACTTAGGCTATCTCAAGAGAGATGATTTGCT 2640  
Db 2512 AATTAAAACTGAAAATGTACAAATATCACTTAGGCTATCTCAAGAGAGATGATTTGCT 2571  
Qy 2641 TCTCAAGGAAATGGAGACAGGATATTCATGGGTATCAAAATCCAGCATACAGTCAA 2700  
Db 2572 TCTCAAGGAAATGGAGACAGGATATTCATGGGTATCAAAATCCAGCATACAGTCAA 2631  
Qy 2701 CACTGAGATCAGCACACACCATATTTCAATATAGAGAGTCATGTACTTGGCAACAG 2760  
Db 2632 CACTGAGATCAGCACACACCATATTTCAATATAGAGAGTCATGTACTTGGCAACAG 2691  
Qy 2761 TAAATCTGAAAAAAGACACTTACTTATTAATAAACCCCAATGCAATCAGCGAAAC 2820  
Db 2692 TAAATCTGAAAAAAGACACTTACTTATTAATAAACCCCAATGCAATCAGCGAAAC 2751  
Qy 2821 ATATTTTACTATTTCTGATATAGTCAAAATGATCATAGCCAGGTTTGTCCACCT 2880  
Db 2752 ATATTTTACTATTTCTGATATAGTCAAAATGATCATAGCCAGGTTTGTCCACCT 2811  
Qy 2881 TCCCTGAAATTTTACTCAGATCATTTTGAACCAAGATAGTCTTACTTATTTAGGG 2940  
Db 2812 TCCCTGAAATTTTACTCAGATCATTTTGAACCAAGATAGTCTTACTTATTTAGGG 2871  
Qy 2941 ACTGAACAAATTTATTGGGAGCAACTCTTTATATGCTAGAAAGTACATTTAAAGATGA 3000

Db 2872 ACTGAACAAATTTATTGGGAGCAAACTCTTTATATGCTAGAAAGTACATTTAAAGATGA 2931  
Qy 3001 CTACTTACGCGAGGAGATGCGAGTCTCTCTAAACGCAATGAATGTATGTGTAGGCA 3060  
Db 2932 CTACTTACGCGAGGAGATGCGAGTCTCTCTAAACGCAATGAATGTATGTGTAGGCA 2991  
Qy 3061 CTGTAGTCAAGTGTATATATGCTCCACACTAGCTCTGATTAACACAAACCTCAGTATTCAG 3120  
Db 2992 CTGTAGTCAAGTGTATATATGCTCCACACTAGCTCTGATTAACACAAACCTCAGTATTCAG 3051  
Qy 3121 TTATTAGGCACACTAGTTTATTAGCCACTACTCTGTTACATAGTAGAGTGTGTTGTTGCC 3180  
Db 3052 TTATTAGGCACACTAGTTTATTAGCCACTACTCTGTTACATAGTAGAGTGTGTTGTTGCC 3111  
Qy 3181 AATAATCTTGAATTTGTTTAAAGAACTGAGGTTTCAGATACATACCATGGAATA 3240  
Db 3112 AATAATCTTGAATTTGTTTAAAGAACTGAGGTTTCAGATACATACCATGGAATA 3171  
Qy 3241 ATCTTACTTTTCTTGTACTACACAAAGCTATTTTAAAGAGATGCTATGTTGGGAGAG 3300  
Db 3172 ATCTTACTTTTCTTGTACTACACAAAGCTATTTTAAAGAGATGCTATGTTGGGAGAG 3231  
Qy 3301 GCGGAGTTGTACTATATGACATAATCAAT 3330  
Db 3232 GCGGAGTTGTACTATATGACATAATCAAT 3261

RESULT 6  
ADA14842  
ID ADA14842 standard; cDNA; 2887 BP.  
XX  
AC ADA14842;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human interphotoreceptor matrix component, IPMC, 150 isoform B cDNA.  
XX  
KW ss; gene; human; IPMC 150 isoform B; gene therapy;  
KW interphotoreceptor matrix component; IPMC; ocular disorder;  
KW macular degeneration; photoreceptor death; retinal detachment.  
XX  
OS Homo sapiens.  
XX  
FH Key  
CDS Location/Qualifiers  
FT 5..2143  
FT /\*tag= a  
FT /partial  
FT /product= "IPMC 150 isoform B"  
FT /note= "No start codon given. Encodes residues 8-719 of  
XX (seqid:4)"  
XX  
XX US2002160954-A1.  
XX  
XX 31-OCT-2002.  
XX  
XX 08-NOV-2001; 2001US-00007270.  
XX  
XX 29-OCT-1998; 98US-00183972.  
XX 29-OCT-1999; 99US-00430195.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX  
XX Hageman GS, Kuehn MH;  
XX WPI; 2003-238235/23.  
XX DR P-PSDS; ADA14843.  
XX  
XX New isolated or recombinant interphotoreceptor matrix component  
XX polynucleotide and polypeptide, useful for diagnosing, preventing,  
XX treating or prognosticating ocular disorders, e.g. macular degeneration  
XX or retinal detachment.  
XX  
XX Claim 3; Page 33-34; 76pp; English.

XX The invention relates to an isolated or recombinant interphotoreceptor  
CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
CC gene operatively linked to the IPMC polynucleotide. The IPMC  
CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
CC preventing, treating or prognosticating ocular disorders, e.g. macular  
CC degeneration, photoreceptor death or retinal detachment. They are also  
CC useful for identifying a compound capable of modulating IPMC gene  
CC expression in a cell. The present sequence represents cDNA encoding human  
CC interphotoreceptor matrix component, IPMC, 150 isoform B.

XX SQ Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;

Query Match 83.1%; Score 2765.8; DB 7; Length 2887;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 2851; Conservative 0; Mismatches 22; Indels 62; Gaps 1;  
396 TTTTAGACAGCTTTCAAGCTTATTATAGATTGAGAGTGTGTCAGGAGCAGTAGTGGGAG 455  
15 TTTTGTGATTTTCTCCAGTTCAAGGAACCAAGTGTGTCAGGAAGCAGTAGTGGGAG 74  
456 CATATCGGATCTTCTGGATCGCATCCCTGCACACAGGGGAAATATCAGGACTGGGTGAGCA 515  
75 CATATCGGATCTTCTGGATCGCATCCCTGCACACAGGGGAAATATCAGGACTGGGTGAGCA 134  
516 TCTGCCAGCAGGAGACCTTCTGCTCTTTTGACATTTGGAAAAAATTTGAGCAATTTCCAGG 575  
135 TCTGCCAGCAGGAGACCTTCTGCTCTTTTGACATTTGGAAAAAATTTGAGCAATTTCCAGG 194  
576 AGCACCCTGGATCTTCTCCAGAGAGATATAACAGAGAGTTTCCCTGCAGAGAAAGATG 635  
195 AGCACCCTGGATCTTCTCCAGAGAGATATAACAGAGAGTTTCCCTGCAGAGAAAGATG 254  
636 AAATATCTGCAGAGAGACATTTGGGAGAGCTGGTGAACCATTTGTCATTTCAACAGCAA 695  
255 AAATATCTGCAGAGAGACATTTGGGAGAGCTGGTGAACCATTTGTCATTTCAAC----- 309  
696 TCTACATTTCAAGACTTTGGGAGTATTTCTAAGAAACCCCTCAGAGAGCAAAATTCAGA 755  
310 -----AGG 312  
756 TGTGCGCAAGCTCTCACTTGGGCTTTCCCTCTCACTCTCCTGATGACACCTCCTCTCAATGA 815  
313 TGTGCGCAAGCTCTCACTTGGGCTTTCCCTCTCACTCTCCTGATGACACCTCCTCTCAATGA 372  
816 AATTTCTCGATAATACACTCAACGACACCAAGATGCTTACACAGAGAGAGAAACAGAAAT 875  
373 AATTTCTCGATAATACACTCAACGACACCAAGATGCTTACACAGAGAGAGAAACAGAAAT 432  
876 CGCTGTGTTGGAGAGCAGAGAGGTGGAGCTCAGCGTCTCTCTGTTAAACGAGAGTTCAA 935  
433 CGCTGTGTTGGAGAGCAGAGAGGTGGAGCTCAGCGTCTCTCTGTTAAACGAGAGTTCAA 492  
936 GGCAGAGCTCGCTGACTCCAGTCCCGATATTTACAGGAGCTAGCAGGAAAGTCCCAACT 995  
493 GGCAGAGCTCGCTGACTCCAGTCCCGATATTTACAGGAGCTAGCAGGAAAGTCCCAACT 552  
996 TCAGATCCAAAAGATATTTAAGAAATTTCCAGGATTCAAAAAATCCATGTGTAGGATT 1055  
553 TCAGATCCAAAAGATATTTAAGAAATTTCCAGGATTCAAAAAATCCATGTGTAGGATT 612  
1056 TAGACCAAGAGAGAGAGAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATCTT 1115  
613 TAGACCAAGAGAGAGAGAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATCTT 672  
1116 TAGAGACACAGTGCAG 1175  
673 TAAGAGACACAGTGCAG 732  
1176 CAAAAATTTGAAGTGAAGAGTCTATCATGGAACCATGGAGGAGGAGCAAGCAACCGAGAGT 1235  
733 CAAAAATTTGAAGTGAAGAGTCTATCATGGAACCATGGAGGAGGAGCAAGCAACCGAGAGT 792

QY 1236 CTATCTCAGCTACAGACCTCAAAAGCTGATCAGCAAGACCTAGAGGAGAACAAATC 1295  
DB 793 CTATCTCAGCTACAGACCTCAAAAGCTGATCAGCAAGACCTAGAGGAGAACAAATC 852  
QY 1296 TTTGATGTGGGACAAATTCAGTTCACTGATGAATTCCTGGATCACTGCCAGCTTTGG 1355  
DB 853 TTTGATGTGGGACAAATTCAGTTCACTGATGAATTCCTGGATCACTGCCAGCTTTGG 912  
QY 1356 TCTTCACACCCCAATCAGAGCTGCCACATCTTTTGGCTGTTATAACAGAGAGTACTTTT 1415  
DB 913 TCTTCACACCCCAATCAGAGCTGCCACATCTTTTGGCTGTTATAACAGAGAGTACTTTT 972  
QY 1416 GAGTCCAGAACTTCTCTCTGTTGAACCCACCTTGAGACAGTGGACGGAGCAGAGCATGG 1475  
DB 973 GAGTCCAGAACTTCTCTCTGTTGAACCCACCTTGAGACAGTGGACGGAGCAGAGCATGG 1032  
QY 1476 TCTACTCAGCACTTCTTGGTCTCCACCTGCTATGGCCCTCTACCTCCCTGTGAGAGCTCC 1535  
DB 1033 TCTACTCAGCACTTCTTGGTCTCCACCTGCTATGGCCCTCTACCTCCCTGTGAGAGCTCC 1092  
QY 1536 ACCTTTCTTTATGGATCAAGCATCTTCTCTGATGATCAAGGACCAAGGACCAAGATCAAT 1595  
DB 1093 ACCTTTCTTTATGGATCAAGCATCTTCTCTGATGATCAAGGACCAAGGACCAAGATCAAT 1152  
QY 1596 GGCACACTCAGCAGACAAATGCTAGTACAGGAGCTCACCATCCCACTGATGATTTCTGC 1655  
DB 1153 GGCACACTCAGCAGACAAATGCTAGTACAGGAGCTCACCATCCCACTGATGATTTCTGC 1212  
QY 1656 AATCAGCAACTGGCTCTGGGAATTTCAATCCACCTGCTGATCTTTCAGATGACAGCCGATC 1715  
DB 1213 AATCAGCAACTGGCTCTGGGAATTTCAATCCACCTGCTGATCTTTCAGATGACAGCCGATC 1272  
QY 1716 AAGTSCAGGTGGCGAAGATATGTCAGACACTAGATGAATGATCTGCTGACACTCC 1775  
DB 1273 AAGTSCAGGTGGCGAAGATATGTCAGACACTAGATGAATGATCTGCTGACACTCC 1332  
QY 1776 TGCCCCATCTCAGGTACAGAGCTCAGCGAATATGTTTCTGTCCAGATCAATTTCTTGA 1835  
DB 1333 TGCCCCATCTCAGGTACAGCGGCTCAGCGAATATGTTTCTGTCCAGATCAATTTCTTGA 1392  
QY 1836 GGATACACTCTCTCAGCTTTACAGTATATCACCACCTAGTTCTATGACATTTGCCCTC 1895  
DB 1393 GGATACACTCTCTCAGCTTTACAGTATATCACCACCTAGTTCTATGACATTTGCCCTC 1452  
QY 1896 CAAGGGCCGAGAGCTGGTAGTGTTCTTCACTCTCGCTGTTGCTTAACATGGCTTTCTCAA 1955  
DB 1453 CAAGGGCCGAGAGCTGGTAGTGTTCTTCACTCTCGCTGTTGCTTAACATGGCTTTCTCAA 1512  
QY 1956 CGACTGTTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACAGCT 2015  
DB 1513 CGACTGTTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACAGCT 1572  
QY 2016 GCTGTTCCATATCTACGATCCAAATCTTACAGGATTTAAGCACTTGAATCTTAACTT 2075  
DB 1573 GCTGTTCCATATCTACGATCCAAATCTTACAGGATTTAAGCACTTGAATCTTAACTT 1632  
QY 2076 CAGAAAACGGAGTGTGATTTGTAATAGCAAAATGAAATTTGCTTAAGTCTGTGCGGTATAA 2135  
DB 1633 CAGAAAACGGAGTGTGATTTGTAATAGCAAAATGAAATTTGCTTAAGTCTGTGCGGTATAA 1692  
QY 2136 CCTCACCAGGCTGTGCAACGGGCTTTGGAGGATTTTCTGTTCTGTCAGCCCAACAACT 2195  
DB 1693 CCTCACCAGGCTGTGCAACGGGCTTTGGAGGATTTTCTGTTCTGTCAGCCCAACAACT 1752  
QY 2196 CCATCTGGAATAGACAGTACTCTCTCAACATTTGAACAGCTGATCAAGAGATCCCTG 2255  
DB 1753 CCATCTGGAATAGACAGTACTCTCTCAACATTTGAACAGCTGATCAAGAGATCCCTG 1812  
QY 2256 CAAGTCTCGCCCTGGCGGAAATTTGCCAATGTGTAAAGCAACGAGCTGAGGAGC 2315  
DB 1813 CAAGTCTCGCCCTGGCGGAAATTTGCCAATGTGTAAAGCAACGAGCTGAGGAGC 1872

```
QY 2316 GGAGTGTGCTGCAACAGGATATGACAGCAGGGAGCGCTGACCGTCTGGACCCAGG 2375
D 1873 GGAGTGTGCTGCAACAGGATATGACAGCAGGGAGCGCTGACCGTCTGGACCCAGG 1932
QY 2376 CCTCTGGCCCTGGCAAAAGGAATGCGAGTCTCTCAGGAAAGGAGCTCCATGCGAG 2435
D 1933 CCTCTGGCCCTGGCAAAAGGAATGCGAGTCTCTCAGGAAAGGAGCTCCATGCGAG 1992
QY 2436 GTTCCAGATCAGTCTGAAATCAAGATACAAACCTAGTGTAAAGGTTCCAAATCA 2495
D 1993 GTTCCAGATCAGTCTGAAATCAAGATACAAACCTAGTGTAAAGGTTCCAAATCA 2052
QY 2496 ACAAAATACAGTATTCAGTAAAGAAATCTGAAATTAAGCTGACCGTGAATATGAAGA 2555
D 2053 ACAAAATACAGTATTCAGTAAAGAAATCTGAAATTAAGCTGACCGTGAATATGAAGA 2112
QY 2556 ATTTAAACCATCAGATGGGAGGAATTAAGCTGAAATTAAGCTGAAATTAAGCTGAA 2615
D 2113 ATTTAAACCATCAGATGGGAGGAATTAAGCTGAAATTAAGCTGAAATTAAGCTGAA 2172
QY 2616 CTATCTCAAGAGATGATTTGCTCTCAAGGAAATGAGACAGCATATTCATGGGT 2675
D 2173 CTATCTCAAGAGATGATTTGCTCTCAAGGAAATGAGACAGCATATTCATGGGT 2232
QY 2676 CATCAAAATCCAGACATACAGTCAACTGAGAAATCAGACACACCATATTCATATATA 2735
D 2233 CATCAAAATCCAGACATACAGTCAACTGAGAAATCAGACACACCATATTCATATATA 2292
QY 2736 GAAGAGTCAATGCTGAGCAACAGTAAATCTGAAATTAAGCTGAAATTAAGCTGAA 2795
D 2293 GAAGAGTCAATGCTGAGCAACAGTAAATCTGAAATTAAGCTGAAATTAAGCTGAA 2352
QY 2796 AAACCCAAATGCAATCAGCAAAATATTTTACTATTTCTGGATGATGATGATGATGAT 2855
D 2353 AAACCCAAATGCAATCAGCAAAATATTTTACTATTTCTGGATGATGATGATGATGAT 2412
QY 2856 TCAATAGCCAGGTTGCTTCCACCTTCCGTAATTTTACTATTTCTGGATGATGATGATGAT 2915
D 2413 TCAATAGCCAGGTTGCTTCCACCTTCCGTAATTTTACTATTTCTGGATGATGATGATGAT 2472
QY 2916 AGCATAGCTTACTATTTGTTAGGAGTGAACAAATTTTGGAGCAAACTCTTTATAT 2975
D 2473 AGCATAGCTTACTATTTGTTAGGAGTGAACAAATTTTGGAGCAAACTCTTTATAT 2532
QY 2976 GCTAGAAATGATTAAGATGATCTTACGAGGAGATGAGGCTCTCTTAAAG 3035
D 2533 GCTAGAAATGATTAAGATGATCTTACGAGGAGATGAGGCTCTCTTAAAG 2592
QY 3036 CATGAATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3095
D 2593 CATGAATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2652
QY 3096 GATAAACAAACCTCAGTATTCAGTATTAAGGACATGATTTTATAGCAACTACTGC 3155
D 2653 GATAAACAAACCTCAGTATTCAGTATTAAGGACATGATTTTATAGCAACTACTGC 2712
QY 3156 TTACATAGTAGCTGTTTGTGCAATATCTTTGATGATGATGATGATGATGATGATGATGAT 3215
D 2713 TTACATAGTAGCTGTTTGTGCAATATCTTTGATGATGATGATGATGATGATGATGATGAT 2772
QY 3216 GTTCAGATACATACATGAGGAAATCTTACTTTTCTGTTTACTACAAAGCTATTTT 3275
D 2773 GTTCAGATACATACATGAGGAAATCTTACTTTTCTGTTTACTACAAAGCTATTTT 2832
QY 3276 AAGAGATGCTATGTTGGAGAGGGGAGTGTGATGATGATGATGATGATGATGATGATGAT 3330
D 2833 AAGAGATGCTATGTTGGAGAGGGGAGTGTGATGATGATGATGATGATGATGATGATGAT 2887
```

RESULT 7

ACC57947

ID ACC57947 standard; cDNA; 2887 BP.

XX

```
AC ACC57947;
XX 11-AUG-2003 (first entry)
XX Human interphotoreceptor matrix IPM 150, isoform B, cDNA.
XX Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
XX receptor; ophthalmological; gene therapy; gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 2..2143
XX FT /tag= a
XX FT /product= "IPM 150"
XX FT /partial
XX FT /note= "No start codon"
XX PN WO2003039346-A2.
XX PD 15-MAY-2003.
XX PF 08-NOV-2002; 2002WO-US036090.
XX PR 08-NOV-2001; 2001US-00077270.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI Hageman GS, Kuehn MH;
XX WIPI; 2003-441440/41.
XX PS Claim 1; Page 78-79; 105pp; English.
XX The present sequence is that of cDNA encoding isoform B of novel human
interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
is located on chromosome 6q13-q15, a region that also contains loci for
progressive bifocal choroidretinal atrophy, autosomal dominant Stargardt's
-like macular dystrophy, North Carolina macular dystrophy and Salla
disease. Members of the IPMC gene family have been identified in humans,
monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
CC Subfamilies are designated IPM 150 (or IPM1) and IPM 200 (or IPM2). The
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
CC antibodies that specifically bind the polypeptides, and vectors
comprising the polynucleotides. A claimed method of treating or
preventing photoreceptor death or retinal detachment involves
administering an IPMC polynucleotide, polypeptide or antibody. Also
CC claimed is a method for identifying a compound capable of modulating IPMC
gene expression
XX Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;
```

```
Query Match 83.1%; Score 2765.8; DB 8; Length 2887;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 2851; Conservative 0; Mismatches 22; Indels 62; Gaps 1;
QY 396 TTTTAGCAGCTCTTCAAGCTTATATAGATGAGTGTGTCAGGAAGCAGATGGGAAG 455
D 15 TTTTGGATTTTCTCCAGTTCAAGAACCAAGTGTGTGAGGAAGCAGATGGGAAG 74
QY 456 CATATCGGATCTTTCTGGATCGCATCCCTGACACAGGGGAATATCAGGCTGGGTGAGCA 515
D 75 CATATCGGATCTTTCTGGATCGCATCCCTGACACAGGGGAATATCAGGCTGGGTGAGCA 134
QY 516 TCTGCCAGCAGGAGACCTTCTGCTCTTTGACATTTGGAAAAAATTCAGCAATTTCCAGG 575
D 135 TCTGCCAGCAGGAGACCTTCTGCTCTTTGACATTTGGAAAAAATTCAGCAATTTCCAGG 194
```

QY 576 AGCACCTGGATCTTCTCCAGCAGAGATAAACAAGAGGTTTCCCTGACAGAAAGATG 635  
Db 196 AGCACCTGGATCTTCTCCAGCAGAGATAAACAAGAGGTTTCCCTGACAGAAAGATG 254  
QY 636 AAATATCTGCAGAGAGACATTTGGAGAGCCTGGTGAACCAATTTGTCATTTCAACAGCAA 695  
Db 255 AAATATCTGCAGAGAGACATTTGGAGAGCCTGGTGAACCAATTTGTCATTTCAAC----- 309  
QY 696 TCTACATTTCAAGACATTTGGCAGTATTCTAAGAAACCCCTCAGAAAGCAATTTCAAGA 755  
Db 310 -----AGA 312  
QY 756 TGTGCCAACGTCTCACCTTGGGCGCTTTCCCTCTCACTCTGATGACACCCCTCTCTCAATGA 815  
Db 313 TGTGCCAACGTCTCACCTTGGGCGCTTTCCCTCTCACTCTGATGACACCCCTCTCTCAATGA 372  
QY 816 AATTTCTCGATTAATACATCAACGACACCAAGATGCCCTAACAGAAAGAGAAACAGAAAT 875  
Db 373 AATTTCTCGATTAATACATCAACGACACCAAGATGCCCTAACAGAAAGAGAAACAGAAAT 432  
QY 876 CGCTGTGTGGAGGAGCAGAGGGGTGGAGCTCAGCGTCTCTGTGTAACCAAGATTCAA 935  
Db 433 CGCTGTGTGGAGGAGCAGAGGGGTGGAGCTCAGCGTCTCTGTGTAACCAAGATTCAA 492  
QY 936 GGCAGAGCTCGCTGACTCCAGTCCCATATTTACAGAGCTAGCAGAAAGTCCCAACT 995  
Db 493 GGCAGAGCTCGCTGACTCCAGTCCCATATTTACAGAGCTAGCAGAAAGTCCCAACT 552  
QY 996 TCAGATGCAAAAGATATTTAAGAACTTCCAGGATTCAGAAATCCATGTGTAGGAT 1055  
Db 553 TCAGATGCAAAAGATATTTAAGAACTTCCAGGATTCAGAAATCCATGTGTAGGAT 612  
QY 1056 TAGACCAAGAAAGAAAGATGCTCAAGTCCACAGAGATGCAACTTACGGCCATCTT 1115  
Db 613 TAGACCAAGAAAGAAAGATGCTCAAGTCCACAGAGATGCAACTTACGGCCATCTT 672  
QY 1116 TAAGAGACACAGTCAGAGCAAAAGCCCTGCAAGTGACCTCTGTCTTTTGAATCCAA 1175  
Db 673 TAAGAGACACAGTCAGAGCAAAAGCCCTGCAAGTGACCTCTGTCTTTTGAATCCAA 732  
QY 1176 CAAAAATTAAGAGTGAAGAGTCTATCATGGAACCATGGAGGAGCAAGCAACCAAGAAAT 1235  
Db 733 CAAAAATTAAGAGTGAAGAGTCTATCATGGAACCATGGAGGAGCAAGCAACCAAGAAAT 792  
QY 1236 CTATCTCACAGCTACAGACCTCAAAAGCTGATCAGCAAAAGCATAGAGAAAGCAATC 1295  
Db 793 CTATCTCACAGCTACAGACCTCAAAAGCTGATCAGCAAAAGCATAGAGAAAGCAATC 852  
QY 1296 TTTGGATGTGGGACAAATTCAGTTCACTGATGAATGTGCTGATCACTGACAGCCCTTTGG 1355  
Db 853 TTTGGATGTGGGACAAATTCAGTTCACTGATGAATGTGCTGATCACTGACAGCCCTTTGG 912  
QY 1356 TCCTGACACCAATCAGAGCTGCCACATCTTTTGTGTTTATAACAGAGATGCTACTTT 1415  
Db 913 TCCTGACACCAATCAGAGCTGCCACATCTTTTGTGTTTATAACAGAGATGCTACTTT 972  
QY 1416 GAGTCCAGAACTTCCCTGTTGAACCCAGCTTGGACAGATGGAGCGAGCAGCATGG 1475  
Db 973 GAGTCCAGAACTTCCCTGTTGAACCCAGCTTGGACAGATGGAGCGAGCAGCATGG 1032  
QY 1476 TCTACCTGACATCTTTGGTCTCCACTGCTATGGCTCTACCTCTGTCAGAAAGCTCC 1535  
Db 1033 TCTACCTGACATCTTTGGTCTCCACTGCTATGGCTCTACCTCTGTCAGAAAGCTCC 1092  
QY 1536 ACCTTTCTTTATGGCATCAAGCATCTTCTCTGATCTGATCAGGCAACCAAGATACAT 1595  
Db 1093 ACCTTTCTTTATGGCATCAAGCATCTTCTCTGATCTGATCAGGCAACCAAGATACAT 1152  
QY 1596 GGCCACTGACAGCAATGTAGTACAGGGGCTCACCATCCCAAGCATGATTTCTGCTC 1655  
Db 1153 GGCCACTGACAGCAATGTAGTACAGGGGCTCACCATCCCAAGCATGATTTCTGCTC 1212  
QY 1656 AATCAGCCAACTGGCTCTGGGAATTTCAATCCACTGCAATCTTCAGATGACAGCGGATC 1715

Db 1213 AATCAGCCAACTGGCTCTGGGAATTTCACTCCACTGCATCTTCAGATGACAGCGGATC 1272  
QY 1716 AAGTGCAGGTGGCGAAGATATGTTGATGAGACACCTAGATGAATGATCTGTCTGACACTCC 1775  
Db 1273 AAGTGCAGGTGGCGAAGATATGTTGATGAGACACCTAGATGAATGATCTGTCTGACACTCC 1332  
QY 1776 TGCCCATCTGAGGTACACAGAGCTCAGCGAATATGTTCTGTCCAGATCAATTTCTTGA 1835  
Db 1333 TGCCCATCTGAGGTACACAGAGCTCAGCGAATATGTTCTGTCCAGATCAATTTCTTGA 1392  
QY 1836 GGATACCACTCTCTGCTCAGCTTTACAGTATATACCACTAGTTCTATGACCAATGCCCC 1895  
Db 1393 GGATACCACTCTCTGCTCAGCTTTACAGTATATACCACTAGTTCTATGACCAATGCCCC 1452  
QY 1896 GAAGGGCCGAGAGCTGTGTGTTCTTCACTGCTGCTTCTTCACTAGCTTCTTCCAA 1955  
Db 1453 GAAGGGCCGAGAGCTGTGTGTTCTTCACTGCTGCTTCTTCACTAGCTTCTTCCAA 1512  
QY 1956 CGACCTGTTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACAGCT 2015  
Db 1513 CGACCTGTTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACAGCT 1572  
QY 2016 GCTGTTTCAATCTPAAGATCCAATCTTACAGGATTTAAGCAACTTGAATTAATTAACCT 2075  
Db 1573 GCTGTTTCAATCTPAAGATCCAATCTTACAGGATTTAAGCAACTTGAATTAATTAACCT 1632  
QY 2076 CAGAAACGGGAGTGTGTTGTAATAGCAAAATGAACTTGAAGTCTGTGCGGTATAA 2135  
Db 1633 CAGAAACGGGAGTGTGTTGTAATAGCAAAATGAACTTGAAGTCTGTGCGGTATAA 1692  
QY 2136 CTTCAACAGGCTGTGCAACGGGCTCTTGGAGGATTTTGGTCTGCTGAGGCCCAACT 2195  
Db 1693 CTTCAACAGGCTGTGCAACGGGCTCTTGGAGGATTTTGGTCTGCTGAGGCCCAACT 1752  
QY 2196 CCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACAGCTGATCAGAGATCCCTG 2255  
Db 1753 CCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACAGCTGATCAGAGATCCCTG 1812  
QY 2256 CAAAGTTCCTGCGCTGCGGCGAATTTGGCCAAATGTGTAAGAAACGAACTGAGGAAGC 2315  
Db 1813 CAAAGTTCCTGCGCTGCGGCGAATTTGGCCAAATGTGTAAGAAACGAACTGAGGAAGC 1872  
QY 2316 GAGTGTCTGCTGCAAAACAGGATATGACAGCCAGGGAGCTTGAAGCTTGGAAACGAG 2375  
Db 1873 GAGTGTCTGCTGCAAAACAGGATATGACAGCCAGGGAGCTTGAAGCTTGGAAACGAG 1932  
QY 2376 CCTCTGCGGCTTGCAAAAGGAAATGCGAGTCTTCCAGGAAAGGAGCTCCATGCGAG 2435  
Db 1933 CCTCTGCGGCTTGCAAAAGGAAATGCGAGTCTTCCAGGAAAGGAGCTCCATGCGAG 1992  
QY 2436 GTTGCAGATCACTCTGAAATCAAGCATCAAAACTAGTGTAAAAAGTTTCCAAATCA 2495  
Db 1993 GTTGCAGATCACTCTGAAATCAAGCATCAAAACTAGTGTAAAAAGTTTCCAAATCA 2052  
QY 2496 ACAGAAATCAAGGATATCAGTAAAGAAATTTCTGAATTTACTGACCGTAGAATGAGA 2555  
Db 2053 ACAGAAATCAAGGATATCAGTAAAGAAATTTCTGAATTTACTGACCGTAGAATGAGA 2112  
QY 2556 ATTTAACCATCAAGATTTGGGAAGGAAATTTAAAACTGAAATTTGTAATTTACTTAGG 2615  
Db 2113 ATTTAACCATCAAGATTTGGGAAGGAAATTTAAAACTGAAATTTGTAATTTACTTAGG 2172  
QY 2616 CTATCTCAGAGAGATGATTTGCTTCTCAAGGAAATGAGAGAGCATATTCATCGGT 2675  
Db 2173 CTATCTCAGAGAGATGATTTGCTTCTCAAGGAAATGAGAGAGCATATTCATCGGT 2232  
QY 2676 CATCAAAATCCAGACATACAGTCAACCTGAGATCAGACACACCATATTTCAAAATATA 2735  
Db 2233 CATCAAAATCCAGACATACAGTCAACCTGAGATCAGACACACCATATTTCAAAATATA 2292  
QY 2736 GAAGAGTCATGTTCTTGGCAACGATTAATTTGAAAAAAGAACACTTACTTATTATA 2795

Db 2293 GAAGAGTCATGCTGCTGCAACCACTAATCTGAAAAAAGACACTTACTTATTATTA 2352

Qy 2796 AAACCCCAATGCAATCAGCAACATATTTTACTATCTTGGATGATAGTCAAAATGA 2855

Db 2353 AAACCCCAATGCAATCAGCAACATATTTTACTATCTTGGATGATAGTCAAAATGA 2412

Qy 2856 TCATAAGCCAGGTTGCTTCCACCTTCCCTGAAATTTTACTACAGATCAATTTGCAACA 2915

Db 2413 TCATAAGCCAGGTTGCTTCCACCTTCCCTGAAATTTTACTACAGATCAATTTGCAACA 2472

Qy 2916 AGCATAGCTTACTTATTTAGGACTGAACAATTTTATTTGGGAAGCAAACTCTTTATAT 2975

Db 2473 AGCATAGCTTACTTATTTAGGACTGAACAATTTTATTTGGGAAGCAAACTCTTTATAT 2532

Qy 2976 GCTAGAAAGTACATTTAAAGATGACTACTTACCGAGGAGATCGAGTCTCTTAAACG 3035

Db 2533 GCTAGAAAGTACATTTAAAGATGACTACTTACCGAGGAGATCGAGTCTCTTAAACG 2592

Qy 3036 CATGAATGATGTAGTGTAGGCACTGTAGTGTATATATGCTTCCACACTACGTCT 3095

Db 2593 CATGAATGATGTAGTGTAGGCACTGTAGTGTATATATGCTTCCACACTACGTCT 2652

Qy 3096 GATAAACAACCTCAGTATTCAGTTATTAGGCACACTAGTTTATACGCAACTACTGC 3155

Db 2653 GATAAACAACCTCAGTATTCAGTTATTAGGCACACTAGTTTATACGCAACTACTGC 2712

Qy 3156 TTACATAGTAGACTGTTTGTGCAATAATCTTTGAATTTCTTTAAAGAACTGAG 3215

Db 2713 TTACATAGTAGACTGTTTGTGCAATAATCTTTGAATTTCTTTAAAGAACTGAG 2772

Qy 3216 GTTCAGATACACATACCATGCAAAATCTTACTTTTCTTTACTACACAAAGCTATTT 3275

Db 2773 GTTCAGATACACATACCATGCAAAATCTTACTTTTCTTTACTACACAAAGCTATTT 2832

Qy 3276 AAAGAAGTGTATGTTGGGAGAGGCGAAGTTGTACTATATGACATATCAAT 3330

Db 2833 AAAGAAGTGTATGTTGGGAGAGGCGAAGTTGTACTATATGACATATCAAT 2887

RESULT 8

AAA46328

ID AAA46328 standard; DNA; 2966 BP.

XX

AC AAA46328;

XX

DT 04-SEP-2000 (first entry)

XX

DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.

XX

KW Interphotoreceptor matrix; IPM; proteoglycan, IPM150; IPMC; IPM200;

KW chromosome 6q13-q15; ocular disease; retinal detachment;

KW chorioretinal degeneration; retinal degeneration; cone degeneration;

KW age related macular degeneration; photoreceptor degeneration;

KW retinal pigment epithelium degeneration; mucopolysaccharidosis;

KW rod- cone dystrophy; cone-rod dystrophy; ss.

XX

OS Homo sapiens.

XX

FN W0200026367-A2.

XX

PD 11-MAY-2000.

XX

PF 29-OCT-1999; 99WO-US025440.

XX

PR 29-OCT-1998; 98US-00183972.

XX

PA (IOWA ) UNIV IOWA RES FOUND.

XX

PI Hageman GS, Kuehn MH;

XX

DR WPI; 2000-365616/31.

XX

PT Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for

preventing, diagnosing and treating ocular disorders such as retinal detachment and chorioretinal degeneration.

Claim 3; Fig 18; 183pp; English.

The present sequence represents a splice variant of an interphotoreceptor matrix (IPM) proteoglycan, designated IPM150. The sequence is missing exon 2. The protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome 6q13-q15, between markers CHLC.GATA11p10 and D6S284. The IPM proteins may be used to supplement a patient's own production of the protein or to rectify alterations in their nucleic acids that result in expression of an inactive protein. The IPM nucleic acids may be used in this way to treat ocular diseases such as retinal detachment, chorioretinal degeneration, retinal degeneration, age related macular degeneration, photoreceptor degeneration, RPE (retinal pigment epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also be used to assay for other modulators of IPM proteoglycan expression and activity that may be used to treat ocular diseases. The nucleic acids and proteins may also be used as diagnostic reagents to detect the presence of IPM nucleic acids and their products in samples from patients according to standard methodologies

Sequence 2966 BP; 918 A; 687 C; 624 G; 737 T; 0 U; 0 Other;

Query Match 81.8%; Score 2724.6; DB 3; Length 2966;

Best Local Similarity 96.9%; Pred. No. 0;

Matches 2845; Conservative 0; Mismatches 24; Indels 66; Gaps 4;

Qy 396 TTTTAGACAGCTCTTCAAGCTTATTATAGATTGAGAGTGTGTCAGGAACGACTATGGGAAG 455

Db 15 TTTTGTGATTTTCTCCAGTTCAAGGAACCAAGTGTGTGAGGACGATATGGGAAG 74

Qy 456 CATATCGGATCTTTCTGGATCGATTCCTGACACAGGGGAATATCAGGACTGGGTACGA 515

Db 75 CATATCGGATCTTTCTGGATCGATTCCTGACACAGGGGAATATCAGGACTGGGTACGA 134

Qy 516 TCTGCCACGACGAGACCTTCTGCTCTTTGACATTTGGAATAAACTTCAGCAATTTCCGAG 575

Db 135 TCTGCCACGACGAGACCTTCTGCTCTTTGACATTTGGAATAAACTTCAGCAATTTCCGAG 194

Qy 576 AGCACTCGATCTTTCTCCAGCAGAGATAAAACAGAGAAGTTTCCCTGACAGAAAAGATG 635

Db 195 AGCACTCGATCTTTCTCCAGCAGAGATAAAACAGAGAAGTTTCCCTGACAGAAAAGATG 254

Qy 636 AAATATCTGCAGAGAAGACATTTGGAGAGCTGTGTGAAACCATTTGTCATTTCACAGCAA 695

Db 255 AAATATCTGCAGAGAAGACATTTGGAGAGCTGTGTGAAACCATTTGTCATTTCACAC 309

Qy 696 TCTACATTTCAAGACTTTGGCAGTATTCTAAGAAAAACCTCAGAGAGCAAAATTCAGA 755

Db 310 -----AGT 312

Qy 756 TGTTCGCAACGCTCTCACTTGGGCTTTCCCTCTCACTTCCTGATGACACCTCTCCTCAATGA 815

Db 313 TGTTCGCAACGCTCTCACTTGGGCTTTCCCTCTCACTTCCTGATGACACCTCTCCTCAATGA 372

Qy 816 AATTCTCGATAATACACTCAACGACACCAAGATGCTTACACAGAGAGAAACAGAAAT 875

Db 373 AATTCTCGATAATACACTCAACGACACCAAGATGCTTACACAGAGAGAAACAGAAAT 432

Qy 876 CGCTGTGTGGAGGAGCAGAGGGTGGAGCTCAGCGTCTCTCTGTAAACAGAGTTCAA 935

Db 433 CGCTGTGTGGAGGAGCAGAGGGTGGAGCTCAGCGTCTCTCTGTAAACAGAGTTCAA 492

Qy 936 GGCAGAGCTCGCTGACTCCCGAGTCCCATATTTACCAGAGCTAGCAGGAAGTCCCACT 995

Db 493 GGCAGAGCTCGCTGACTCCCGAGTCCCATATTTACCAGAGCTAGCAGGAAGTCCCACT 552

Qy 996 TCAGATCAAAAAGATATTTAAGAAACTTCCAGGATTCAAAAAATCCATGTGTAGGATT 1055

Db 553 TCAGATCAAAAAGATATTTAAGAAACTTCCAGGATTCAAAAAATCCATGTGTAGGATT 612



QY 1056 TAGACCAAGAGAGAAAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATCTT 1115  
DB |||||  
DB 613 TAGACCAAGAGAGAAAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATCTT 672  
QY 1116 TAAGAGACACAGTCAGAGAGCAAAAAAGCCCTGCAAGTGACCTCTGCTTTTGAATCCAA 1175  
DB |||||  
DB 673 TAAGAGACACAGTCAGAGAGCAAAAAAGCCCTGCAAGTGACCTCTGCTTTTGAATCCAA 732  
QY 1176 CAAAATTGAAAGTAGAGAGAGCTATCATGGAACCATAGGAGAGACAAAGCAACAGAAAT 1235  
DB |||||  
DB 733 CAAAATTGAAAGTAGAGAGAGCTATCATGGAACCATAGGAGAGACAAAGCAACAGAAAT 792  
QY 1236 CTATCTCAGAGTCAGAGACCTCAAAAGGCTGATCAGCAAAAGCTATAGAGGAAGAACATC 1295  
DB |||||  
DB 793 CTATCTCAGAGTCAGAGACCTCAAAAGGCTGATCAGCAAAAGCTATAGAGGAAGAACATC 852  
QY 1296 TTTGGATGTGGGGA CAATTCAGTTCACTGATGAAATTTGCTGGATCACTGCCAGCCTTTGG 1355  
DB |||||  
DB 853 TTTGGATGTGGGGA CAATTCAGTTCACTGATGAAATTTGCTGGATCACTGCCAGCCTTTGG 912  
QY 1356 TCCTCAGACCCCAATCAGAGCTGCCACATCTTTTGGCTTTATACAGAGGATGCTACTTT 1415  
DB |||||  
DB 913 TCCTCAGACCCCAATCAGAGCTGCCACATCTTTTGGCTTTATACAGAGGATGCTACTTT 972  
QY 1416 GAGTCCAGAACTTCCTCTGTTGAACCCAGCTTGAGACAGTCGAGCGAGCAGATGG 1475  
DB |||||  
DB 973 GAGTCCAGAACTTCCTCTGTTGAACCCAGCTTGAGACAGTCGAGCGAGCAGATGG 1032  
QY 1476 TCTACCTCAGACTTCTTGGTCTCCACCTGCTATGGCTCTACCTCCCTGTCAGAGCTCC 1535  
DB |||||  
DB 1033 TCTACCTCAGACTTCTTGGTCTCCACCTGCTATGGCTCTACCTCCCTGTCAGAGCTCC 1092  
QY 1536 ACCTTTCTTTATGGCATCAAGCATCTCTCTGACTGATCAAGGCAACCCACAGATACAAT 1595  
DB |||||  
DB 1093 ACCTTTCTTTATGGCATCAAGCATCTCTCTGACTGATCAAGGCAACCCACAGATACAAT 1152  
QY 1596 GGCCACTGACCAGACAAATGCTAGTACAGGCTCAACATCCCAACCAAGTGAATTTCTGC 1655  
DB |||||  
DB 1153 GGCCACTGACCAGACAAATGCTAGTACAGGCTCAACATCCCAACCAAGTGAATTTCTGC 1212  
QY 1656 AATCAGCCAACTGGCTCTGGGAATTTACATCCACCTGCATCTTCAGATGACAGCCGATC 1715  
DB |||||  
DB 1213 AATCAGCCAACTGGCTCTGGGAATTTACATCCACCTGCATCTTCAGATGACAGCCGATC 1272  
QY 1716 AAGTSCAGGTGGCGAAGATATGGTCAGACACCTAGATGAAATGGATCTGTCTGACACTCC 1775  
DB |||||  
DB 1273 AAGTSCAGGTGGCGAAGATATGGTCAGACACCTAGATGAAATGGATCTGTCTGACACTCC 1332  
QY 1776 TGCCCATCTGAGGTACAGAGCTCAGGGAATATGTTCTGTCCAGATCAATTTCTTGA 1835  
DB |||||  
DB 1333 TGCCCATCTGAGGTACAGGCTCAGGGAATATGTTCTGTCCAGATCAATTTCTTGA 1392  
QY 1836 GGATACCACTCTGCTCTCAGCTTTACAGTATATCAACCACTAGTTCTATGACCATTTGCC 1895  
DB |||||  
DB 1393 GGATACCACTCTGCTCTCAGCTTTACAGTATATCAACCACTAGTTCTATGACCATTTGCC 1452  
QY 1896 CAAGGCGGAGAGCTGGTAGTGTCTTCAGTCTGGGTGTTGCTAAACATGGCTTTCTCCAA 1955  
DB |||||  
DB 1453 CAAGGCGGAGAGCTGGTAGTGTCTTCAGTCTGGGTGTTGCTAAACATGGCTTTCTCCAA 1512  
QY 1956 CGACTGTCTCAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACAGCT 2015  
DB |||||  
DB 1513 CGACTGTCTCAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACAGCT 1572  
QY 2016 GCTGTTCCATATCTAOSATCAATCTTTACAGGATTTAAGCAACTTGAATTTAACTTAACTT 2075  
DB |||||  
DB 1573 GCTGTTCCATATCTAOSATCAATCTTTACAGGATTTAAGCAACTTGAATTTAACTTAACTT 1632  
QY 2076 CAGAAACGGAGTGTGATTTGAATAGCAAAATGCTTTGCTAGTCTGTCGGCTATAA 2135  
DB |||||  
DB 1633 CAGAAACGGAGTGTGATTTGAATAGCAAAATGCTTTGCTAGTCTGTCGGCTATAA 1692

2136 CCTCACCAAGGCTGTGCACGGGCTCTTGAGAGATTTTGGTTCTGCTGCAGGCCCAACAAT 2195  
DB |||||  
DB 1693 CCTCACCAAGGCTGTGCACGGGCTCTTGAGAGATTTTGGTTCTGCTGCAGGCCCAACAAT 1752  
QY 2196 CCAATCTGGAAAATAGACAGCTACTCTCTCAACATTCGAAACAGCTGATCAAGCAGATCCCTG 2255  
DB |||||  
DB 1753 CCAATCTGGAAAATAGACAGCTACTCTCTCAACATTCGAAACAGCTGATCAAGCAGATCCCTG 1812  
QY 2256 CAAATTTCTGGCTCGGGCGAAATTTGGCCCAATGTGTAAAGAACGAAACGGACTGAGGAAGC 2315  
DB |||||  
DB 1813 CAAATTTCTGGCTCGGGCGAAATTTGGCCCAATGTGTAAAGAACGAAACGGACTGAGGAAGC 1872  
QY 2316 GAGTGTCTGCTCCCAACACAGGATATGACAGCCAGGAGGCTTGGACGCTCTGGAACCAAG 2375  
DB |||||  
DB 1873 GAGTGTCTGCTCCCAACACAGGATATGACAGCCAGGAGGCTTGGACGCTCTGGAACCAAG 1932  
QY 2376 CTTCTGTGGCTCGGCACAAAGGAATGCGAGTCTCCAGGAAAGGAGCTCCATGAG 2435  
DB |||||  
DB 1933 CTTCTGTGG - CTTCTGTGG - CTTCTGTGG - CTTCTGTGG - CTTCTGTGG - CTTCTGTGG - 1989  
QY 2436 GTTCCAGATCACTCTGAAAATCAAGCATACAAAATCTAGTGT - AAAAGTTCCTCAAAATCA 2495  
DB |||||  
DB 1990 GTTCCAGATCACTCTGAAAATCAAGCATACAAAATCTAGTGT - AAAAGTTCCTCAAAATCA 2048  
QY 2496 ACAAATTAACAAGTAAATCAGTAAAGGAATTTCTGAATTTACTGACCGTAGAATATGAAGA 2555  
DB |||||  
DB 2049 ACAAATTAACAAGTAAATCAGTAAAGGAATTTCTGAATTTACTGACCGTAGAATATGAAGA 2108  
QY 2556 ATTTAACCATCAAGATTTGGAGGAATTTAAACCTGAAATGTACAAATTTACTCATTAG 2615  
DB |||||  
DB 2109 ATTTAACCATCAAGATTTGGAGGAATTTAAACCTGAAATGTACAAATTTACTCATTAG 2168  
QY 2616 CTATCTCAAGAGAGATGATTTGCCCTTCTCAAGGAAATGGAGACAGGATATTTCAATGGT 2675  
DB |||||  
DB 2169 CTATCTCAAGAGAGATGATTTGCCCTTCTCAAGGAAATGGAGACAGGATATTTCAATGGT 2228  
QY 2676 CATCAAAATCCAGACATACAGTCAACCTGAGAAATTCAGACACACCATATTTCAAATATA 2735  
DB |||||  
DB 2229 CATCAAAATCCAGACATACAGTCAACCTGAGAAATTCAGACACACCATATTTCAAATATA 2288  
QY 2736 GAAGAGTCAATGCTGCTGCAACCTGAAATTTCTGAAAAGAAAGACACTTACTTATTTA 2795  
DB |||||  
DB 2289 GAAGAGTCAATGCTGCTGCAACCTGAAATTTCTGAAAAGAAAGACACTTACTTATTTA 2346  
QY 2796 AAACCCCAATCAATCAGCGAAACATATTTTACTATTTCTGGATGATGCTCAAAATGA 2855  
DB |||||  
DB 2349 AAACCCCAATCAATCAGCGAAACATATTTTACTATTTCTGGATGATGCTCAAAATGA 2408  
QY 2856 TCATAAGCCAGGTTTGGCTTCCACCTTCCCTGAAAATTTTACTCAGAGATCAATTTGCAACA 2915  
DB |||||  
DB 2409 TCATAAGCCAGGTTTGGCTTCCACCTTCCCTGAAAATTTTACTCAGAGATCAATTTGCAACA 2468  
QY 2916 AGCATAGCTTTACTTATTTGTTAGGACTGAAACATTTTATTTGGGAGCAAACTCTTTATAT 2975  
DB |||||  
DB 2469 AGCATAGCTTTACTTATTTGTTAGGACTGAAACATTTTATTTGGGAGCAAACTCTTTATAT 2528  
QY 2976 GCTAGAGATACATTTAAAGATGATCTTACGCGAGGAGATGCGAGTCTCTCTAAAGC 3035  
DB |||||  
DB 2529 GCTAGAGATACATTTAAAGATGATCTTACGCGAGGAGATGCGAGTCTCTCTAAAGC 2588  
QY 3036 CATGAATGTATGTAGTGTGAGGACTGCTAGTGTATATATGCTCCACACTACGCTCT 3095  
DB |||||  
DB 2589 CATGAATGTATGTAGTGTGAGGACTGCTAGTGTATATATGCTCCACACTACGCTCT 2648  
QY 3096 GATAACCAAAACCTCAGTATTTAGGCACTAGTTTTATAGCAACTTACTGTC 3155  
DB |||||  
DB 2649 GATAACCAAAACCTCAGTATTTAGTATTTAGGCACTAGTTTTATAGCAACTTACTGTC 2708  
QY 3156 TTACATAGTAGACTGTTTTGTTGGCAATACTTTGAAATGCTTTTAAAGAACTGAG 3215  
DB |||||  
DB 2709 TTACATAGTAGACTGTTTTGTTGGCAATACTTTGAAATGCTTTTAAAGAACTGAG 2769  
QY 3216 GTTCAGATACATACCATGGAATACTTACTTTTCTTGTGTACTACAAAGGCTATTTT 3275



```
Db 2769 GTTCAGATACATACCAATGGAATAATCTTACTTTCTGTATACACAAAGCTATTTT 2828
QY 3276 AAAGAAGATGCTATGTTGGGAGAGGGCGAAGTTGTACTATATACATAATCAAT 3330
Db 2829 AAAGAAGATGCTATGTTGGGAGAGGGCGAAGTTGTACTATATACATAATCAAT 2883

RESULT 9
AAA46329
ID AAA46329 standard; DNA; 2244 BP.
XX AAA46329;
XX
XX
XX 04-SEP-2000 (first entry)
XX
XX Interphotoreceptor matrix proteoglycan (IPM150) splice variant.
XX
XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPW200;
XX chromosome 6q13-q15; ocular disease; retinal detachment;
XX choriorretinal degeneration; retinal degeneration; cone degeneration;
XX age related macular degeneration; photoreceptor degeneration;
XX retinal pigment epithelium degeneration; mucopolysaccharidosis;
XX rod- cone dystrophy; cone-rod dystrophy; ss.
XX
XX Homo sapiens.
XX
XX WO200026367-A2.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025440.
XX
XX 29-OCT-1998; 98US-00183972.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2000-365616/31.
XX
XX
XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
XX preventing, diagnosing and treating ocular disorders such as retinal
XX detachment and chorioretinal degeneration.
XX
XX Claim 3; Fig 19; 183pp; English.
XX
XX The present sequence represents a splice variant of an interphotoreceptor
XX matrix (IPM) proteoglycan, designated IPM150. The sequence comprises an
XX additional intron after exon 5. The protein is an IPM component (IPMC).
XX Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
XX is located on chromosome 6q13-q15, between markers CHLC.GATA11P10 and
XX D6S284. The IPM proteins may be used to supplement a patient's own
XX production of the protein or to rectify alterations in their nucleic
XX acids that result in expression of an inactive protein. The IPM nucleic
XX acids may be used in this way to treat ocular diseases such as retinal
XX detachment, choriorretinal degeneration, retinal degeneration, age related
XX macular degeneration, photoreceptor degeneration, KPE (retinal pigment
XX epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-
XX cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
XX also be used to assay for other modulators of IPM proteoglycan expression
XX and activity that may be used to treat ocular diseases. The nucleic acids
XX and proteins may also be used as diagnostic reagents to detect the
XX presence of IPM nucleic acids and their products in samples from patients
XX according to standard methodologies
XX
XX Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
XX
XX Query Match 65.6%; Score 2184.2; DB 3; Length 2244;
XX Best Local Similarity 99.5%; Pred. No. 0;
XX Matches 2211; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
XX
XX 1 TAAACCAAGAGGTTATCCTCAATCATCTGGTATCAATATATATATTTTTCACATTTC 60
```

```
Db 22 TAAACCAAGAGGTTATCCTCAATCATCTGGTATCAATATATATTTTTCACATTTC 81
QY 61 TGTACTTTTAAATGAGATTTGAGGTTGTTCTGTGATTTGTTATCAGAATTACCAATGCAC 120
Db 82 TGTACTTTTAAATGAGATTTGAGGTTG-TCTGTGATTTGTTATCAGAATTACCAATGCAC 140
QY 121 AAAAGCCAGAATGTATTTTGGAACTAGAGAGCTATTTTGTGTTTGGATTTTCTCCA 180
Db 141 AAAAGCCAGAATGTATTTTGGAACTAGAGAGCTATTTTGTGTTTGGATTTTCTCCA 200
QY 181 AGTTCAAGGACCAAGATATATCTCAATTAAATATACATATACCAATCTGAAACTAAGACATAGA 240
Db 201 AGTTCAAGGACCAAGATATATCTCAATTAAATATACATATACCAATCTGAAACTAAGACATAGA 260
QY 241 CAATCCCCCAAGAAATGAACAACTGAAAGTACTGAAATAATGTACAAAATGTCAACTAT 300
Db 261 CAATNCCCCCAAGAAATGAACAACTGAAAGTACTGAAATAATGTACAAAATGTCAACTAT 320
QY 301 GAGACGAATATTCGATTTGGCAAGCATCGAAACAAAAGATCCGCAATTTTCCCAACGGG 360
Db 321 GAGACGAATATTCGATTTGGCAAGCATCGAAACAAAAGATCCGCAATTTTCCCAACGGG 380
QY 361 GGTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTAGACAGTCTTCAAGCTTATTA 420
Db 381 GGTAAAGTCTGTCCACAGGAATCCATGAAACAGATTTAGACAGTCTTCAAGCTTATTA 440
QY 421 TAGATTGAGAGTGTGTCAGGAAGCAGTATGGAAAGCATATCGGATCTTTCTGGATCGCAT 480
Db 441 TAGATTGAGAGTGTGTCAGGAAGCAGTATGGAAAGCATATCGGATCTTTCTGGATCGCAT 500
QY 481 CCCTTGACACAGGGGAATATCAGGACTGSGTCAGCATCTGCCAGCAGGAGAGACCTTCTGCT 540
Db 501 CCCTTGACACAGGGGAATATCAGGACTGSGTCAGCATCTGCCAGCAGGAGAGACCTTCTGCT 560
QY 541 CTTTGACATTGGAAAAAATCTTCAGCAATTCAGGAGCAGCTGGATCTTCTCCAGCAGAG 600
Db 561 CTTTGACATTGGAAAAAATCTTCAGCAATTCAGGAGCAGCTGGATCTTCTCCAGCAGAG 620
QY 601 AATAAACAAGAGAGTTTCCCTGACAGAAAGATGAATATCTGCAGAGAGACATTTGGG 660
Db 621 AATAAACAAGAGAGTTTCCCTGACAGAAAGATGAATATCTGCAGAGAGACATTTGGG 680
QY 661 AGAGCCTGTGTGAAACCATTTCTCATTTCAACAGCAATCTACATTTCAAGAGCTTTGGGCGT 720
Db 681 AGAGCCTGTGTGAAACCATTTCTCATTTCAACAGCAATCTACATTTCAAGAGCTTTGGGCGT 740
QY 721 ATTCTAAGAAAAACCTCAGAAAGCAGCAATTCAGAGTGTTCGCAACGCTCTCACTTGGGCT 780
Db 741 ATTCTAAGAAAAACCTCAGAAAGCAGCAATTCAGAGTGTTCGCAACGCTCTCACTTGGGCT 800
QY 781 TTCCTCTCACTCTCATGACACCCCTCCTCAATGAATTTCTGATATATACACTCAACGAC 840
Db 801 TTCCTCTCACTCTCATGACACCCCTCCTCAATGAATTTCTGATATATACACTCAACGAC 860
QY 841 ACCAAGATGCTTACACAGAAAGAGAAACAGAAATTCGCTGTGTGGAGGAGCAGAGGGTG 900
Db 861 ACCAAGATGCTTACACAGAAAGAGAAACAGAAATTCGCTGTGTGGAGGAGCAGAGGGTG 920
QY 901 GAGCTCAGCGTCTCTCTGTTAAACAGAGAGTTCAAGGAGAGCTGCTGACTCCAGTCC 960
Db 921 GAGCTCAGCGTCTCTCTGTTAAACAGAGAGTTCAAGGAGAGCTGCTGACTCCAGTCC 980
QY 961 CCATATTACAGGAGCTAGCAGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAA 1020
Db 981 CCATATTACAGGAGCTAGCAGAAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAA 1040
QY 1021 CTTCCAGGATTCAAAAAATCCATGTTAGGATTTAGACCAAGAGAGAGAGAGAGTGGC 1080
Db 1041 CTTCCAGGATTCAAAAAATCCATGTTAGGATTTAGACCAAGAGAGAGAGAGTGGC 1100
QY 1081 TCAAGCTCCACAGAGATGCAACTTTCAGGCGCATCTTTAAGAGACACAGTGCACAGACAAA 1140
```



SQ	Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;	
	Query Match 65.6%; Score 2184.2; DB 7; Length 2244;	
	Best Local Similarity 99.5%; Fred. No. 0;	
	Matches 2211; Conservative 0; Mismatches 10; Indels 2; Gaps 2;	
QY	1 TAAACCAAGAGGTTATCCTCAATCATCTGGTATCAATATATATATTTTTCACATTTC	60
DB	22 TAAACCAAGAGGTTATCCTCAATCATCTGGTATCAATATATATATTTTTCACATTTC	81
QY	61 TGTACTTTTTTAAGTGAATTTGAGGTTGTTCTGTGATGTTATCAGAAATACCAATGCAC	120
DB	82 TGTACTTTTTTAAGTGAATTTGAGGTTG-TCTGTGATTTGTTATCAGAAATACCAATGCAC	140
QY	121 AAAAGCCAGAGATGATTTGGAAACTAGAGAGCTATTTTGGTTTTTGGATTTTCTCCA	180
DB	141 AAAAGCCAGAGATGATTTGGAAACTAGAGAGCTATTTTGGTTTTTGGATTTTCTCCA	200
QY	181 AGTTCAAGAACCAAGATATCTCCATTAACATATACCATTTCTGAACATAAGACATAGA	240
DB	201 AGTTCAAGAACCAAGATATCTCCATTAACATATACCATTTCTGAACATAAGACATAGA	260
QY	241 CAATCCCCCAAGAAATGAAACAACTGAAGTACTGAAAATATGTAACAAATGTCAACTAT	300
DB	261 CAATNCCCCAAGAAATGAAACAACTGAAGTACTGAAAATATGTAACAAATGTCAACTAT	320
QY	301 GAGACGAATATTCGATTTGGCAAGCATCGAACCAAAAAGATCCGCATTTTCCCAACGGG	360
DB	321 GAGACGAATATTCGATTTGGCAAGCATCGAACCAAAAAGATCCGCATTTTCCCAACGGG	380
QY	361 GGTATAAGTCTGTCCACAGAAATCCATGAACAGATTTTGAAGATCTTCAGACTTATTA	420
DB	381 GGTATAAGTCTGTCCACAGAAATCCATGAACAGATTTTGAAGATCTTCAGACTTATTA	440
QY	421 TAGATTGAGAGTGTGTGAGAGCAGTATGGGAAGCATATCGCATCTTCTGTGATCGCAT	480
DB	441 TAGATTGAGAGTGTGTGAGAGCAGCATGGGAAGCATATCGCATCTTCTGTGATCGCAT	500
QY	481 CCCTGACACAGGGGAATATCAGACTGGGTGACATCTGTCAGCAGGAGACCTTTCGCT	540
DB	501 CCCTGACACAGGGGAATATCAGACTGGGTGACATCTGTCAGCAGGAGACCTTTCGCT	560
QY	541 CTTTGACATTTGAAAAAACTTTCAGCAATTTCCAGAGGACCTTGGATCTTCTCCAGCAGAG	600
DB	561 CTTTGACATTTGAAAAAACTTTCAGCAATTTCCAGAGGACCTTGGATCTTCTCCAGCAGAG	620
QY	601 AATAAACAAGAGTTTCCTGACAGAAAGATGAAATATCTGACAGAGACATTTGG	660
DB	621 AATAAACAAGAGTTTCCTGACAGAAAGATGAAATATCTGACAGAGACATTTGG	680
QY	661 AGAGCCTGGTGAACCATTTGTCATTTTCAACAGCAATCTACATTTCAAGACTTTGGGCAGT	720
DB	681 AGAGCCTGGTGAACCATTTGTCATTTTCAACAGCAATCTACATTTCAAGACTTTGGGCAGT	740
QY	721 ATTCTAAGAAAAACCTTCAGAGAGCAAAATTCAGATGTTTGCACAGCTCTCACTTGGGCT	780
DB	741 ATTCTAAGAAAAACCTTCAGAGAGCAAAATTCAGATGTTTGCACAGCTCTCACTTGGGCT	800
QY	781 TTCCCTCTCACTCCTGTATGACACACCTTCTCAATGAAATTTCTCGATAATACACTCAACAC	840
DB	801 TTCCCTCTCACTCCTGTATGACACACCTTCTCAATGAAATTTCTCGATAATACACTCAACAC	860
QY	841 ACCAAGATCCCTACACAGAAAGAGAAACAGAAATTCGCTGTGTTGGAGAGCAGAGGGTG	900
DB	861 ACCAAGATCCCTACACAGAAAGAGAAACAGAAATTCGCTGTGTTGGAGAGCAGAGGGTG	920
QY	901 GAGCTCAGGCTCTCTGTGTAACAGAGATTTCAAGGAGAGCTCGCTGATCTCCAGTCC	960
DB	921 GAGCTCAGGCTCTCTGTGTAACAGAGATTTCAAGGAGAGCTCGCTGATCTCCAGTCC	980
QY	961 CCATATTACAGAGCTAGCAGGAAGTCCCAACTTCAGATGCGAAAGATATTTAAGAA	1020
DB	981 CCATATTACAGAGCTAGCAGGAAGTCCCAACTTCAGATGCGAAAGATATTTAAGAA	1040

QY	1021 CTTCCAGGATTCAAAAAATCCATGTTTAGATTTTAGACCAAGAAAGAAAAAGATGCG	1080
DB	1041 CTTCCAGGATTCAAAAAATCCATGTTTAGATTTTAGACCAAGAAAGAAAAAGATGCG	1100
QY	1081 TCAAGTCCACAGAGATGCAACTTACGGCCATCTTTAAAGAGACACAGTGCAGAACAAA	1140
DB	1101 TCAAGTCCACAGAGATGCAACTTACGGCCATCTTTAAAGAGACACAGTGCAGAACAAA	1160
QY	1141 AGCCCTGCAAGTGAACCTCTGTCTTTTGAATTCACAAAAATTTGAAGTGAAGAGTCTAT	1200
DB	1161 AGCCCTGCAAGTGAACCTCTGTCTTTTGAATTCACAAAAATTTGAAGTGAAGAGTCTAT	1220
QY	1201 CATGAAACCATGGAGAGGACCAAGCAACCAAGAAATCTATCTCACAGCTACAGACCTCAA	1260
DB	1221 CATGAAACCATGGAGAGGACCAAGCAACCAAGAAATCTATCTCACAGCTACAGACCTCAA	1280
QY	1261 AGGCTGATCAGCAAAAGCACTAGAGAGAAACAATCTTTGGATGTGGGACAAATTCAGTTC	1320
DB	1281 AGGCTGATCAGCAAAAGCACTAGAGAGAAACAATCTTTGGATGTGGGACAAATTCAGTTC	1340
QY	1321 ACTGATGAATTTGCTGGATCACTGCGAGCCTTTGGTCTCTGACACCCCAATCAGAGCTGCC	1380
DB	1341 ACTGATGAATTTGCTGGATCACTGCGAGCCTTTGGTCTCTGACACCCCAATCAGAGCTGCC	1400
QY	1381 ACATCTTTTGTCTGTATTAACAGAGATGCTACTTTTGTGTCAGAACTTCTCTCTGTTGAA	1440
DB	1401 ACATCTTTTGTCTGTATTAACAGAGATGCTACTTTTGTGTCAGAACTTCTCTCTGTTGAA	1460
QY	1441 CCCCAGCTTGAGACAGTGGACGGAGCAGAGCATGGTCTTACCTGACACACTTCTTGTCTCCA	1500
DB	1461 CCCCAGCTTGAGACAGTGGACGGAGCAGAGCATGGTCTTACCTGACACACTTCTTGTCTCCA	1520
QY	1501 CCTGCTGAGCCTCTACCTCCCTGTGAGAGCTCCACCTTCTTTTATGGGATCAAGCATC	1560
DB	1521 CCTGCTGAGCCTCTACCTCCCTGTGAGAGCTCCACCTTCTTTTATGGGATCAAGCATC	1579
QY	1561 TTCTCTCTGATGATCAAGGCCACACAGATACATGCGCACTGACAGACATCTAGTA	1620
DB	1580 TTCTCTCTGATGATCAAGGCCACACAGATACATGCGCACTGACAGACATCTAGTA	1639
QY	1621 CCAGGCTCACCATCCCAACAGAGTATTTCTGCAATTCAGCCAACTTGGCTCTGGGAAT	1680
DB	1640 CCAGGCTCACCATCCCAACAGAGTATTTCTGCAATTCAGCCAACTTGGCTCTGGGAAT	1699
QY	1681 TCACATCCACCTGATCTTTCAGATGACAGCGCATCAAGTGCAGCGGATCAAGTGCAGGATGGAC	1740
DB	1700 TCACATCCACCTGATCTTTCAGATGACAGCGGATCAAGTGCAGGATGGAGTGGAC	1759
QY	1741 AGACACCTAGATGAATGATGATCTGTGACACTCTGCCCCCATCTGAGGTACCAGAGCTC	1800
DB	1760 AGACACCTAGATGAATGATGATCTGTGACACTCTGCCCCCATCTGAGGTACCAGAGCTC	1819
QY	1801 AGCGAATATGTTCTGTCCAGATCACTTCTGGAGGATACCACTCTCTCTCAGCTTTA	1860
DB	1820 AGCGAATATGTTCTGTCCAGATCACTTCTGGAGGATACCACTCTCTCTCAGCTTTA	1879
QY	1861 CAGTATATACCACTAGTCTTATGACCAATTTGCCCAAGGCGGAGAGCTGGTAGTGTTC	1920
DB	1880 CAGTATATACCACTAGTCTTATGACCAATTTGCCCAAGGCGGAGAGCTGGTAGTGTTC	1939
QY	1921 TTCAAGTCTGGTGTGCTTAACATGGGCTTCTCCAGACCTGTTTCAACAGAGCTCTCTG	1980
DB	1940 TTCAAGTCTGGTGTGCTTAACATGGGCTTCTCCAGACCTGTTTCAACAGAGCTCTCTG	1999
QY	1981 GAGTACCGAGCTCTGGAGCAACAAATTCACACAGCTCTGTTTCCATATCTTACGATCCAAT	2040
DB	2000 GAGTACCGAGCTCTGGAGCAACAAATTCACACAGCTCTGTTTCCATATCTTACGATCCAAT	2059
QY	2041 CTTACAGGATTTAAGCACTTGAAATATCTTAATCTTCAGAAACGGGAGTGTGTAAT	2100
DB	2060 CTTACAGGATTTAAGCACTTGAAATATCTTAATCTTCAGAAACGGGAGTGTGTAAT	2119



[illegible]

Db	2000	GAGTACCGAGCTGTGGAGCAACAATTACACAGCTGCTGGTTCATATCTACGATCCAAT	2050
Qy	2041	CTTACAGGATTTAAGCAACTTGAATACTTTAACTTCAGAAACGGGAGTGTGATTGTGAAT	2100
Db	2060	CTTACAGGATTTAAGCAACTTGAATACTTTAACTTCAGAAACGGGAGTGTGATTGTGAAT	2119
Qy	2101	AGCAAAATGAAGTTTGTAAAGTCTGTGCCGTATAAAGCTTCAACGAAGCTGTGCACGGGGTC	2160
Db	2120	AGCAAAATGAAGTTTGTAAAGTCAAGTCCGTATAAAGCTTCAACGAAGCTGTGCACGGGGTC	2179
Qy	2161	TTGAGGAGTTTCCTTCTGCTGCAGGCCAACAACTTCATCTGGAATATAGACACTACTCT	2220
Db	2180	TTGAGGAGTTTCCTTCTGCTGCAGGCCAACAACTTCATCTGGAATATAGACACTACTCT	2239
Qy	2221	CTC 2223	
Db	2240	CTC 2242	
RESULT 12			
ADAI14847			
ID	ADAI14847 standard; cDNA; 3668 BP.		
XX	ADAI14847;		
DT	06-NOV-2003 (first entry)		
XX	Mouse interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.		
KW	ss; gene; mouse; IPMC 150 isoform A; gene therapy;		
KW	interphotoreceptor matrix component; IPMC; ocular disorder;		
KW	macular degeneration; photoreceptor death; retinal detachment.		
OS	Mus sp.		
FH	Key	Location/Qualifiers	
FT	CDS	196..2592	
FT		/*tag= a	
FT		/product= "IPMC 150 isoform A"	
PN	US2002160954-A1.		
XX			
PD	31-OCT-2002.		
XX			
PF	08-NOV-2001; 2001US-00007270.		
XX			
PR	29-OCT-1998; 98US-00183972.		
PR	29-OCT-1999; 99US-00430195.		
XX			
PA	(IOWA ) UNIV IOWA RES FOUND.		
XX			
PI	Hageman GS, Kuehn MH;		
XX			
PI	WPI; 2003-238235/23.		
DR	P-PSDB; ADAI14848.		
DR			
XX			
FT	New isolated or recombinant interphotoreceptor matrix component		
PT	polynucleotide and polypeptide, useful for diagnosing, preventing,		
PT	treating or prognosticating ocular disorders, e.g. macular degeneration		
PT	or retinal detachment.		
XX			
PS	Claim 3; Page 39-41; 76pp; English.		
XX			
CC	The invention relates to an isolated or recombinant interphotoreceptor		
CC	matrix component (IPMC) polynucleotide. Also disclosed is a vector		
CC	comprising a promoter of an interphotoreceptor matrix component (IPMC)		
CC	gene operatively linked to the IPMC polynucleotide. The IPMC		
CC	polynucleotides, polypeptides and antibodies are useful for diagnosing,		
CC	preventing, treating or prognosticating ocular disorders, e.g. macular		
CC	degeneration, photoreceptor death or retinal detachment. They are also		
CC	useful for identifying a compound capable of modulating IPMC gene		
CC	expression in a cell. The present sequence represents cDNA encoding mouse		
CC	interphotoreceptor matrix component IPMC, 150 isoform A.		

XX SQ Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;

Query Match 41.3%; Score 1375.6; DB 7; Length 3668;  
Best Local Similarity 70.7%; Pred. No. 0;  
Matches 2172; Conservative 1; Mismatches 730; Indels 169; Gaps 19;

QY 1 TAAACCAAGAGGTTATCTCAATCATCTGGTATCAATATATAATATTTTTCACATTTTC 60  
DB 62 TAAACCAAGAGGTTATCTCAATCATCTGGTATCAATATATAATATTTTTCATATTTTC 121  
QY 61 TGTACTTTT-----AATGAGATTGAGTTGTTCTGTGATGTATCAGAAATPACC 113  
DB 122 AGTCACTTTTCTTTAAAGTGTGACTGGTATTTGTTCTGTGATTTT--TCAGAAATPACC 179  
QY 114 AATGCACAAAAGCCAGAAATGATTTGAAACCTAGAAGAGCTATTTTGTGTTTGTGATTT 173  
DB 180 AGTATACAGAA--CCAGATGAATTTCAAATTAACATGCTATCTTTGTTTGGGATTT 238  
QY 174 TTCTCCAAGTTCAAGGAACCAAAGATATCTCCATTAACATATACCATCTGAAACTAAAG 233  
DB 239 TTCTCCAAGTTCAAGGAATCAAGGATCAAGATACCTCTATTAAATATTCAGTTCTGAAATTA 298  
QY 234 ACATAGACAATCCCCCAAGAAATGAACAACCTGAAGTACTGAAAAATCTCAAAATGT 293  
DB 299 ACATAGACAACCCCAAGAAATGAACAANTGAAGTACTTCAAGTGCACAAAGTGT 358  
QY 294 CAATATGAGACGAATATTCGATTTGGCAAGCATCGAACAAAAGATCCGCAATTTTTC 353  
DB 359 CAACCATGAACGAATATTCGATTTGCCAAGCTTCGAACCAAAAGATCAGCACTTTTTC 418  
QY 354 CAACGGGGTTAAAGTCTGTCCACAGGATCCATGAACACAGATTTAGACAGTCTTCAAG 413  
DB 419 CA---GCTGCTAAACATCTGTCCACAGGAATCTTGTAGACAGATTTTAGCAAGTCTTCAAG 475  
QY 414 CTTATTATAGATTGAGAGTGTGTGAGAAAGCAGTATGGGAAGCATATCGGATCTTTCTGG 473  
DB 476 AATATTATAGACTGAGAGTATGTCAGAGAGTCTGTGTGGGAGCATATCGTATCTTTCTGG 535  
QY 474 ATCCATCCCTGACACAGGGGAATATCAGGATGGGTGACGATCTGCCACAGAGACCT 533  
DB 536 ACCGAATCTCTGACACAGAGGAATATCAAGATGGGTGAGCCTCTGCCAGAAAGAACCT 595  
QY 534 TCTGCCCTTTTGACATTTGGAAAAAATTCAGCAATTCACAGGAGCCTCGGATCTTCTCC 593  
DB 596 TCTGCCCTTTTGACATTTGGGAAAAAATTCAGCAATTCACAGGAGCCTTAGATCTTCTTC 655  
QY 594 AGCAGAGATTAATAACAGAGAAGTTTCCCTGACAGAAAAGATGAATATCTGCAGAGAAGA 653  
DB 656 AGCAGAGATTAATAACAGAGAAGTTTCCCTGGAGGAAGATGAGACAGCCTCCATGGAGA 715  
QY 654 CATTTGGGAGAGCTGGTGAACCATTTGCTATTTCAACAGCAATCTACATTTCAAGACTT 713  
DB 716 CACTGGAAGCACCTTACTGAAAGCCCTGTGTGATCCAC----- 752  
QY 714 GGGCAGTATTCTAAGAAAAACCTCAGAAAGACAAATTCAGAGATGTTGCCAACTCTCACT 773  
DB 753 -----AGATGTTTCCAGGATGTCCT 773  
QY 774 TGGCCCTTTCCCTCTCACTCTGTATGACACCTCTCTCAATGAATTTCTGATTAATACAT 833  
DB 774 GGGCCCTTTCCCTCTCTGTATGACACAGACCTCAAGGAGATTTCTCAGTGTCACTCT 833  
QY 834 CAACGACACCAAGATGCTCAACAGAAAAGAGAAAACAGAA-----TTCCCTGT 881  
DB 834 CAAGGACATTAAGAGCCCAACAGAAAAGTAAACAGAACTTATTCAGTGTCTGAATTT 893  
QY 882 GTTGGAGAGCAGAGGTGGAGTCTCAGCTCTCTCTGTGTAACAGAGTTCAAGGCAGA 941  
DB 894 CTCAATCAGAGAGAGGTGAATTCAGATCTCTCTGCCAAACCAACAGGTTCAAGGCAGA 953  
QY 942 GCTCGCTGACTCCCACTTATACAGGAGCTAGCAGGAAGTCCCACTTCAGAT 1001

DB 954 GCTCACCAACTCTGGGTCAACCATCTACAGGAACCTGGTGGGACAGTCCCAACTCAGTT 1013  
QY 1002 GCAAAAGATATTTAAGAAACTTCCAGGATTCAAAATAATCCATGTGTTAGATTTAGACC 1061  
DB 1014 GCAAAAGATATTTAAGAAACTTCCAGGATTCGGAGAAATCCGTGTATTTAGGATTTAGACC 1073  
QY 1062 AAGAGAAAGAAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGGCATCTTTAAAGAG 1121  
DB 1074 AAGAGAAAGAAAGATGGTTCAAGCTCCACAGAAATACAGCTTATGGCACTTTAAGAG 1133  
QY 1122 ACACAGTGCAGAAAGAAAAGCCCTGCAAGTGAACCTCTCTGCTTTTGTATTCACAAAAT 1181  
DB 1134 GGACCATGCAGAAAGAAAAGCCCTGATAGTCACTACTGTCTCTGTGATTCACAAAAAT 1193  
QY 1182 TGAAAGTGAAGGAAGTCTATCTATGGAACCATGGAGGAGCAAGCAACAGAAATCTATCT 1241  
DB 1194 TGAAAGTGAAGGAATCCATCATGAGTCTATAGAA---GACAAAACACAGAAACCTACT 1250  
QY 1242 CACAGCTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGAGGAAGAACAACTTTTGA 1301  
DB 1251 CACAGCTACAGACCTCAAAAGGCTGATCATCACTACTAGATGGAGACCTGTCTCTGGT 1310  
QY 1302 TGTGGGGAATTTCAAGTTTCACTGATGAATTTGCTGGATCACTGCCAGGCTTTGTCCTGA 1361  
DB 1311 AGAAGGGAATTTCCATTCGGTGTGAAGTTACTGGGACCT-----CTTCAGACCTGT 1364  
QY 1362 CACCAATCAGAGCTGCCACATCTTTTGTCTGTTATTAACAGAGGATGCTACTTTGAGTCC 1421  
DB 1365 CACTGAACAGATCTGCCCAAGCCCTTGTCTGATGTACAGAGGATGCCACTTTGAGTCC 1424  
QY 1422 AGAATCTCTCTGTTGAACCCAGCTTGACAGAGTGGACGGAGCAGAGATGTCCTACC 1481  
DB 1425 AGAATCTCTCTGTTGAGCCTTAGGCTTGAGGCACTGGACAGAGAAGATCTGAGCTGCC 1484  
QY 1482 T-----GACACTTCTTGCTCTCCACCTGTCTATGCTGCTCTACTCTCCCTGTC 1526  
DB 1485 TGAATGTCTCTCCAAAGACAGTTCTTGTCTCCACCTGTATCAGGCTCAATTTCCCGATC 1544  
QY 1527 AGAAGCTCACTTTCTTTATGGAATCAAGCATTTCTCTCTGACTGATCAAGGACACAC 1586  
DB 1545 AGAAAATCTAGCTTCGTTTA---CACCTAGCATCTTCTCTAGATGCTCAAGGCCCCCC 1601  
QY 1587 AGATACATGCGCACTGACACAGACAATGCTAGTACCAGGCTCACCCTCCCAAGGATGA 1646  
DB 1602 TCCCTTGATGACCTGAGCCCAACAGACACTCATCCCAAGCCCACTCTCCCACTATGA 1661  
QY 1647 TTATTCTCAATCAGCCAACTGGCTCTGGGAATTTCACTCCACTGCTCATCTTCAGATGA 1706  
DB 1662 TTATTCTACCATCCGCCAATTTGCTCTGGAATCGTCACTTGGCTGCTCATCTCCAGTGA 1721  
QY 1707 CAGCCGATCAAGTGCAGGTGGCGAAGATATGGTGCAGACACCTAGATGAATGGATCTGTC 1766  
DB 1722 CAGAGAGCTGATCAAAAGCAGCCATGACAAATCCGAGACCTAGATGGCATGGATGTC 1781  
QY 1767 TGCACTCTCTCCCACTCTGAGGTACAGAGCTCAGCGAATATATTTCTGTCCCCAGATCA 1826  
DB 1782 TGACAGCCGACCTTGTGAGAAATATCAGAACTCAGTGGATACGATTTGCTCGGTGCA 1841  
QY 1827 TTTCTTGAGGATACCACTCTCTGCTCAGCTTTTACATATACCACTAGTTCTATGAC 1886  
DB 1842 GTTCTTGAGATGACCAACCCCACTCCCAAGTAGTGTTCATCACCAGCTCCGAGAC 1901  
QY 1887 CATTTGCCCCCAAGGGCGAGAGCTGTGTTCTTCCAGTCTGCTGTGCTAATACATGGC 1946  
DB 1902 CATTTGCCCAAGGGCGAGAGCTGTGTTCTTCCAGCTGCTGTGCTAATACATGGC 1961  
QY 1947 CTTCTCCAAAGCCTGTTCAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAT 2006  
DB 1962 GTTCTCTATGACCTGTTCAAGAGTCTCTGAGTATCAAGCCCTGGAAACAAGAT 2021  
QY 2007 CACAGAGTGTCTGTTCCATATCTACGATCCAATCTTACAGGATTTAAGCACTTGAAT 2066  
DB 2022 CACAGAGTGTCTGTTCCCTATCTACGATCGAATCTTTACGGGATTTAAGCAACTGGAAT 2081







```

Db 2382 GACCCGTGAACCTCTGTGCTCCCTGG---AAGACITGTGTGCGCGCGAGACAGCAAC 2438
Qy 2427 TCCATGCGAGGTGCGAGATCACTCTGAAATCAAGCATACAAACTAGTGTATAAAAGTT 2486
Db 2439 TCCATGCGAGGCCACAGATCACTCTTACAACCAAGCTCAGGAACCTGCTGTATAAAAGCT 2498
Qy 2487 CCAAAATCAACAAATACAAAGGTAATCAGTAAAGAAATTTCTCAATTTACTGACCGTAGA 2546
Db 2499 ACGTCAGCAA-----AATAGGTAGTCAAGAAAGAAATTTCTAACTATCAGCTATAGG 2552
Qy 2547 ATATGAAGAATTTAACCATCAAGATTTGGAAAGAAATTTAAAACTGAAA-----2595
Db 2553 AITTTGAAGAATTTGAAGCAGGACTGGAGGAAATTTAAAGCTGGAATCATATGCATT 2612
Qy 2596 -----ATGTCAATTTATCACTTAGGCTATCTCAGAGAGATGATTGCGCT 2640
Db 2613 ATGTTGCAAACTCTGTTGAAGGAACTTTATTTCTTAAAGAGGTGTATCTGTTCTGT 2672
Qy 2641 TCTCAAGGAAATGGAGACAGGCAATTTTCATGCTCATCAAAATCCAGACATACAGTCAA 2700
Db 2673 TAACCTTCTGAAAAACAGAGGAGAGATTCAGTGGTCAATTCGAATACAGGCATGTAATCAA 2732
Qy 2701 CACTGAGAATCAGCACACACATATTTCAATATAGAGAGTCACTGTTGCTGCAACCCAG 2760
Db 2733 CTTTGAGACTCAG-----CATGCTTGAACAAGAGCACAGGCGTGTATTGTATGA-CAG 2784
Qy 2761 TAAATCTGAAAAAAGACACACTTACTTATTATTA--AAACCCCAAGATCAATCAGCGAA 2818
Db 2785 TTAAGCCTGTTGGGGGGGGGACATATTTTGTAGTCAAACTCAAGCAATCATTTGA 2844
Qy 2819 ACATATTTTACTATTTCTTGATGATAGTCAAAATGATCAATAGCAGGTTGCTTCCAC 2878
Db 2845 ACACA-TTGACTATTTTGGACAGTACTC--AAGTAGCAAAAGATAAGGTAGCTTTT 2901
Qy 2879 CTTCCCTGAAAAATTTACTCACAGATCATTTGCAACAGCATAGCTTACTTATTTGTTAG 2938
Db 2902 CTTTCTTTAAATTTATACATAAARCTATTTCAATAAATACAAAC-----TTGTTTGA 2954
Qy 2939 GGAAGTGAACAAATTTATGGGAACAACTTTTATATGCTAGAAAGTACATTTAAAGAT 2998
Db 2955 TGGGTTGTACAATTTAGGATCTGATCTTTTATATGTTAGATATACAGTTAAAGAT 3014
Qy 2999 GACTACTTACGC 3010
Db 3015 TATCATTTGGGC 3026

```

## RESULT 14

AAA46309  
ID AAA46309 standard; cDNA; 3206 BP.

XX  
AC AAA46309;

XX  
DT 04-SEP-2000 (first entry)

XX  
DE cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).

XX  
KW Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
KW chromosome q13-q15; ocular disease; retinal detachment;  
KW choriorretinal degeneration; retinal degeneration; cone degeneration;  
KW age related macular degeneration; photoreceptor degeneration;  
KW retinal pigment epithelium degeneration; mucopolysaccharidosis;  
XX rod- cone dystrophy; cone-rod dystrophy; 88.

OS Mus sp.

XX  
FH Location/Qualifiers  
CDS 1..2130

XX  
FT /\*tag= a

FT /transl\_except= (pos: 16..18, aa: Val)

FT /transl\_except= (pos: 55..57, aa: Ala)

FT /transl\_except= (pos: 58..60, aa: Tyr)

FT  
FT /transl\_except= (pos: 73, aa: Asp)  
FT /transl\_except= (pos: 234..236, aa: Xaa)  
FT /transl\_except= (pos: 271..273, aa: Xaa)  
FT /transl\_except= (pos: 403..405, aa: Xaa)  
FT /transl\_except= (pos: 2107..2109, aa: Xaa)  
FT /product= "interphotoreceptor matrix proteoglycan IPM150"  
FT /note= "Xaa is an unspecified amino acid"

XX WO200026367-A2.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US025440.

XX 29-OCT-1998; 98US-00183972.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;

XX WPI: 2000-365616/31.

XX P-PSDB; AAY93338.

XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for preventing, diagnosing and treating ocular disorders such as retinal detachment and chorioretinal degeneration.

XX Claim 2; Fig 6A; 183pp; English.

XX The present sequence encodes an interphotoreceptor matrix (IPM) proteoglycan, designated IPM150. The protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome q13-q15, between markers CHLC.GAT1110 and D6S284. The IPM proteins may be used to supplement a patient's own production of the protein or to rectify alterations in their nucleic acids that result in expression of an inactive protein. The IPM nucleic acids may be used in this way to treat ocular diseases such as retinal detachment, chorioretinal degeneration, retinal degeneration, age related macular degeneration, photoreceptor degeneration, RPE (retinal pigment epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also be used to assay for other modulators of IPM proteoglycan expression and activity that may be used to treat ocular diseases. The nucleic acids and proteins may also be used as diagnostic reagents to detect the presence of IPM nucleic acids and their products in samples from patients according to standard methodologies

XX Sequence 3206 BP; 937 A; 778 C; 686 G; 793 T; 0 U; 12 Other;

Query Match 33.8%; Score 1127.2; DB 3; Length 3206;  
Best Local Similarity 68.9%; Pred. No. 9.9e-291;  
Matches 1824; Conservative 5; Mismatches 665; Indels 152; Gaps 15;

Qy 418 TTATAGATTGAGAGTGTCAGGAACGAGTATGGAGCATATCGGATCTTTTGGATCG 477  
Db 18 TCAAGGAATCAAGATATGTCAGAGATCGTGTGGAGATGATCGTATCTTTCTGNNAG 77  
Qy 478 CATCCCTGCACAGGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAGGAGACCTTCTG 537  
Db 78 AATTCCTGCACAGAGGAATATCAAGCTGGGTGAGCATCTGCCAGAGAAACCTTCTG 137  
Qy 538 CCCTTTTGACATTTGGAAAAAATTCAGCAATTCAGAGGAGCAGCTGATCTTCTCCAGCA 597  
Db 138 CCCTTTTGACATTTGGAAAAAATTCAGCAATTCAGAGGAGCAGCTGATCTTCTCCAGCA 197  
Qy 598 GAGATAAATAACAGAGAGATTTTCCCTGCACAGAAAGATGAAATATCTGCAGAGAGACATT 657  
Db 198 GAGATAAATAACAGAGAGATTTTCCCTGGAGGAAGATGAGCAGCTTCCATGAGACACT 257  
Qy 658 GGGAGAGCCTTGTAACCAACATTTGATCAATTTCAACAGCAATCTTACATTTCAAGACTTGGGC 717  
Db 258 GGAAGCAGCCTTACTGRAGCCCTCTGTGTACCCAC-----290

QY 718 AGTATTCTTAAGAAAAACCTTCAGAGAGCAAAATTCAGATGTTGCCAAGCTCTCACTTGGG 777  
DB 291 -----AGATGTTTCCAGGATGTCCTTGGG 315  
QY 778 CTTTTCCCTCTCACTCCCTGATGACACCCCTCTCTCAATGAATTCGATAAATACACTCAAC 837  
DB 316 CMTTCCCACTTCCCTTCTGATGACACAGACCTTCAGGGAGATTCTCAGTGTCAACCTCAAG 375  
QY 838 GACACCAAGATGCCCTACACAGAAAGAGAAACAGAA-----TTGCTGTGTTG 885  
DB 376 GACATTCAAAAGCCCAACAGAAAGTAAACAGAACCTATTCAATGCTCTGAATTTCTCA 435  
QY 886 GAGGAGCAGAGGTGGAGCTCAGCGTCTCTCTGTGTAAACAGAAAGTTCAAGCGAGCTC 945  
DB 436 TCAGAGGAGAGGTGGATTCAGCATCTCTGTGCCAAACACAGGTTCAAGCGAGAGCTC 495  
QY 946 GCTGACTCCAGTCCCACTATTTACCAGGAGCTAGCAGGAAGTCCCACTTCAGATCNA 1005  
DB 496 ACCAATCTGGGTCAACATACTACCAAGGACTGTGGGACAGTCCCACTCAGTTGCA 555  
QY 1006 AAGATATTAAAGAACTTCCAGGATTCAAAAAATCCATGTGTAGGATTTAGACCAAG 1065  
DB 556 AAGATATTAAAGAACTTCCAGGATTCGAGAAATCCGTGTATTAGGATTTAGACCAAG 615  
QY 1066 AAAGAAAAGATGGCTCAAGCTCCACAGAGATGCAATTTACGGCCATCTTTAGAGACAC 1125  
DB 616 AAAGAAAGAGATGGTTCAAGCTCCACAGAAATACAGCTTATGGGCCATCTTTAAGAGGGAC 675  
QY 1126 AGTCAGAGCAAAAGCCCTGCAAGTGACCTCTCTGTTTGTATTCACAAACAAATTTGAA 1185  
DB 676 CATGCAGAAACAAAAGCCCTGATAGTACTCTGTCTCTGATTCACACAAATTTGAA 735  
QY 1186 AGTGAGGAGTCTATCATGGAACCATGAGAGAGACAAAGCAACAGAAATCTATCTCA 1245  
DB 736 AGTGAAGAAATCCATCTATGGAGTCTAT---AGAAGACAAACCAACAGAAACCTACCTCACA 792  
QY 1246 GCTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGAGGAAGAACTTTTGGAGTG 1305  
DB 793 GCTACAGACCTCAAAAGGCTGATCAGCAAGCACTAGAGGAAGAACTTTTGGAGTG 852  
QY 1306 GGGACAAATCAGTTCACTGATGAATTTGCTGGATCACTGCCAGCCCTTGGTCTGACACC 1365  
DB 853 GGGAAATTTCCATTCGGTGTGAAGTTACTGGGACACT-----CTTCAACCTGTCACT 906  
QY 1366 CAATCAGAGCTGCCACATCTTTTGTGTTATACAGAGGATGCTACTTTGATGCTCAGAA 1425  
DB 907 GAACAGATCTGCCAAAGCCCTTGTGTGTACAGAGATGCCATTTGATGCTCAGAA 966  
QY 1426 CTTCTCTGTGTGAACCCAGCTTGACAGTGGAGCGAGCAGAGATGCTTACCT--- 1482  
DB 967 CTTCTCTGTGTGAGCTTAGGCTTGAGGAGTGGACAGAGATCTGAGCTGCTGGA 1026  
QY 1483 -----GACACTTCTGTCTGACCTGATCAGGCTCACATCCCAACAGCTGAT 1066  
DB 1027 ATGTCCTTCCAAAGACAGTTCTTGTCTCCACCTGTATCAGCCTCAATTTCCCGATCAGAA 1086  
QY 1531 GCTCCACTTTCTTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGCTCAGATCAGAT 1590  
DB 1087 AATCTACTCTTGTTA---CACCTAGCATCTTCTCTAGATGCTCAAGGCCCTCC 1143  
QY 1591 ACATGGCCACTGACAGCAATGCTAGTACAGGGCTCACATCCCACTCCCAAGATGAT 1650  
DB 1144 TTGATGACCACTGGCCCAACAGCACTCATCCCAAGCCCACTCTCCCACTATCGATTTAT 1203  
QY 1651 TCTGCAATCAGCAACTGGCTCTGGGAATTTACATCCCACTCCCACTCTCCCACTATCGATTTAT 1710  
DB 1204 TCTACCACTCCCAATGCTCTGGATCGTCAATTTGGCTGCACTCTCCCACTATCGATTTAT 1263  
QY 1711 CGATCAAGTGGAGGAGATATGGTCAGACACCTAGATGAATGGATCTGTCTGAC 1770  
DB 1264 GAGCTGATCAAGAGCAGCCATGACAAATCCGAGACCTAGATGGCATGATGTCTGAC 1323  
QY 1771 ACTCCTGCCCACTCTGAGGTACAGAGCTCAGGAAATATGTTCTGCTCCCAATCATTTTC 1830

DB 1324 ACCCGACCTTGTCAAGAAATATCAGAACTGAGTGGANATCGATTTGCTCTGGGTGAGTTTC 1383  
QY 1831 TTGGAGATACCACTCTCTCTCAGCTTTTACAGTATATCACCACTAGTTCTTATGACCAAT 1890  
DB 1384 TTGGAGATGACCAACCCATCCCAACAGTACGTTTCTCATCCACCACTGCTCCGAGACCAAT 1443  
QY 1891 GCCCCCAAGGGCGAGAGCTGTGTCTTCTCAGTCTCGGTGTTGCTAACTAGGCTTTC 1950  
DB 1444 GCCCAAGGGCGAGAGCTGTGTCTTCTCAGCTCGGTGTTGCTAACTAGGCTTTC 1503  
QY 1951 TCCAAAGACCTGTTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAAATTCACA 2010  
DB 1504 TCTATGACCTGTTCACCAAGAGTTCTCTGGAGTATCAAGCCCTGGAACAAAGTTTCA 1563  
QY 2011 CAGCTGCTGTTTCCATATCTAGATCCAAATCTTACAGATTTTAAAGCACTTGAATATCT 2070  
DB 1564 GACCTGCTGTTTCCATATCTAGATCCAAATCTTACAGATTTTAAAGCACTTGAATATCT 1623  
QY 2071 AACTTCAGAAAAGGGAGTGTGATTTGTAATAGCAAAATGAAAGTTTGTAAAGTCTGTGCG 2130  
DB 1624 AGCTTCAGAAAAGGGAGTGTGATTTGTAACAGCAAGTGGGTTTGAAGGGCTGATCC 1683  
QY 2131 TATAACCTCACCAGGCTGTGCAAGGGTCTTGGAGATTTTGTCTGTGCTGACGCCAA 2190  
DB 1684 TACAACCTCACCAGGCTGTGCGGGTCTTGGAGATCTTGGTCTCCACCGAGCTCAA 1743  
QY 2191 CAACTCCATCTGAAATAGACAGTACTCTCTACATTTGAACAGCTGATCAAGCAAT 2250  
DB 1744 GGGCTCAATCTGAAATCGAAAGTACTCTCTCGACATTTGAACAGCTGATCAAGCGGAT 1803  
QY 2251 CCCTCCAAAGTCTCTGGCTCGCGGAAATTTGCCAAATGTGTAAAGAAACGAACGAGCTGAG 2310  
DB 1804 CCCTCCAAAGTCTCTAGACTGTGGCAAAATTTGCCCAAGTGTGTAAAGATGAGTGGACAG 1863  
QY 2311 GAAGCGAGTGTGCTGCAACAGGATATGACAGCCAGGGAGGCTGAGCGGTCTGAA 2370  
DB 1864 GAAGCAGAGTGTGCTGCAACAGGATATGACAGCCAGGGAGGCTGAGCGGTCTGAA 1923  
QY 2371 CCAGGCTCTCTGGGCTCGGCAAGAAATGCGAGGCTCTCCAGGGAAGAGGAGCTCCA 2430  
DB 1924 CTGAACCTCTGTCCCTCTGG---AAAGACTTGTGTGGCCGCGCGAGACAAAGCACTCCA 1980  
QY 2431 TGCAGTTGCGAGATCACTCTGAAATTCAGACATACAAACTAGTTTAAAGAGTTCCAA 2490  
DB 1981 TGCAGGCGCCAGATCACTCTACAAACCAAGCTCAGGAACCTGTTGTTTAAAGAGTACGT 2040  
QY 2491 AATCAACAAATTAACAGGTAATCAGTAAAGAAATTTCTGAATTTACTCACCGTATGATAT 2550  
DB 2041 CAGCA-----AATAGGTAGTCAAGAAAGAAATTTCTAAACTATCAGCTATAGGATTT 2094  
QY 2551 GAAGATTTAAACCAATCAAGATTTGGAAAGGAAATTTAAAGAACTGAAATTTGA-CAAATTATCA 2609  
DB 2095 GAAGAAATTTGAARACCAAGGAGTGGGAGGAAATTTAAAGCTGGAATCATATGCTATTTATGT 2154  
QY 2610 CTTAGGCTATCTCAAGAGAGATGATTTGCTTTCTCAAGGA----- 2649  
DB 2155 TGCAAACTCTGTTGAAGGAAACCTTTATTTCTTAAAGAAAGGTGTATCTGTTCTGTATTAAC 2214  
QY 2650 -----AAATGGAGACAGGCATATTTATGGGTCTATCAAAATCCAGACATACAGTCAACACT 2704  
DB 2215 TTTGAAAAAAGAGGAGAGATTTCACTGTGTCTATTTGAATACAGGCATGTAATCAACTTT 2274  
QY 2705 GAGATCAGCACACACCATATTTCAATATATAGAGAGTCAATGCTGCTGAGCAACAGTAAA 2764  
DB 2275 GAGACTCAGATGC-----TTGAACAGAGACAGGAGGTGTTTGTATGACAGTTAAGCCT 2330  
QY 2765 TTTGAAAAAAGAGACACTTTACTTTATTTAAACCCCAATGCAATCAGCGAAACATAT 2824  
DB 2331 GGTGGGGCGGGGGCACATATTTTAGTCAAACTC---AAAGCAATCATTTGGAACACA- 2387  
QY 2825 TTTTACTATTTCTTGGATGATGATCAAAATGATCAAGCCAGGTTTGTCTTCCACTTCC 2884

Db 2398 TTGACTATTTTGGACAGTACTC--AAGTAGCAAGATAAGGTAGCTTTTCTTTCT 2445  
 QY 2885 TGAAATTTTACTCACAGATCATTTGCAACAAGCATAGCTTACTTATTGTTAGGACTG 2944  
 Db 2446 TTAATATTATCAATAAATCTTATTTCAATTA-----ATACAACTGTTTAGTGGTT 2498  
 QY 2945 AACAAATTTATGGGAGCAAACTCTTTATATGCTAGAAATACATTTAAAGATGACTAC 3004  
 Db 2499 GTACAATATTGAGGATCTGATTTCTTTATATGTTAGATATACAGTTAAAGATTATCAT 2558  
 QY 3005 TTACGC 3010  
 Db 2559 TTGGGC 2564

## RESULT 15

ID ADA14849 standard; cDNA; 1726 BP.

AC ADA14849;

DT 06-NOV-2003 (first entry)

XX Mouse interphotoreceptor matrix component, IPMC, 150 isoform D cDNA.

DE ss: Gene; mouse; IPMC 150 isoform D; gene therapy;  
 XX interphotoreceptor matrix component; IPMC; ocular disorder;  
 XX macular degeneration; photoreceptor death; retinal detachment.

OS Mus sp.

XX Key Location/Qualifiers  
 FH 140..1540  
 FT CDS  
 FT /\*tag= b  
 FT /product= "IPMC 150 isoform D"  
 FT 140..199  
 FT /\*tag= a  
 FT /label= Signal\_sequence  
 FT 200..1537  
 FT /\*tag= C  
 FT /label= Mature\_IPMC\_150\_isoform\_D  
 XX US2002160954-A1.

XX 31-OCT-2002.

XX 08-NOV-2001; 2001US-00007270.

XX 29-OCT-1998; 98US-00183972.

XX 29-OCT-1999; 99US-00430195.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;

XX WPI; 2003-238235/23.

XX P-PSDB; ADA14850.

XX New isolated or recombinant interphotoreceptor matrix component  
 PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 PT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.

XX Claim 3; Page 43-44; 76pp; English.

XX The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene

CC expression in a cell. The present sequence represents cDNA encoding mouse  
 CC interphotoreceptor matrix component, IPMC, 150 isoform D.

XX Sequence 1726 BP; 541 A; 383 C; 388 G; 414 T; 0 U; 0 Other;

SQ Query Match 16.0%; Score 534; DB 7; Length 1726;  
 Best Local Similarity 72.0%; Pred. No. 5.5e-132;

Matches 792; Conservative 0; Mismatches 225; Indels 83; Gaps 4;

QY 396 TTTTAGACAGTCTTCAAGCTTATTATAGATTGAGAGTGTGTCAGGAAGCAGTATCGGAAG 455  
 Db 171 TTTTGGGATTTTCTCCAAGTTCAGGAATCAAAAGTATGTCAAGAGTCGTGTGGGAAG 230

QY 456 CATATCGGATCTTCTCGATCGCATCCCTGCACAGGGGAATATCAGACACTGGGTCACGA 515  
 Db 231 CATATCGTATCTTCTGGACCGAATCTCTGCACAGAGAAATATCAAGCTGGGTCAGCC 290

QY 516 TCTGCCAGCAGGAGACTTCTTCTGCTTCTTGTGACATTTGGAAAAAATTCAGCAATTTCCAGG 575  
 Db 291 TCTGCCAGAAAAAACCTTCTGCTCTTTGACATTTGGAAAAAATTCAGCAATTTCCAGG 350

QY 576 AGCACTCGATCTTCTCCAGCAGAGATAAAACAGAGAGAGTTTCCCTGACAGAAAAAGATG 635  
 Db 351 AGCACTAGATCTTCTTCAGCAGAGATAAAACAGAGAGAGTTTCCCTGGGAGGAAAGATG 410

QY 636 AAATATCTGCAGAGAAAGACATTTGGGAGAGCCTGTGAAACCAATTTGTCATTTCAACAGCAA 695  
 Db 411 AGCAGCCTCCATGGAGACACTTGAAGCACCTACTGAAGCCCTGTGTATCCAC----- 465

QY 696 TCTACATTTCAAAGACTTGGGAGTATTTTAAGAAAAACCTTCAGAAAGCAAAATTCAGAA 755  
 Db 466 -----AGG 468

QY 756 TGTGCCAAACGTCTCACTTGGGCTTTCCCTCTCACTCTCTGATGACACCTCTCTCAATGA 815  
 Db 469 TGTTCAGGATGTCTCTGGGCCATTTCCCACTTCTCTGATGACACACCTCTCAAGGA 528

QY 816 AATTCCTGATTAATACATCTCAACAGACACCAAGATCCCTACACAGAAAGAGAAACAGAA-- 873  
 Db 529 GATTCCTAGTGTCACTCCCTCAAGGACATTTCAAAAGCCCAACAGAAAGTATAACAGAAACC 588

QY 874 -----TTCCGCTGTGTGGAGGAGCAGAGGTGGAGCTCAGCGTCTCTCTGTGTA 923  
 Db 589 TATTCAGTGTCTGAATTTCTATCAGAGGAGAGGTGGAGTTTCAAGCATCTCTCTGCCAAA 648

QY 924 CCAGAAGTTCAAGGCAGAGCTCGCTGATCCCTCCATATATTACCAGAGCTAGCAGG 983  
 Db 649 CCAGAGTTCAAGGCAGAGCTCACCACTCTGGGTCACTACTACCAGGACTGTGTGG 708

QY 984 AAGTCCCACTTCAGATGCAAAAGATATTAGAAACTTCCAGGATTCAAAAAATCCA 1043  
 Db 709 ACAGTCCCACTGCAGTTGCCAAAAGATATTAAAGAACTTCCAGGATTCGAGAAATCCG 768

QY 1044 TGTGTAGGATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAACT 1103  
 Db 769 TGTATTAGGATTTAGACCAAGAAAGAAAGATGGTTCAAGCTCCACAGAAATACAGCT 828

QY 1104 TACGGCATTTTAAGAGACACAGTGCAGAAAGCAAAAGCCCTGCAAGTACCTCTCTGTC 1163  
 Db 829 TATGCCATCTTTAAGAGGAGCACTGCAAGCAAAAGCCCTGATAGTATCTACTCTGTC 888

QY 1164 TTTTGTATCCAAACAAATTCAGAGTGGAGAGTCTATCATGGAAACCATGGAGAGAGCA 1223  
 Db 889 TCTTGATTCACAAATTTGAAAGTGAAGAAATCCCATCATGGAGTCTAT---AGAAGACAA 945

QY 1224 GCAACCAAGAAATCTATCTCACAGCTACAGACCTCAAAAGCTGATCAGCAAAAGCACTAGA 1283  
 Db 946 ACAACCAAGAAACCTACTCTCACAGCTACAGACCTCAAAAGCTGATCAGCAAAAGCACTAGA 1005

QY 1284 GGAAGAAACATCTTTGGATGTTGGGACAAATTCAGTTCACTGATGAAATTCCTGGATCACT 1343  
 Db 1006 TGGAGACCTGTCTCTGGTAGAGGGGAAATTCATTCGGTGTGATGAAGTTACTGGGACACT 1065

Search completed: March 1, 2004, 14:40:02  
Job time : 1281 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2004, 20:29:14 ; Search time 4968 Seconds  
(without alignments)  
4790.692 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117

Sequence: 1 MYLTTTAAVFVFIQVQV.....NSELTVVEEFPNQWEGN 797

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_p2n.model -DEV=xlh  
-Q/cgnt2\_1/USPTO.spool/US10007270/runat\_25022004.164207\_27210/app.query.fasta\_1.967  
-DB=EST-QFMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=bicsum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10007270 @CGN\_1\_1\_3609@runat\_25022004.164207\_27210 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmi.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_htc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_red.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2801	68.0	1665	29	AY415971	AY415971 Homo sapi
2	1683	40.9	1647	29	AY415973	AY415973 Mus muscu
3	1054	25.6	626	13	BQ639265	BQ639265 hg33d04.y
4	971	23.6	1587	29	AY415972	AY415972 Pan trogl
5	955	23.2	598	13	BQ636596	BQ636596 hdl1h02.y
6	902	21.9	3713	29	AY418611	AY418611 Homo sapi
7	893	21.7	690	13	BX510244	BX510244 DKFZp686P
8	829	20.1	963	13	BU506195	BU506195 AGENCOURT
9	819.5	19.9	3734	29	AY418613	AY418613 Mus muscu
10	817.5	19.9	3713	29	AY418612	AY418612 Pan trogl
11	815	19.8	508	14	CA393958	CA393958 cs44g04.y
12	799	19.4	472	13	EX097138	EX097138 BX097138
13	759	18.4	510	9	AL713229	AL713229 DKFZp686P
14	751	18.2	618	14	CA391789	CA391789 cs18h07.y
15	738	17.9	561	14	W26960	W26960 16h10 Human
16	730.5	17.7	914	13	BX743511	BX743511 BX743511
17	714.5	17.4	824	12	BI738733	BI738733 603358767
18	708	17.2	797	11	AK020862	AK020862 Mus muscu
19	686	16.7	422	12	BM726533	BM726533 UI-E-EJO-
20	685	16.6	886	14	CF549501	CF549501 AGENCOURT
21	674	16.4	753	12	BI735383	BI735383 603356869
22	649	15.8	448	12	BM681190	BM681190 UI-E-EJO-
23	637	15.5	393	13	BQ636351	BQ636351 rd07h06.y
24	636	15.4	851	12	BI733865	BI733865 603353151
25	634	15.4	836	12	BI752112	BI752112 60302362
26	631	15.3	813	13	BX743512	BX743512 BX743512
27	624	15.2	802	12	BI735091	BI735091 603356230
28	612	14.9	405	14	H38604	H38604 YP48e04.r1
29	584	14.2	878	14	CF549297	CF549297 AGENCOURT
30	561.5	13.6	963	13	BU287197	BU287197 603604306
31	528	12.8	666	13	BY742200	BY742200 BX742200
32	507	12.3	322	9	AA326863	AA326863 EST30113
33	493	12.0	309	14	H38594	H38594 YP48c06.r1
34	487	11.8	701	29	AG128736	AG128736 Pan trogl
35	437.5	10.6	567	28	AZ974344	AZ974344 2M0248F20
36	435.5	10.6	481	9	AI510373	AI510373 mp95e12.y
37	435.5	10.6	435	9	AA116463	AA116463 mp95e12.y
38	387	9.4	678	28	AZ876525	AZ876525 2M0191104
39	344	8.4	872	29	CNS032A8	AL224585 Tetraodon
40	338	8.2	418	14	CB766257	CB766257 AMGNNUC:S
41	327.5	8.0	420	13	BX521328	BX521328 BX521328
42	279	6.8	706	10	BB646928	BB646928 BB646928
43	279	6.8	3802	11	AK047356	AK047356 Mus muscu
44	273	6.6	3250	11	BC026456	BC026456 Mus muscu
45	259	6.3	852	29	CNS03M89	AL250434 Tetraodon

# ALIGNMENTS

RESULT 1  
AY415971  
LOCUS  
DEFINITION Homo sapiens IMPG1 gene, VIRTUAL TRANSCRIPT, partial sequence, 1665 bp DNA linear GSS 17-DEC-2003  
ACCESSION AY415971  
VERSION AY415971.1 GI:39771931  
KEYWORDS GSS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1665)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D., and Cargill, M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1665)  
 :AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D., and Cargill, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
 FEATURES  
 source Location/Qualifiers  
 1..1665  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 gene <1..>1665  
 /gene="TMPC1"  
 ORIGIN /locus\_tag="HCMS735"  
 Alignment Scores:  
 Pred. No.: 6,05e-268 Length: 1665  
 Score: 2801.00 Matches: 546  
 Percent Similarity: 98.56% Conservations: 0  
 Best Local Similarity: 98.56% Mismatches: 8  
 Query Match: 98.03% Indels: 0  
 DB: 29 Gaps: 0  
 US-10-007-270-2 (1-797) x AY415971 (1-1665)  
 QY 244 AsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAla 263  
 DB 1 AACAGAGATTCAAGGAGAGCTCGCTGACTCCAGTCCCATATTACCAGGAGCTAGCA 60  
 QY 264 GlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIle 283  
 DB 61 GGAAAGTCCCAACTTCAGATGCAGAAAGATATTAAAGAACTTCAGGATTCAGAAATATC 120  
 QY 284 HisValLeuGlyPheArgProLysLysGluLysAspGlySerSerGlnMetGln 303  
 DB 121 CATGTGTAGGATTAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTCAAGCTCCACAGAGATGCAA 180  
 QY 304 LeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeu 323  
 DB 181 CTTACGGCCATCTTTAAGAGACACAGTGCAGAAAGCAAAAGCCCTCGAAGTCAACCTGCTG 240  
 QY 324 SerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThrMetGluGluAsp 343  
 DB 241 TCTTTTGATTCCCAACAAATTTGAAGTGAAGAGTCTATCATGGAACCATGGAGGAGGAC 300  
 QY 344 LysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuLysSerLysAlaLeu 363  
 DB 301 AAGCAACCAAGAAATCTATCTCAGAGCTACAGACCTCAAAAGGCTGATCAGAAAGACATTA 360  
 QY 364 GluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySer 383  
 DB 361 GAGGAACAAATCTTTGGATGTGGGACAAATTCAGTTCACATGATGAATTCCTGGATCA 420  
 QY 384 LeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThr 403  
 DB 421 CTGCGACCTTTTGGTCTGTACACCCCAATCAGAGCTGCCACATCTTTTCTGCTTTAACA 480  
 QY 404 GluAspAlaThrLeuSerProGluLeuProValGluProValGluProGlnLeuThrValasp 423  
 DB 481 GAGGATGCTACTTTGAGTCCAGAACTCTCTCTCTGTTGAACCCCAAGCTTGAGACAGTGGAC 540

QY 424 GlyAlaGluHisGlyLeuProAspThrSerTrpSerProProAlaMetAlaSerThrSer 443  
 DB 541 GGAGCAGACATGGTCTACCTCAGCACTTCTTGGTCTCCACCTGCTATGGCCTCTACCTCC 600  
 QY 444 LeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGly 463  
 DB 601 CTGTCAAGAGCTCCACCTTCTTTATGGCATCAAGCATCTTCTCTGACTGATCAGGC 660  
 QY 464 ThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThr 483  
 DB 661 ACCACAGATACCAATGGCCACTGACCAGCAATAGTACACAGGGCTCACCATCCCAACC 720  
 QY 484 SerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSer 503  
 DB 721 AGTGATTATCTTGCAATCAGCCAACTGGCTCTGGGAATTCACATCCACCTGCACTTCA 780  
 QY 504 AspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAsp 523  
 DB 781 GATGACAGCCGATCAAGTGCAGGTGGCGAAGATATGGTCAGACACTAGATGAATGGAT 840  
 QY 524 LeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrValSerValPro 543  
 DB 841 CTGTCTGACACTCTCTGCCCCATCTGAGGTACAGAGCTCAGCGAATATGTTCTGTCCCA 900  
 QY 544 AspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSer 563  
 DB 901 GATCATTTCTTGGAGGATACCACTCTCTCTCAGCTTTACAGTATATCACCACCTAGTTCT 960  
 QY 564 MetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeuArgValAlaAsn 583  
 DB 961 ATGACCATGTCGCCCAAGGGCCGAGAGCTGGTAGTGTCTTCAGTCTGCTGTTGCTAAC 1020  
 QY 584 MetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGln 603  
 DB 1021 ATGGCTTCTCCACGACCTGTTCAACAGAGACTCTCTGAGTACCGAGCTCTGGAGCAA 1080  
 QY 604 GlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeu 623  
 DB 1081 CAATTCAACAGCTGCTGTTTCCATATCTACGATCCAACTTTACAGGATTTAAGCACTT 1140  
 QY 624 GluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLys 643  
 DB 1141 GAATATCTTAATCTCAGAAACGGAGGTGTATTGTGAATAGCAAAATGAAGTTTGTGAAG 1200  
 QY 644 SerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAla 663  
 DB 1201 TCAGTGCCTGATAACCTCACCAGGCTGTGCACGGGTCTTGGAGGATTTTCGTTCTGCT 1260  
 QY 664 AlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAsp 683  
 DB 1261 GCAGCCCAACAACTCCATCTGGAATAGACAGCTACTCTCTCAACATTTGAACCCAGCTGAT 1320  
 QY 684 GlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGlu 703  
 DB 1321 CAAGCAGATCCTCGAAGTTCTTGCCCTGGCGGAAATTTGCCCAATGTGTAAAGAACAA 1380  
 QY 704 ArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAsp 723  
 DB 1381 CGGACTGAGGAAGCGAGTGTCTGCTGCAAAACCAAGATATGACAGCCAGGGAGCTGGAC 1440  
 QY 724 GlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLys 743  
 DB 1441 GGTCTGGAACCAAGCCCTCTGTGGCCCTGGCAAAAGGATGCGAGGTCCTCCAGGGAAAG 1500  
 QY 744 GlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLys 763  
 DB 1501 GGAGCTCATGCAAGTTGCCAGATCACTCTGAAATCAAGCATACAAACCTAGTGTGTAAA 1560  
 QY 764 LysPheGlnAsnGlnGlnAsnLysValIleSerLysArgAsnSerGluLeuLeuThr 783  
 DB 1561 AAGTTCAAAATCAACAAAATAAAGGTAATCAGTAAAAAGAAATCTTGAATTAAGTACGAC 1620



QY 704 ArgThrGluGluAlaGluCysArgCysIysProGlyTyrAspSerGlnGlySerLeuAsp 723  
 Db 1369 TGGACAGAGGAGGAGAGTGTCTGACAGAGGACATGAGCCACCGGAGCCCTGGAC 1428  
 QY 724 GlyLeuGluProGlyLeuGlyGlyProGlyThrIysGluCysGluValLeuGlnGlyLys 743  
 Db 1429 TACCAGACCTTGACCTGTGTCCTCCCTGGA---AAGACTGTGTGGCGCCGCGAACA 1485  
 QY 744 GlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLys 763  
 Db 1486 GCAACTCATGACGAGCCACAGATCTCTACAAACCAAGCTCAGGAACCTGTGTATAA 1545  
 QY 764 LysPheGlnAsnGlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThr 783  
 Db 1546 AAGCTAGCT---CAGCAATAAGCTAGTAGTCAAGAAAGAAATCTTAACTATCAGCT 1602  
 QY 784 ValGluTyrGluGluPheAsnHisGlnAspTyrGluGlyAsn 797  
 Db 1603 ATAGGATTGAAGAAATTGAAGACCGAGCTGGGAGGGAAT 1644  
 RESULT 3  
 BQ639265  
 LOCUS  
 DEFINITION h433d04.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he  
 Homo sapiens cDNA clone h433d04 5', mRNA sequence.  
 VERSION BQ639265.1 GI:21763724  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1. (bases 1 to 626)  
 Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A.,  
 Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.  
 Expressed sequence tag analysis of human retina for the NEIBank  
 Project: Rebindin, an abundant, novel retinal cDNA and alternative  
 splicing of other retina-preferred gene transcripts  
 Mol. Vis. 8 (4), 196-204 (2002)  
 22103461  
 12107411  
 CONTACT: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 33 row: d column: 04  
 Seq primer: M13RPI reverse primer (ABT).  
 Location/Qualifiers  
 1. .626  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="h433d04"  
 /tissue\_type="Retina"  
 /dev\_stage="Adult"  
 /lab\_host="EMDH103"  
 /clone\_lib="Human Retina cDNA (Un-normalized,  
 unamplified): hd/he"  
 /notes="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
 was dissected from two 80 year old donors with no observed  
 eye disease. 100ug of total RNA was used for library  
 construction. A directionally cloned cDNA library in the  
 pSPORT1 vector (life technologies) was essentially following  
 the protocols of the SuperScript Plasmid System full  
 details of which are contained in the manufacturer's  
 instruction manual (http://www.lifetech.com/). First  
 strand synthesis was carried out using a Not I  
 primer-adaptor

[5'-PGACTAGTCTTAGATCGGAGCGCGCCG(T)15-3']. EST analysis  
 was performed on the unamplified library at the NIH  
 Intramural Sequencing Center (NISC)."

ORIGIN

Alignment Scores:  
 Pred. No.: 2,378-94 Length: 626  
 Score: 1054.00 Matches: 208  
 Percent Similarity: 100.00% Conservations: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 25.60% Indels: 0  
 DB: 13 Gaps: 0

US-10-007-270-2 (1-797) x BQ639265 (1-626)

QY 260 GlnGluLeuAlaGlyLysSerGlnLeuMetGlnIysIlePheLysLeuProGly 279  
 Db 3 CAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAGAAAGATATTTAAGAAACTTCCAGGA 62  
 QY 280 PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer 299  
 Db 63 TTCAAAAAATCCATGTGTAGGATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCC 122  
 QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
 Db 123 ACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAAGAAAGCCCTGCA 182  
 QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThr 339  
 Db 183 AGTGACCTCTGTCTTTGATTCACACAAATTTGAAAGTGGAGAGTCTATCATGGAAACC 242  
 QY 340 MetGluGluAspLysGlnProGluIleTyrIleuThrAlaThrAspLeuLysArgLeuIle 359  
 Db 243 ATGGAGGAGGACCAAGCAACAGAAATCTATCTACAGCTACAGACCTCAAAAGCTGATC 302  
 QY 360 SerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
 Db 303 AGCAAGCAGCTAGAGGAGAAACAATCTTTGATGTGGGACAATTCAGTTCACGTGATGAA 362  
 QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
 Db 363 ATTGCTGGATCACTGCCAGGCTTTGGTCTTGACACCAATCAGAGCTGCCACATCTTT 422  
 QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
 Db 423 GCTGTATTAACAGAGGATGCTACTTTGAGTCCAGAACTCTCTCTGTGTGAACCCAGCTT 482  
 QY 420 GluThrValAspGlyValAlaGluHisGlyLeuProAspThrSerTrpSerProAlaMet 439  
 Db 483 GAGACAGTGGACGAGGAGAGCATGGTCTACCTGACACTTCTTGGTCTCCACCTGCTATG 542  
 QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
 Db 543 GCCTCTACCTCCCTGTGTCAGAAAGCTCCACCTTCTTTATGGCATCAAGCATCTTCTCTG 602  
 QY 460 ThrAspGlnGlyThrThrAspThr 467  
 Db 603 ACTGATCAGGCACCACAGATACA 626

RESULT 4

AY415972

LOCUS

DEFINITION

AY415972

ACCESION

AY415972

VERSION

AY415972.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AY415972 1587 bp DNA linear GSS 17-DEC-2003  
 Pan troglodytes IMPG1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.

AY415972 GI:39771932

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1. (bases 1 to 1587)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios

JOURNAL  
 PUBLISHED  
 REFERENCE  
 2 (bases 1 to 1587)

CLARK, A.G., GLANOWSKI, S., NIELSEN, R., THOMAS, P., KEJARIWAL, A.,  
 TODD, M.A., TANENBAUM, D.M., CIVELLO, D.R., LU, F., MURPHY, B.,  
 FERREIRA, S., WANG, G., ZHENG, X.H., WHITE, T.J., SHINSKY, J.J.,  
 ADAMS, M.D. and CARGILL, M.  
 Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA

COMMENT  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment

## FEATURES

source

Location/Qualifiers  
 1..1587  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 <1..>1587  
 /gene="INFG1"  
 /locus\_tag="HCM5735"

## ORIGIN

## Alignment Scores:

Pred. No.: 2,05e-85 Length: 1587  
 Score: 971.00 Matches: 239  
 Percent Similarity: 45.27% Conservative: 0  
 Best Local Similarity: 45.27% Mismatches: 289  
 Query Match: 23.59% Indels: 0  
 DB: 29 Gaps: 0

US-10-007-270-2 (1-797) x AY415972 (1-1587)

QY 270 MetGlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArg 289  
 Db 1 ATGCAAAAGATATTTAAGAACTCCAGGATTCAGAAAAATCCATGTGTAGGATTTAGN 60  
 QY 290 ProLysLysGluLysAspGlySerSerThrGluMetGlnLeuThrAlaIlePheLys 309  
 Db 61 NNN 120  
 QY 310 ArgHisSerAlaGluAlaLysSerProLaserAspLeuLeuSerPheAspSerAnlys 329  
 Db 121 NNN 180  
 QY 330 IleGluSerGluGluValTyHisGlyThrMetGluGluAspLysGlnProGluIleTyR 349  
 Db 181 NNN 240  
 QY 350 LeuThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeu 369  
 Db 241 NNN 300  
 QY 370 AspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyPro 389  
 Db 301 NNN 360  
 QY 390 AspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSer 409  
 Db 361 GACACCAATCAGAGCTGCCACATCTTTTGTCTTATTAACAGAGNATGCTTACCTTAGT 420  
 QY 410 ProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeu 429  
 Db 421 CCAGAACTTCCTCTTTGTTGAACCCAGCTTCAGACAGTGGACGAGCAGCATGGTCTA 480  
 QY 430 ProAspThrSerTrpSerProProAlaValaserThrSerLeuSerGluAlaProPro 449  
 Db 481 CCTGNN 540

RESULT 5

QY 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469  
 Db 541 NNN 600  
 QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTySerAlaIle 489  
 Db 601 NNN 660  
 QY 490 SerGlnLeuAlaLeuGlyIleSerHisProAlaSerSerAspAspSerArgSerSer 509  
 Db 661 NNN 720  
 QY 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529  
 Db 721 NNN 780  
 QY 530 ProSerGluValProGluLeuSerGluTyValSerValProAspHisPheLeuGluAsp 549  
 Db 781 CCACTGAGGTACCAGAGCTCAGCGAATATGTTCTGTCCAGATCATTTCTGGAGGAT 840  
 QY 550 ThrThrProValSerAlaLeuGlnTyIleThrThrSerSerMetThrIleAlaProLys 569  
 Db 841 ACCACTCTGTCTGTCTTTACAGTATATCACCAGTATGTTCTATGACCATTTGCCCAAG 900  
 QY 570 GlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSerAspAsp 589  
 Db 901 GGCCGAGAGCTGGTAGTGTCTTCAGTCTCGTGTGCTAACATGGCTTCTCAACGAC 960  
 QY 590 LeuPheAsnLysSerSerLeuGluTyArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609  
 Db 961 CTGTTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGAGCAANNNNNNNNNNNNNNCTG 1020  
 QY 610 ValProTyLeuArgSerLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg 629  
 Db 1021 GTTCCATATCTACGATCCAACTTNNCAGGATTTAAGCAACTTGAATACCTTAACCTCAGA 1080  
 QY 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyAsnLeu 649  
 Db 1081 AACGGAGTGTGATTTGTAATACCAAAATGAAGTTTNCATAGTCAGTCGCGTATNNNNNC 1140  
 QY 650 ThrIleAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 659  
 Db 1141 ACCAAGCTGTGCACGGGGTCTTTGGAGGATTTTCGTCTGCMNCAGCCCAACCACTCCAT 1200  
 QY 670 LeuGluIleAspSerTySerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 699  
 Db 1201 CTGGAATAGANACNACTCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1260  
 QY 690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709  
 Db 1261 NNN 1320  
 QY 710 CysArgCysLysProGlyTyAspSerGlnGlySerLeuAspGlyLeuProGlyLeu 729  
 Db 1321 NNN 1380  
 QY 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749  
 Db 1381 NNN 1440  
 QY 750 ProAspHisSerGluAsnGlnAlaTyLysThrSerValLysPheGlnAsnGlnGln 769  
 Db 1441 NNN 1500  
 QY 770 AsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyGluGluPhe 789  
 Db 1501 NNN 1560  
 QY 790 AsnHisGlnAspTrpGluClyAsn 797  
 Db 1561 AACCATCAAGATTGGGAAGGAAAT 1584

```

B0636596
LOCUS      B0636596          598 bp      mRNA      linear      EST 15-JUL-2002
DEFINITION hdl1h02.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he
Homo sapiens cDNA clone hdl1h02 5', mRNA sequence.
ACCESSION  B0636596
VERSION    B0636596.1  GI:21761055
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1. (bases 1 to 598)
AUTHORS   Wistow,G., Bernstein,S.I., Wyatt,M.K., Ray,S., Behal,A.,
            Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
TITLE     Expressed sequence tag analysis of human retina for the NEIBank
            Project: Retbindin, an abundant, novel retinal cDNA and alternative
            splicing of other retina-preferred gene transcripts
JOURNAL    Mol. Vis. 8 (4), 196-204 (2002)
MEDLINE    22103461
PUBMED     12107411
COMMENT    Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 11 row: h column: 02
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES   Location/Qualifiers
            1..598
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="hdl1h02"
             /tissue_type="Retina"
             /dev_stage="adult"
             /lab_host="EMDH108"
             /clone_lib="Human Retina cDNA (Un-normalized,
             unamplified): hd/he"
             /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue
             was dissected from two 80 year old donors with no observed
             eye disease. 100ug of total RNA was used for library
             construction. A directionally cloned cDNA library in the
             pSPORT1 vector (Life Technologies) was constructed at
             Bioerve Biotechnology (Laurel MD) essentially following
             the protocols of the SuperScript Plasmid System full
             details of which are contained in the manufacturer's
             instruction manual (http://www.lifetech.com/). First
             strand synthesis was carried out using a Not I
             primer-adaptor
             [5'-pGCTAGTCTAGTCGAGCGGCGCC(7)15-3']. EST analysis
             was performed on the unamplified library at the NIH
             Intramural Sequencing Center (NISC)."]
ORIGIN
Alignment Scores:
Pred. No.:      1..66e-84      Length:      598
Score:          955.00         Matches:     190
Percent Similarity: 98.47%      Conservative: 3
Best Local Similarity: 96.94%   Mismatches: 3
Query Match:    23.20%         Indels:     0
DB:             13             Gaps:       0

US-10-007-270-2 (1-797) x B0636596 (1-598)

QY      432 ThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProPhephe 451
Db      ::::
Db      11 TCGCITGGTCTCCACCTGCTATGGCTCTACCTCCCTGTGAGAGCTCCACCTTCTTT 70
QY      452 MetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAsp 471
Db      71 ATGGCATCAGCACTCTCTCTGACTGATCAAGGCACACACATATGGCCACTGAC 130

472 GlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGln 491
131 CAGACAATCTAGTACCAGGCGCCACCATCCCCACAGTGATTATCTTGCATACAGCCAA 190
492 LeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArgSerSerAlaGly 511
191 CTGGCTCTGGGAATTTTCATCCCTCCCTGCTTCCAGATGACGCGCATCAAGTCAGT 250
512 GlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSer 531
251 GCGCAAGATATGCTCAGAGACCTAGATGAAATGGATCTGTCTGCACACTCTCTGCCCATCT 310
532 GluValProGluLeuSerCluTyrValSerValProAspHisPheLeuGluAspThrThr 551
311 GAGGTACCAAGACCTCAGCGAATATGTTCTTGTGCCAGATCATTTCTTGGAGATACCACT 370
552 ProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProIlysglyArg 571
371 CCTGTCTCAGCTTTACAGTATATACCACTAGTCTTATGACCAATGCCCCACAGGCGCA 430
572 GluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591
431 GAGCTGGTAGTGTCTTCAATCTGGCTTGTCTTCAATCTGGCTTGTCTTCAACAGCACTTTC 490
592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuValPro 611
491 AACAAAGACTCTCTGGAGTACCGAGCTCTGGAGCAACATTCACACAGCTGCTGGGTCCA 550
612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627
551 TATCTACGATCCAATCTTACAGGATTTAAGCAACTTGAATACTTAAC 598

RESULT 6
LOCUS   AY418611          3713 bp      DNA      linear      GSS 17-DEC-2003
DEFINITION Homo sapiens IMPC2 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION AY418611
VERSION   AY418611.1  GI:39774571
KEYWORDS  GSS.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 3713)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL   Science 302 (5652), 1960-1963 (2003)
PUBMED    14671302
REFERENCE 2 (bases 1 to 3713)
AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
            Direct Submission
            Submitted (15-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
            These sequences were made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
            1..3713
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             <1..>3713
             /gene="IMPC2"
             /locus_tag="HCM6615"
ORIGIN

```



## Alignment Scores:

Pred. No.: 6,22e-78 Length: 3713  
 Score: 902.00 Matches: 290  
 Percent Similarity: 39.08% Conservative: 145  
 Best Local Similarity: 26.06% Mismatches: 274  
 Query Match: 21.91% Indels: 405  
 DB: 29 Gaps: 34

US-10-007-270-2 (1-797) x AV418611 (1-3713)

QY 2 TyrLeuGluThrArgAlaIlePheValPheThrIlePheLeuGlnValGlnGlyThr 21  
 DB 11 TTCTCTTTTGGGAAGATTCTCTGGTATTTC-ATATTTGCTGTATAGACGAC 69  
 QY 22 ---LysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro--- 39  
 DB 70 TTTCATCATTAACAGCACAAACCTACTTATCT---ATAGAGGAGATCCAGAACCCCAAG 126  
 QY 40 -----ProArgAsnGluThr-----ThrGluSer 47  
 DB 127 AGTGCAGTTTCTTTCTCTGCTGGAAGATCAACAGACCTTTCTCTAGCTACCAAAAG 186  
 QY 48 ThrGluLysMetTyrLysMetSerThrMetArgAlaIlePheAspLeuAlaLysHisArg 67  
 DB 187 AAACAGCCTCTGGACCGCAGAGAAACTGAAGACAGTGGTTA-----ATCAGA 234  
 QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87  
 DB 235 AGCGGAGATCTATTCTGTTCTTAATGGAGTGAATACTGCCAGATGAAGTGTGCA 294  
 QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTrp 107  
 DB 295 GAGGTGTGGCAAAATCATGTGAAGTATTTAAAGTCCGAGTGTGTCAAGAAAGTGTCTGG 354  
 QY 108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTrpVal 127  
 DB 355 GAAGCCTTCAGACACTTTTGGGATCGACTCTCTGGCGTGAAGATATCATATCTGGATG 414  
 QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147  
 DB 415 AATTTGTGTGGATGGAGTGCACAGTATATTTGAATGGGCACAAATTTTGTGTAATCT 474  
 QY 148 GlnGluHisLeuAspLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
 DB 475 GTGGAACTAGAACGCTTATCATGAAGAACTGACTTAT-----GCAAG 519  
 QY 168 AspGluIleSerAlaGluLysThrLeuGlyGluPro-----GlyGluThrIleVal 184  
 DB 520 GAAACTGTAAAGCAGCTCTGAA--CTGTCTCTCCAGTTCCTGTGTGTGTACTTCAACA 576  
 QY 185 IleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr----- 200  
 DB 577 TTGGGAGACACTACTCTCAGTGT-----CCATCCAGAGAGGTGGACGCTATGAA 627  
 QY 201 -----ProAspAspThrLeuLeuAsnGluIleLeuAsp 211  
 DB 628 GGTGCTCAGAGACGCTTGGAAAGCCAGAGAGATATACCAATGAAT---GAG 684  
 QY 212 AsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeu 231  
 DB 685 AATGTGTAGAGAAGACCCACAAACACGAGCTGAACAGATTGCGAATTC----- 735  
 QY 232 GluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeu 251  
 DB 736 -----AGTATCCACTTTTGGGAAGCAGATGACAGGGAAGAACTA 774  
 QY 252 AlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGln 271  
 DB 775 CAGGATTCCTCCAGCTTCCACCAGCACCTTGAAGAGAATTTATTTTCAGAGGTGAA 834  
 QY 272 LysIlePheLysLysLeuProGlyPheLysIleHisValLeuGlyPheArgProLys 291

DB 835 AATGCATTTACTGGGTACCAAGGCTACAAGAAATTCGTGTACTGTAATTTAGNNNNNN 894  
 QY 292 LysGluLysAspGlySerSerThrGluMetGlnLeuThrAlaIlePheLysArgHis 311  
 DB 895 NNNNNNNNNNTGCGTAGATGTTTACTATCATGCTTACC-----TTC 939  
 QY 312 SerAlaGluAlaLysSerProAlaSer---AspLeuLeuSerPheAspSerAsnLysIle 330  
 DB 940 AATGCTGAGGCCATCAGCAATACCACTGGGACCTCATTAGCCTTCTCAACACAGGTG 999  
 QY 331 GluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeu 350  
 DB 1000 GAAAC-----CATGGCTGTGAACTGATGATATAACCACTCTGTGTATTAT 1047  
 QY 351 ThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGlu----- 365  
 DB 1048 ACAATCATGAATTCAGAGATTATATTGCTGAGACATTGCAGCAATTTTGTCTGGGG 1107  
 QY 365 ----- 365  
 DB 1108 AACTTCTCTGATCCAGATCCTGATTCTCCTGAGCTTATCAATGTGAGAGAGTTTG 1167  
 QY 366 ---GluGlnSerLeuAspVal-----GlyThrIleGlnPheThr--- 377  
 DB 1168 CGTCAACCAACTGAAGATCTAGTTTGGAAACACCAAGTTCAAGTCTTCAGGCAACGCCG 1227  
 QY 378 -----AspGluIleAla 381  
 DB 1228 TCATCTATTCTGATTAATACCTTTCAAGCTGCATGCCCTCAGCAGATGAATCACTCAC 1287  
 QY 382 GlySerLeuPro-----AlaPheGlyProAspThr 391  
 DB 1288 AGCAGTATCCACCACTTGATTTCAGCTCTGGTCTCCCTCAGCCACTGGCAGGGAACCTC 1347  
 QY 392 GlnSerGluLeuPro----- 396  
 DB 1348 TGCTCAGAAAGCTCTTGGGTGATTAGTGTCTACACAAATTAGCCTTTCCCTCGAAG 1407  
 QY 396 ----- 396  
 DB 1408 ATGGGCTCAGCTCTCCCCAGAGGTTTAGAGGTTAGCAGCTTGACTCTTCACTTCTGTC 1467  
 QY 397 -----ThrSerPheAlaValIleThrGluAspAlaThrLeuSerPro 410  
 DB 1468 ACCCGCGCAGTGTTCAGACTGGCTTGCCTGTGGCTTCTGAGGAAAGGACTTCTGATCT 1527  
 QY 411 GluLeuProValGluProGlnLeuGluThrValAspGlyAlaGlu----- 426  
 DB 1528 CACTTG-----GTAGAAGATGGATTAGCCAATGTTGAAGAGTCAAGAATTTCTTTCT 1581  
 QY 427 ---HisGlyLeuProAspThrSerTrpSerProAlaMetAlaSerThr----- 442  
 DB 1582 ATTGATTCTTCCCTTCAAGTTTCATCTCAACCTGTGCCAAAGAAACATACCATCC 1641  
 QY 443 -----SerLeuSerGluAlaPro-----ProPhe 450  
 DB 1642 ATGGAAGACTGTGTGTCTTAACTATTCACCATATCTGACCTCTTCTATACCTTTT 1701  
 QY 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470  
 DB 1702 GCTTGGACTCTTGTACCTCCAAAGTCAAGACCAATTAAGAGTGAGCCCTTCTCTGCCA 1761  
 QY 471 AspGlnThrMet----- 474  
 DB 1762 GATGCATCCATGGAAAAAGAGTTAATATTTCACGCTGTTTAGGTTTCCAGGCTCTGGCAA 1821  
 QY 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494  
 DB 1822 AAGGTAGATCTGATTACTTGGCCATGGAGTGAGACTTCTATCA---GAGAAGAGCGCTGAA 1878  
 QY 495 GlyIleSerHisProProAlaSerSerAspSerArgSerSerAlaGlyGlyGluAsp 514  
 DB 1879 CCACTGTCCAAAGCGGTGGCTTGAAGATGATGATTCACTTTTGGCCAGCTTGAGATTGAAGAC 1938

```
QY 515 -----MetValArgHisLeuAspGluMetAsp----- 523
Db 1939 AAGAACTAGTTTGTAGTTGACAAATCGATTCACAGACCAGAAATTAGTAGCACTCAAAA 1998
QY 523 ----- 523
Db 1999 TATGAACATGATGACAGATCCATACACTTTCCAGAGGAAGAGCCTCTTAGTGGCCCTGCT 2058
QY 524 -----LeuSerAspThrProAlaPro----- 530
Db 2059 GTGCCCATCTTCGAGATATCGAGCTGAATCTCGCTCTTAACCCCTCCCAAGACATCA 2118
QY 531 SerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThr 550
Db 2119 TCAGAGTACTGCTGTGTGATGATTACTCAGTTACCAAGCACCTCTTATACTGACATCT 2178
QY 551 ThrProValSerAla----- 555
Db 2179 GTACCAATCTCTGCTCTTACTGTATAATCATGACGACATGCCATCTCTAAGGGAGGAT 2238
QY 556 LeuGlnTyrIleThrThrSerSer----- 563
Db 2239 ATGGAACAAATTAATGAGTATCACTCACTAATGAATGTTTACAGAGTGGTTTCAATGCTA 2298
QY 564 -----MetThrIleAlaProLysGlyArgGlu----- 572
Db 2299 AAGCCAGATATGCAAACTTTGTGACTATATTCGCCAATTCAGAGAGATTTGGACAAGA 2358
QY 572 ----- 572
Db 2359 ACTTCTCCCTAGAGAAATTTCCAGAGACATATTGGCAAGTACACACAGAGTGTGTGAC 2418
QY 572 ----- 572
Db 2419 AGGCTCTGTTATCTGTGACACAGTCTACCAAAATTCCTCCAAACCAATCTCCACCCCTG 2478
QY 572 ----- 572
Db 2479 CTAGAGATGAGTAATATTGGGTGTACAGGATATTTCGTAGACTGACCGGATAGGC 2538
QY 572 ----- 572
Db 2539 ACAGATTACTATCAGCTGAGCAAGTCCAGAGCAAAATGGCAAGTTGGTAGTTATGTG 2598
QY 572 ----- 572
Db 2599 GAAATGTCAACAAGTGTCTACTCCACAGAGATGGTTAGTGTGGCTTGGCCCAAGAGGA 2658
QY 573 -----LeuValValPhePheSerLeuArg 580
Db 2659 GGAGATGACTTGAGTTATACCCAGACTTCAGGAGCTTTGGTGTGTTTCTTCAGCCTCGA 2718
QY 581 ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerLeuGluTyrArgAla 600
Db 2719 GTGACTAACATGATGTTTTCAGAAGATCTGTTTAAATAAAACTCCCTTGGAGTATAAGCC 2778
QY 601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620
Db 2779 CTGGAGCAAGATCTTAGAATTTGGTTTCCCTATCTCCAGTCAAAATCTCAGCGGGTTC 2838
QY 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640
Db 2839 CAGAACTTAGAAATCTCAACTTCAGAAATGGCAGCATTTGGTGAACAGTCAATGAAG 2898
QY 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660
Db 2899 TTTGCCAATTTCTCTCCCTCTTAACGTCACAAATGGCGGTGTACATGATTTCTGGAAGACTTT 2958
QY 661 ArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680
Db 2959 TGTACCAGCTGCCTACATACCACTGAACTTGGCTATTGATGAATAATCTCTCTTGTATGGAA 3018
```

```
QY 681 ProAlaAspGlnAlaAspProCysValysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700
Db 3019 TCAGGTGATGAAGCAACCCCTTGAAGTTTCAGCCCTGTAATGAATTTTCAGAGTCTG 3078
QY 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGln--- 719
Db 3079 GTCAACCCCTGGAGTGGAGAAGCAAGTGCAGATGCTTCCCTGGATACCTGAGTGTGAA 3138
QY 720 -----GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLys 735
Db 3139 GAACGGCCCTGTACAGTCTCTGTGACCTACAGCTGACTTCTCTTGAATGATGGAAAG 3198
QY 736 GluCysGluValLeuGlnGlyLysGlyAlaProCysArg 748
Db 3199 --TGTGACATTATGCTCTGGGCACGGGCCCATTTGTAGG 3234
RESULT 7
BX510244 690 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp686P2496_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFZp686P2496 5', mRNA sequence.
ACCESSION BX510244
VERSION BX510244.1 GI:32050551
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 690)
AUTHORS Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
TITLE EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I.,
Wellenreuther,R., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFZp686P2496) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source 1..690
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686P2496"
/dev_stage="adult"
/lab_host="DH103"
/clone_lib="686 (synonym: hlcc3)"
/notes="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
ORIGIN
Alignment Scores:
Pred. No.: 3,2e-78 Length: 690
Score: 893.00 Matches: 168
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21.69% Indels: 0
DB: 13 Gaps: 0
US-10-007-270-2 (1-797) x BX510244 (1-690)
QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuValGlnGly 20
```





Db 1345 AGGGAAGTCCAGTCCAAAGTGGCTTTCGGTGAAGTGTCTACCTCCAAAGTTAGCTTCT 1404  
Qy 393 ----- 393  
Db 1405 CCCAGAGGTGGTCCCTCAGTTCCTCCAGAGATTTAGGGGTAGCAGCTTGACTCTT 1464  
Qy 394 ----- GluLeuPro-----Thr 397  
Db 1465 CATTCGTGTACCCAGCAGTGCCTTCAGCCTGACCTGCTGTGGCTCCTGAGGAAGACT 1524  
Qy 398 SerPheAlaValIleThrGluAspAlaThrLeuSerProGlu----- 411  
Db 1525 TCTGGATCGTTCATATTAGAGATGGGTAGCAGCAGTCAAGAAATAGAGATCTTCT 1584  
Qy 412 ----- -LeuProPro 414  
Db 1585 ATTGATGATTCCTTCAAGCCCATTAATCAACCTGTGCCAAAGAAACAGTACCACCT 1644  
Qy 415 ValGlu-----ProGlnLeuGlu----- 420  
Db 1645 ATGGAGACTCTGACAGGGTCTCTTGTCCACACCATCTGACCTTCTGCTATAGAA 1704  
Qy 421 -----ThrValAsp-----GlyValaGluHisGlyLeu----- 429  
Db 1705 GACCTTACTAAGACATAGGACACCTTCTGGCTTGGAGTCCCTTGGCTTCCAACATCTCA 1764  
Qy 430 -----ProAspThrSer----- 433  
Db 1765 GACCAAGTGAAGTATGCCATGGTTTCCAGACACCTCTGTGGAAGAAAGACTTCATTTT 1824  
Qy 434 -----TrpSer 435  
Db 1825 GAAAGTGGCTTGGTCTTGGGTCTGGGAAGATGTAGATGTGATGATGGCCCATGGAGT 1884  
Qy 436 ProProAlaMetAlaSerThr-----SerLeuSerGluAlaPro----- 448  
Db 1885 GAGACTTCATTAGAGAGACCACTAAACCACTGTCAAAGTCATGGTCTGAAGAACAGGAT 1944  
Qy 448 ----- 448  
Db 1945 GCACATTACCAACTGAGGGTGAAGAAATATACATATAGATGGCAGATAGTCCACA 2004  
Qy 448 ----- 448  
Db 2005 GAACAAATTATGAATCATCAGAACATAGATAGGATAGGCCCATACATTTTATAGAG 2064  
Qy 449 -----ProPheMetAlaSerSer----- 455  
Db 2065 GAAGAATCCCATGTAGATCTACTATACCATCTTTGTAGAGTCCGCAACTCCACATCA 2124  
Qy 456 -----IlePheSer-----LeuThrAspGlnGlyThrThrAspThrMetAlaThrAsp 471  
Db 2125 TCTCAATCTTTCAAACACACATCTAGATGTACAGACATTCATTCCTTACTCCTTACC 2184  
Qy 472 GlnThrMetLeuValPro---GlyLeuThrIleProThrSerAspThrSerAlaIleSer 490  
Db 2185 AAACCAACCTCTTACCGGTAACTATAGCAATCCCTGCTCCACTAAGAAACACAGATGAG 2244  
Qy 491 GlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAsp-----AspSerArg 507  
Db 2245 GTACTCAAGGAAGATATGTGTACATACAGAAATCATCTCCAGTCAACAAAGCTGACAGT 2304  
Qy 508 SerSerAlaGlyGlyGluAspMet----- 515  
Db 2305 GTTCCAGTGTCAAGCCAGATATGACCTGTGTGGACCATGTGCGCAATACAGATACA 2364  
Qy 516 -----ValArgHisLeuAspGluMetAspThrPro 528  
Db 2365 GTTTGACAAGAAGCTTCTTCTTAGGGAATTTGTCAGAGACATGTGCAAGTACACCA 2424  
Qy 529 -----AlaProSerGluValPro--- 534  
Db 2425 GAGAGCACTGACAGCTCTGGTGAAGCTTCCATGACAGACAGTCCACTGAATGGCTTCA 2484

Qy 535 -----GluLeuSerGluThrValSerVal----- 542  
Db 2485 ACCACCCACTCCAGCCAGCTAGAGGAGAGTAATAATGGCGGTCCAGGATATTTCATTA 2544  
Qy 542 ----- 542  
Db 2545 GAACATAGATCAGTATGACACAGATTTATATATCAGTCGAGCTAAGTGAAGAACACATGGC 2604  
Qy 543 ---ProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnThrIleThr 561  
Db 2605 AAGGCTGACAGCTATGTGGAATGTCTACCAAGTTI-----CACTACACAGAGATG 2655  
Qy 562 SerSerMetThrIleAlaProLysGly-----ArgGlu 572  
Db 2656 CCTATTGTGCTCTGCCCAAGAGAGGTGCTTGGAGTCACACCAGACTCGAGGAGCA 2715  
Qy 573 LeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsn 592  
Db 2716 TTGGTGGTTTCTTCAGCCTCCGCGTGACAAACATGTGTTTTCAGAACACTGTTTAAAC 2775  
Qy 593 LysSerSerLeuGluThrArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProThr 612  
Db 2776 AAAAAGCTTTTGAATATATAAGCCCTGGAACAAAGATCTTAGAACTGCTGTGTCCTAT 2835  
Qy 613 LeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySer 632  
Db 2836 CTCAGTCAATCTGTCCAGGTTCCAGAACCTAGAAATCTCGAGTTTCAGAAACCGCAGC 2895  
Qy 633 ValIleValAsnSerLysMetLysPheAlaLysSerValProThrAsnLeuThrLysAla 652  
Db 2896 ATTGTGTGTAACGCGCAGTGGAGTTGCGCGAGTCTGCCCTCTTAATGTCAACAGGCGC 2955  
Qy 653 ValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHisLeuGluIle 672  
Db 2956 ATGTATAGATCTGGAAGACTTTTGTACCACTGCTTACCAACCATGAAGTTGGATATC 3015  
Qy 673 AspSerThrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAla 692  
Db 3016 GATAAGTACTCTCTGACGCTGGAATCAGGTGATGAGGCCAACCTTGCAGGCTTTCAGGCC 3075  
Qy 693 CysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCys 712  
Db 3076 TGTAAATGAATTTCTGAGTGTGTGTAAATCCATGAGTGGAGAGCAAGTCAATGC 3135  
Qy 713 LysProGlyThrAspSerGlnGly-----SerLeuAspGlyLeuGluPro 727  
Db 3136 TACCTGGGTACCTGAGTGTGATGAATGACCTTGTCAAAGTCTCTGTGATCTACAGCT 3195  
Qy 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747  
Db 3196 GACTTCTGTTGAACGATGGAAG---TGTGACATTATGCTGGGCATGAGCCATTGT 3252  
Qy 748 Arg 748  
Db 3253 AGA 3255

## RESULT 10

AY418612

LOCUS

DEFINITION

Pan troglodytes IMPG2 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION

AY418612

VERSION

AY418612.1

GI:39774572

KEYWORDS

SOURCE

ORGANISM

Pan troglodytes (chimpanzee)

REFERENCE

1 (bases 1 to 3713)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,

Todd, M.A., Tansbaum, D.M., Civallo, D.R., Lu, P., Murphy, B.,

Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

AY418612 3713 bp DNA linear GSS 17-DEC-2003

Pan troglodytes IMPG2 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION

AY418612

VERSION

AY418612.1

KEYWORDS

SOURCE

ORGANISM

Pan troglodytes (chimpanzee)

REFERENCE

1 (bases 1 to 3713)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,

Todd, M.A., Tansbaum, D.M., Civallo, D.R., Lu, P., Murphy, B.,

Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,









QY 493 AlaLeuGlyIleSerHisProProAlaIleSerSerAspAspSerArgSerSerAlaGlyGly 512  
 DB 363 GCTCTGGGAATTTTCAATCCACTTGCATCTTCAGATGACAGCCGATCAAGTGCAGGTGC 422

QY 513 GluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrPro 528  
 DB 423 GAAGATATGTCAGACACACCTAGATGAATGATCTGTCGACACTCT 470

RESULT 13  
 LOCUS AL713229 510 bp mRNA linear EST 04-SEP-2003  
 DEFINITION DXFZp686P1295\_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
 ACCESSION AL713229  
 VERSION AL713229.1 GI:19696585  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 510)  
 AUTHORS Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and  
 Wiemann, S.  
 TITLE EST (Bloeker, H., Boecker, M., Brandt, P., Mewes, H.W., Weil, B. and  
 Wiemann, S.)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: MIPS  
 MIPS Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by GSF (National Research Centre for Biotechnology Ltd.,  
 Braunschweig/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No sl sequence available.  
 This clone (DXFZp686P1295) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
 source Location/Qualifiers  
 1..510  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DXFZp686P1295"  
 /dev\_stage="adult"  
 /lab\_host="DH103"  
 /clone\_lib="686 (synonym: hlcc3)"  
 /note="Vector: pTriplex2; Site\_1: SfiI; Site\_2: SfiIb;  
 cDNA-collection"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4,58e-65 Length: 510  
 Score: 759.00 Matches: 156  
 Percent Similarity: 66.53% Conservative: 1  
 Best Local Similarity: 66.11% Mismatches: 0  
 Query Match: 18.44% Indels: 79  
 DB: 9 Gaps: 1

US-10-007-270-2 (1-797) x AL713229 (1-510)

QY 1 MetTyrLeuGluThrArgAlaIlePheValPheTrrPheLeuGlnValGlnGly 20  
 DB 37 AIGTATTGGAAACATAGAGATCTATTGTGTTTGGATTTTCTCCAAAGTTCAGGA 96

QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro 40  
 DB 97 ACCAAA----- 102

QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60

DB 102 ----- 102  
 QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 DB 102 ----- 102  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 DB 102 ----- 102  
 QY 101 ValCysGlnGluAlaValTrrPgluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 103 GTGTGTGAGGAAGCAGATATGGAGACATATCGATCTTTCTGGATCCATCCCTGACACA 162  
 QY 121 GlyGluTyrGlnAspTrrPvalSerIleCysGlnGlnThrPheCysLeuPheAspIle 140  
 DB 163 GGGGAATATCAGGACTGGGTGAGCATCTGCAGCAGGAGACCTTCTCCCTCTTGACATT 222  
 QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnArgIleLysGln 160  
 DB 223 GGAATAAACTTCAGCAATTCAGGAGCACCTGGATCTTCTCCAGCAGAGAAATAAAACAG 282  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 DB 283 AGAAGTTTCCCTGACAGAAAAGATGAAATATCTGCAGAGAAGACATTCGGAGAGCCTGGT 342  
 QY 181 -GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuTh 200  
 DB 343 TGAACCACTTGTCTATTCAACAGATGTTGCCAAGCTCTCACTTGGGCTTTCCCTCTCAC 402  
 QY 200 rProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPr 220  
 DB 403 TCCTGATGACACCTCTCAATGAAATTCGATATATACACTCAACGACACCAAGATGCC 462  
 QY 220 oThrThrGluArgGluThrGluPheAlaValLeuGluGluGlnArg 235  
 DB 463 TACAACAGAAAGAAACAGATTCGCTGTGTGGAGGAGCAGAGG 508

RESULT 14  
 LOCUS CA391789 618 bp mRNA linear EST 06-NOV-2002  
 DEFINITION cs18h07.y1 Human Retinal pigment epithelium/choroid cDNA  
 (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs18h07  
 5', mRNA sequence.  
 ACCESSION CA391789  
 VERSION CA391789.1 GI:24723977  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 618)  
 AUTHORS Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A.,  
 Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.  
 TITLE Expressed sequence tag analysis of human RPE/choroid for the  
 NEIBank Project: Over 6000 non-redundant transcripts, novel genes  
 and splice variants  
 JOURNAL Mol. Vis. 8 (4), 205-220 (2002)  
 MEDLINE 22103460  
 PUBMED 12107410  
 COMMENT Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: graeme@helix.nih.gov  
 Plate: 18 row: h column: 07  
 Seq primer: M13RPI reverse primer (ABI).  
 FEATURES  
 source Location/Qualifiers  
 1..618  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

```

/db xref="taxon:9606"
/clone="csl8h07"
/tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH108"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA
(Un-normalized, unamplified): cs"
/notes="Organ: Eye; Vector: pCMVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pCMVSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the SuperScript
Plasmid System (Invitrogen Corp).
<http://www.invitrogen.com/>". The library code
designation was cs. For this library, cDNA inserts were
cloned into the NotI/MluI sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."
ORIGIN
Alignment Scores:
Pred. No.: 3,938-64 Length: 618
Score: 751.00 Matches: 152
Percent Similarity: 66.09% Conservative: 0
Best Local Similarity: 66.09% Mismatches: 0
Query Match: 18.24% Indels: 78
DB: 14 Gaps: 1
US-10-007-270-2 (1-797) x CA391789 (1-618)
QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
Db 161 AUGTATTGGAACTAGAGAGCGTATTTTGTGTTTGGATTTTCTCCAGTTCAAGGA 220
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
Db 221 ACCAAA----- 226
QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgile 60
Db 226 ----- 226
QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80
Db 226 ----- 226
QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
Db 226 ----- 226
QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
Db 227 GTGTGTCCAGGAGCAGTATGGGAGCATATCGGATCTTCTGATCGCATCCCTGACACA 286
QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGlnGluThrPheCysLeuPheAspIle 140
Db 287 GGGGAATATCAGGACTGGGTGTCAGCATCTGCCAGCAGGAGACCTTCTGCTCTTTCACATT 346
QY 141 GlyLysAsnPheSerAsnSerGlnGlnHisLeuAspLeuLeuGlnGlnArgIleLysGln 160
Db 347 GGGAAAACTTCAGCAATTCAGAGGACCTTGGATCTCTCCAGCAGAGATATAACAG 406
QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180
Db 407 AGAAGTTCCCTGCACAGAAAAGATGAATATCTGCAGAGAGACATTCGGAGAGCGCTGGT 466
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
Db 467 GAAACCATTTGCTATTTCACACAGATGTGCCAACGCTCTCACTTGGGCCCTTCCCTCACT 526
QY 201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220
Db 526 ----- 526
Db 527 CCTGATGACACCTCTCTCATGAATTCGATATACACTCAACGACCAAGATGCCT 586
QY 221 ThrThrGluArgGluThrGluPheAlaVal 230
Db 587 AACACAGAAAGAGAAACAGAAATTCGCTGTG 616
RESULT 15
LOCUS W26960 561 bp mRNA linear EST 08-MAY-1996
DEFINITION 16h10 Human retina cDNA randomly primed sublibrary Homo sapiens
cDNA, mRNA sequence.
ACCESSION W26960
VERSION W26960.1 GI:1306188
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 561)
AUTHORS Macke, J., Smallwood, P. and Nathans, J.
TITLE Adult Human Retina cDNA
JOURNAL Unpublished (1996)
COMMENT Contact: Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
Tel: 410 955 4678
Fax: 410 614 0827
Email: jeremy.nathans@gmail.bs.jhu.edu
Clones from this library are NOT available.
PCR Primers
FORWARD: CTTTTCAGCAAGTTCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTCTTCAGGGTAA
Seq primer: GGGTAAAGCAAGAAATTT.
FEATURES
Location/Qualifiers
1..561
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="mixed (males and females)"
/tissue_type="retina"
/dev_stage="adult"
/lab_host="E. coli strain K802"
/clone_lib="Human retina cDNA randomly primed sublibrary"
/notes="Organ: eye; Vector: lambda gt10; Site 1: EcoRI;
Site 2: EcoRI; The library used for sequencing was a
sublibrary derived from a human retina cDNA library.
Inserts from retina cDNA library DNA were isolated,
randomly primed, PCR amplified, size-selected, and cloned
into lambda gt10. Individual plaques were arrayed and
used as templates for PCR amplification, and these PCR
products were used for sequencing."
ORIGIN
Alignment Scores:
Pred. No.: 6,658-63 Length: 561
Score: 738.00 Matches: 150
Percent Similarity: 93.21% Conservative: 1
Best Local Similarity: 92.59% Mismatches: 10
Query Match: 17.93% Indels: 1
DB: 14 Gaps: 0
US-10-007-270-2 (1-797) x W26960 (1-561)
QY 355 LeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIle 374
Db 501 CTCANAGGCTGATCANCNAAGCACATAGGGAGACCAATCTTTGGATGTGGGCAATT 442
QY 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394
Db 441 CAGTTCACCTGATGAATTCGTGGATCACTGCCAGCGCTTTGGTCTGACACCAATCAGAN 382

```

```
QY 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGlnLeuProPro 414
Db |||||||
381 CTGCCACATCTTTGCTGTATACAGAGGATGCTACTTTGAGTCCAGAACTTCCTCT 322
QY 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrp 434
Db |||||||
321 GTTGAACCCAGCTTGAGACAGTGGACGGAGCAGACATGGTCTACTGACACTTCTTGG 262
QY 435 SerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSer 454
Db |||||||
261 TCTCCACCTGCTATGGCCTCTACTCCTCTGTCAAGAGCTCCACCTTCTTTATGGCATCA 202
QY 455 SerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMet 474
Db |||||||
201 AGCATCTTCTCTGACTGATCAGGCACCAAGANACATGGCCACTGACCAGACATG 142
QY 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494
Db |||||||
141 CTAGTACCAGGGGTCCACCATCCCAACAGTGATTATTCTNCAATCAGCCCACTGGGCTCTG 82
QY 495 GlyIleSerHisProProAlaSerSerAspSerSerSerSerSerSerSerSerSerSer 514
Db |||||||
81 GGAATTTACATCCACTGCACTTTCAGATGACGNCGATCAAGTGAAGAGGTGGCGAATA 22
QY 514 pMet 515
Db |||
21 AATG 18
```

Search completed: March 2, 2004, 00:40:46  
Job time : 5032 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2004, 20:51:36 ; Search time 668 Seconds  
(without alignments)  
4304.118 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117

Sequence: 1 MYLERRAIFVFWIFLQVQ.....NSLELTVEEENHQQWEGN 797

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2353733 seqs, 1803733377 residues

Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame-p2n.model -DEV=xlh

-Q=/cgn2\_1/USPTO.spcol/US10007270/runat\_25022004\_164209\_27253/app\_query.fasta\_1.967

-DB=Published Applications NA -QWMT=fastap -SUFFIX=rnpb -MINMATCH=0.1

-LOOPCL=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=Dblum62

-FRAS=human40.cdi LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100

-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0

-MAXLEN=2000000000 -USER=US10007270.@CGN 1.1.423 @runat\_25022004\_164209\_27253

-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -27253

-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
17:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
18:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
No.	Score	Match	Length	ID	Description

1	4073	58.9	3330	13	US-10-007-270-1	Sequence 1, Appli
2	4024.5	97.8	3261	13	US-10-007-270-27	Sequence 27, Appl
3	3619	87.9	2887	13	US-10-007-270-3	Sequence 3, Appli
4	3323	80.7	2244	13	US-10-007-270-5	Sequence 5, Appli
5	2548.5	61.9	3668	13	US-10-007-270-8	Sequence 8, Appli
6	1342.5	32.6	1725	13	US-10-007-270-10	Sequence 10, Appl
7	929.5	22.6	1321	13	US-10-007-270-12	Sequence 12, Appl
8	927	22.5	4166	13	US-10-007-270-16	Sequence 16, Appl
9	885	21.5	555	13	US-10-007-270-14	Sequence 14, Appl
10	846.5	20.6	2964	13	US-10-007-270-18	Sequence 18, Appl
11	841	20.4	4204	13	US-10-007-270-23	Sequence 23, Appl
12	194.5	4.7	2026	14	US-10-198-846-12589	Sequence 12589, A
13	189.5	4.6	4139	9	US-09-964-824A-105	Sequence 105, App
14	189.5	4.6	4139	9	US-09-964-824A-578	Sequence 578, App
15	189.5	4.6	4139	9	US-09-864-864-334	Sequence 334, App
16	189.5	4.6	4139	9	US-09-880-107-2121	Sequence 2121, Ap
17	189.5	4.6	4139	14	US-10-171-311-157	Sequence 157, App
18	189.5	4.6	4139	14	US-10-177-293-310	Sequence 310, App
19	189.5	4.6	4139	15	US-10-440-464-155	Sequence 155, App
20	188.5	4.6	1721	9	US-09-864-864-280	Sequence 280, App
21	188.5	4.6	1721	9	US-09-967-768A-224	Sequence 224, App
22	188.5	4.6	1721	14	US-10-097-340-211	Sequence 211, App
23	188.5	4.6	1721	14	US-10-171-311-155	Sequence 155, App
24	188.5	4.6	1721	14	US-10-007-926A-58	Sequence 58, Appl
25	188.5	4.6	1721	14	US-10-029-517-3	Sequence 3, Appli
26	188.5	4.6	2678	14	US-10-252-157-103	Sequence 103, App
27	187	4.5	2297	15	US-10-406-317-41	Sequence 41, Appl
28	185.5	4.5	1527	14	US-10-057-136-19	Sequence 19, Appl
29	183.5	4.5	1428	15	US-10-447-839A-20	Sequence 20, Appl
30	183.5	4.5	1739	15	US-10-447-839A-19	Sequence 19, Appl
31	183.5	4.5	1804	9	US-09-964-824A-573	Sequence 573, App
32	183.5	4.5	1804	14	US-10-029-517-17	Sequence 17, Appl
33	183.5	4.5	1823	14	US-10-101-510-339	Sequence 339, App
34	173	4.2	1424	15	US-10-447-839A-75	Sequence 75, Appl
35	165	4.0	5718	15	US-10-259-194A-85	Sequence 85, Appl
36	158	3.8	2792	12	US-10-424-535A-10187	Sequence 10187, A
37	158	3.8	2792	12	US-10-424-599-29212	Sequence 29212, A
38	153	3.7	13815	15	US-10-149-736-2	Sequence 2, Appli
39	153	3.7	2166	14	US-10-101-510-326	Sequence 326, App
40	149	3.6	1788	12	US-10-282-122A-22431	Sequence 22431, A
41	149	3.6	1888	9	US-09-881-752A-165	Sequence 165, App
42	145	3.5	8224	12	US-10-240-425-1534	Sequence 1534, Ap
43	145	3.5	8224	14	US-10-177-293-89	Sequence 89, Appl
44	145	3.5	9647	14	US-10-198-846-11006	Sequence 11006, A
45	145	3.5	11185	9	US-09-880-107-3311	Sequence 3311, Ap

ALIGNMENTS

RESULT 1  
US-10-007-270-1  
; Sequence 1, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3330  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IPM 150 CDNA, isocform A



## US-10-007-270-1

## Alignment Scores:

Pred. No.: 0 Length: 3330  
 Score: 4073.00 Matches: 796  
 Percent Similarity: 97.31% Conservative: 0  
 Best Local Similarity: 97.31% Mismatches: 1  
 Query Match: 98.93% Indels: 22  
 DB: -13 Gaps: 1

## US-10-007-270-2 (1-797) x US-10-007-270-1 (1-3330)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
 DB 131 ATGTAATTCGAACTAGAGAGCATATTTTGTGTTTGGATTTTCTCCAAGTTCAGGA 190  
 QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
 DB 191 ACCAAGATATCTCCATTAACTATACCATCTCGAACTAAAGACATAGACAATCCCCA 250  
 QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgile 60  
 DB 251 AGAATGAAACAACTGAAAGTACTGAAATAATGTACAAATGTCAACTATGAGACGATA 310  
 QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 DB 311 TTCGATTTGGCAAGCATCGAACAAAGATCCGCATTTTCCCAACGGGGTTAAAGTC 370  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrArgLeuArg 100  
 DB 371 TGTCCACAGGAATCCATGAAACAGATTITAGACATCTTCAAGCTTATTAGATTGAGA 430  
 QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 431 GTGTGTCCAGAAAGCATGAGTGGGAAGCATATCGGATCTTCTGGATCGCATCCCTGACACA 490  
 QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 491 GGGGAATATCAGACTGGGTGAGCATCTGCCAGCAGGAGACCTTCTGCTCTTTTGACATT 550  
 QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGln 160  
 DB 551 GGAAAAAATTCAGCAATTCAGAGGACCTGGATCTTCTCCAGCAGAGAATAAACAAG 610  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGluGluProGly 180  
 DB 611 AGAAGTTTCCCTGACAGAAAGATGAAATAATCTGCAGAGAGACATTCGGAGAGCCCTGGT 670  
 QY 181 GluThrIleValIleSerThr----- 187  
 DB 671 GAAACCATTTGTATTTCAC-AGCAATCTACATTTCAAAGACTTGGGCAGATTCTAAGA 729  
 QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
 DB 730 AAACCTCAGAAAGACAAATTCAGATGTGCAACAGTCTCACTTGGGCCCTTTCCCTCTC 789  
 QY 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
 DB 790 ACTCTCTGATGACACCTCTCTCAATGAATTTCTCGATATATACATCAACAGCACCAAGATG 849  
 QY 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGluGlnArgValGluLeuSer 239  
 DB 850 CCTCAACAGAAAGAAAGAACAGAAATTCCTGTGTGGAGGAGCAGAGGGTGGAGCTCAGC 909  
 QY 240 ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
 DB 910 GTCTCTCTGGTAACACAGAGTTTCAGACAGAGCTCGTCTGACTCCAGTCCCATATATAC 969  
 QY 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGly 279  
 DB 970 CAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAAAAGATATTAAAGAACTTCCAGGA 1029  
 QY 280 PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSer 299

DB 1030 TTCAAAAATCCATGTGTAGGATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCC 1089  
 QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
 DB 1090 ACAGAGATGCAACTTACGGGCATCTTTAAGAGACACAGTGCAGAAAGCAAAAGCCCTGCA 1149  
 QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThr 339  
 DB 1150 ATGACCTCTGTCTTTGATTCACAAATTTGAAGTGGAGAGCTATCATGGAACC 1209  
 QY 340 MetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIle 359  
 DB 1210 ATGGAGGAGCAAGCAACCCAGAAATCTATCTCACAGCTACAGACCTCAAAAGCTGATC 1269  
 QY 360 SerLysAlaLeuGluGlnGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
 DB 1270 AGCAAGACCTAGAGGAAGAACAACTTTTGGATGTGGGACAAATTCAGTTCATGTATGAA 1329  
 QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
 DB 1330 ATTGCTGGATCACTGCCAGCCTTTGGTCTGTGACACCAATCAGAGCTGCCACATCTTT 1389  
 QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
 DB 1390 GCTGTATTAAACAGAGGATGCTACTTTGAGTCAGAACTTCTCTCTGTAACCCAGCTT 1449  
 QY 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTipSerProAlaMet 439  
 DB 1450 GAGCAGTGGACGAGCAGAGCATGGTCTACCTGACACTTCTTGTCTCCACTGCTATG 1509  
 QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
 DB 1510 GCCTCTACCTCCCTGTGAGAAGCTCCACCTTTCTTATGGCATCAAGCATCTTCTCTCTG 1569  
 QY 460 ThrAspGlyGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
 DB 1570 ACTGATCAGGACACACAGATACATATGGCCACTGACAGACAAATGCTAGTACAGGGCTC 1629  
 QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
 DB 1630 ACCATCCCAACAGTGTATTTCTGCAATCAGCAACTGGCTCTGGGAATTTTCAATCCA 1689  
 QY 500 ProAlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeu 519  
 DB 1690 CTTGCATCTTCAGATGACACCGCATCAAGTCAGGTGGCGAAGATATGTCAGACACCTA 1749  
 QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539  
 DB 1750 GATGAAATGGATCTGTCTGACACTCTGCCCCCATCTGAGGTACAGAGCTCAGCGAATAT 1809  
 QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
 DB 1810 GTTCTGTCCCCAGATCATTTCTTGGAGGATACCACTCTCTGTCTCAGCTTTACAGATATATC 1869  
 QY 560 ThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeu 579  
 DB 1870 ACCACTAGTCTTATGACCATTTGCCCAAGGCGCAGAGCTGTAGTGTCTTCTCAGTCTG 1929  
 QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArg 599  
 DB 1930 CGTGTGTAAACATGGCCCTTCTCCAACGACCTGTTCACAAAGAGCTCTCTGAGTACCGA 1989  
 QY 600 AlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGly 619  
 DB 1990 GCTCTGGACCAACATTCACAGCTGTGGTTCATATCTACGATCCCATCTTACAGGA 2049  
 QY 620 PheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMet 639  
 DB 2050 TTTTAGCAACTTCAAACTACTTAACCTTCAAAACGGGAGTGTGATTGTGAATAGCAAAATG 2109  
 QY 640 LysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAsp 659



Db 1268 GTTGATCACTGCCAGCCTTTGGTCTGTGACACCCCAATCAGAGCTGCCACATCTTTGCT 1327  
Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeuGlu 420  
Db 1328 GTTATAACAGAGAGATGCTACTTTGAGTCCAGAACTCTCTCTGTTGAACCCAGCTTGAG 1387  
Qy 421 ThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProProAlaMetAla 440  
Db 1389 ACAGTGGACGGAGCAGAGATGCTTACTGACACTTCTTGCTCCACCTGCTATGGCC 1447  
Qy 441 SerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThr 460  
Db 1448 TCTACTCTCTGTAGAGCTCCACCTTCTTTATGGCATCAGACATCTTCTCTGACT 1507  
Qy 461 AspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThr 480  
Db 1508 GATCAAGGCACACAGATACATGGCCACTGACCAACAATGCTAGTACCAAGGCTCACC 1567  
Qy 481 IleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro 500  
Db 1568 ATCCCCACCAAGTATTTCTGCAATCAGCCACTGGCTCTGGGAATTCACATCCACCT 1627  
Qy 501 AlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAsp 520  
Db 1628 GCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGATATGGTCAGACACCTAGAT 1687  
Qy 521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrVal 540  
Db 1688 GAATGGATCTGTCTGACACTCTGCCCATCTGAGGTACCAAGCTCAGCGAATATGTT 1747  
Qy 541 SerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThr 560  
Db 1748 TCTGTCCAGATCAATTTCTTGAGGATACCACTCTCTGTCTCAGCTTTACAGTATATCACC 1807  
Qy 561 ThrSerSerMetThrIleAlaProIleGlyArgGluLeuValValPhePheSerLeuArg 580  
Db 1808 ACTAGTTCTATGACCAATTTGCCCCCAAGGGCGAGAGCTGGTAGTGTCTTCAGTCTCGT 1867  
Qy 581 ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAla 600  
Db 1868 GTTGCTAACTGGCTCTCTCCAAAGACCTGTTCAACAAGAGCTCTCTGGAGTACCGAGCT 1927  
Qy 601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
Db 1928 CTGGAGCAACAATTCACACAGCTGCTGTGTCTCCATATCTACGATCCAAATCTTACAGGATTT 1987  
Qy 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
Db 1988 AAGCACTTGAATACTTAACTTCAGAAACGGGAGTGTGATGTGAATAGCAAAATGAAG 2047  
Qy 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660  
Db 2048 TTTGCTAAGTCTGTGCCGTATATAACTCAACAAGCTGTGCACGGGGTCTTGAGAGATTTT 2107  
Qy 661 ArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680  
Db 2108 COTTCTGCTGAGCCCAACACTCTCACTGGAATAGACAGTACTCTCTCAACATTGAA 2167  
Qy 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
Db 2168 CCAGCTGATCAAGCAGATCCCTGCAAGTTCTGTCCTGGCGGAATTTGGCCATGTGTA 2227  
Qy 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGly 720  
Db 2228 AAGACGAACCGAGCTGAGGAAGCGAGGTGCTGCTGCAACACGAGATATGACGCCAGGG 2287  
Qy 721 SerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740  
Db 2288 AGCTTGACGCTCTGGAACCAAGGCTCTGTGG - CTTGGCACAAGAGATGCGAGGTCTTC 2346  
Qy 741 GlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThr 760  
:::

Db 2347 CAGGGAAGGGAGCTCCATGGG--GTTCCAGATCACTCTGAAAAATCAAGCATACAAAAC 2404  
Qy 761 SerValLysLysPheGlnAsnGlnGlnAsnAsnLysValIleSerLysArgAsnSerGlu 780  
Db 2405 AGTGTAA--AAGTTCCAAAATCAAAAAATAACAAGTAAATCAGTAAAAAGAAATTCGAA 2463  
Qy 781 LeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTyrGluGlyAsn 797  
Db 2464 TTACTGACCGTGAATATGAAGATTTAAACCATCAAGATTGGGAAGGAAAT 2514  
RESULT 3  
US-10-007-270-3  
; Sequence 3, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2887  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform B  
US-10-007-270-3  
Alignment Scores:  
Pred. No.: 0 Length: 2887  
Score: 3619.00 Matches: 711  
Percent Similarity: 90.00% Conservative: 0  
Best Local Similarity: 90.00% Mismatches: 1  
Query Match: 87.90% Indels: 78  
DB: 13 Gaps: 1  
US-10-007-270-2 (1-797) x US-10-007-270-3 (1-2887)  
Qy 8 AlaIlePheValPheTrpIlePheLeuGlnValGlnGlyThrLysAspIleSerIleAsn 27  
Db 5 GTATTTTGTGTTTTTGGATTTTCTCCAGTTCAGGAACCAA----- 49  
Qy 28 IleTyrHisSerGluThrLysAspIleAspAsnProProArgAsnGluThrThrGluSer 47  
Db 49 ----- 49  
Qy 48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67  
Db 49 ----- 49  
Qy 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87  
Db 49 ----- 49  
Qy 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTrp 107  
Db 50 -----GTGTGTGCAGGAAGCAGTATGG 70  
Qy 108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTrpVal 127  
Db 71 GAAGCATATCGGATCTTTCTGGATCGATCCCTGACACAGGGGAATATCAGGACTGGGTC 130  
Qy 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147  
Db 131 AGCATCTGCCAGCAGAGACCTTCTGCCTCTTTGACATTGGAAAAAACTTCAGCAATTC 190

QY 148 GlnGluHisLeuAspLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
DB 191 CAGGAGCACCTGGATCTTCTCCAGCAGAGAAATPAAACAGAGAAGTTTCCCTGACAGAAAA 250  
QY 168 AspGluIleSerAlaGluLysThrLeuGlyGluProGlyGluThrIleValIleSerThr 187  
DB 251 GATGAAATATCTCCAGAGAAGACATTTGGAGAGCCTGGTGAAACCATTTGATTTCAACA 310  
QY 188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
DB 311 GATGTTGCCAACGTCATCTGGGCGCTTTCCCTCTCACTCTCGATGACACCCCTCCTCAAT 370  
QY 208 GluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGlu 227  
DB 371 GAAATTCGATAATATACACTCAACGACACCAAGATGCTACACAGAAAGAGAAACAGAA 430  
QY 228 PheAlaValLeuGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPhe 247  
DB 431 TTCCGTGTGTTGGAGAGCAGAGGCTGGAGCTCAGCGTCTCTCTGGTAAACCAAGAAGTTC 490  
QY 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGln 267  
DB 491 AAGGAGCAGGCTGCTGACTCCAGTCCCATATACAGAGGAGCTAGCAGGAAAGTCCAA 550  
QY 268 LeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGly 287  
DB 551 CTTCCAGATGCAAAAGATATTTAAGAACTTCAGGATTCAGGATTCAGGATTCAGGATTC 610  
QY 288 PheArgProLysLysGluLysAspGlySerSerThrGluMetGlnLeuThrAlaIle 307  
DB 611 TTTAGACCAAGAAAGAAAGATGGCTCAGCTCCAGAGATGCAACTTACCGGCCATC 670  
QY 308 PheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSer 327  
DB 671 TTTAAGACACAGTGCAAGAGCAAAAGCCCTGCAAGTGACCTCCTGCTCTTTGATTCC 730  
QY 328 AsnLysIleGluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGlu 347  
DB 731 AACAAATTTGAAGTGAAGAGTCTATCATGGAACCATGGAGGAGGCAAGCAACACAGAA 790  
QY 348 IleTyrLeuThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGln 367  
DB 791 ATCTATCTCAGACTACAGACTCAGAGCTCAGAGGCTGATCAGCAAGCAGCTAGAGGAAGAA 850  
QY 368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
DB 851 TCTTTGGATGTGGGACAAATTCAGTTCACTGATGAAATTTGCTGATCACTGCCAGCCTTT 910  
QY 388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407  
DB 911 GGTCTGACACCCCAATCAGAGCTGCCACATCTTTGCTGTATACAGAGGATGCTACT 970  
QY 408 LeuSerProGluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGluHis 427  
DB 971 TTGAGTCAGAACTTCTCTCTGTTGAACCCAGCTTCAGACAGTGGAGCGAGCAGCAT 1030  
QY 428 GlyLeuProAspThrSerTyrPheProProAlaMetAlaSerThrSerLeuSerGluAla 447  
DB 1031 GGTCTACCTGACATCTTGTGCTGCCACTGCTATGAGCTCTACCTCCCTGTGAGAGCT 1090  
QY 448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467  
DB 1091 CCACCTTTCTTATGGCATCAAGCATCTTCTCTGACTGATCATGAGCAGCAGCAGATACA 1150  
QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487  
DB 1151 ATGGCCACTGACCAAGAAATCTAGTACAGGCTCACCATCCCACTGATGATTTCT 1210  
QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArg 507  
DB 1211 CCAATCAGCCAACTGGCTCTGGGAATTTCACTCCACTGATCTTCAAGATGACAGCCGA 1270

QY 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527  
DB 1271 TCAAGTGCAGGTGGCAAGATATGGTTCAGACACCTAGATGAAATGGATCTGTGTGCACT 1330  
QY 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547  
DB 1331 CTTGCCCATCTCAGGTACCAAGGCTCAGGGAATAGTTTCTGTCAGATCATTTCTTG 1390  
QY 548 GluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567  
DB 1391 GAGGATACCATCTCTGCTCAGCTTTACAGTATATCACCACCTAGTTCTATGACCATGGC 1450  
QY 568 ProLysIleValGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587  
DB 1451 CCCAAGGCGAGAGCTGTAGTTTCTCAGTCTCGGTGTTGCTTAACATGGCTTCTCC 1510  
QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln 607  
DB 1511 AACGACTGTTCACCAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACACAG 1570  
QY 608 LeuLeuValProTyrLeuArgSerLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627  
DB 1571 CTCTGTTTCCATATCTAGATCCCAATCTTACAGGATTTAAGCAACTTGAAATACTTAAC 1630  
QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647  
DB 1631 TTCAGAAACGGGAGTGTGATTGTGAATACCAAAATGAAGTTTGCTAAGTCTGTGCGGTAT 1690  
QY 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667  
DB 1691 AACCTCACCAGAGCTGTGCACGGGTCTTTGGAGGATTTTCTGTTCTGTCAGCCCAACAA 1750  
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687  
DB 1751 CTCCATCTCGAATAGACAGCTACTCTCTCAACATTTGAACAGCTGATCAACAGATCCC 1810  
QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707  
DB 1811 TGCAAGTCTCTGCGCTGCGGCAATTTGCCAATGTGTAAAGAACGAAACGACTGAGGAA 1870  
QY 708 AlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727  
DB 1871 GGGAGTGTGCTGCAACAGGATATGACCCAGGAGGAGCTGGAGCGTCTGGAACCA 1930  
QY 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747  
DB 1931 GGCCTCTGTGGCCCTGGCACAAAGGAATGCGAGGTCTCCAGGAAAGGAGCTCCATGC 1990  
QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767  
DB 1991 AGGTTGCCAGATCACTCTGAAATCAAGCATACAAAACTAGTGTATAAAGAGTCCAAAAT 2050  
QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787  
DB 2051 CAACAAATAACAAGTAATCACTAAGAAATTTCTGAATTACTGACCCGTAGATATGAA 2110  
QY 788 GluPheAsnHisGlnAspTyrGluLysAsn 797  
DB 2111 GAATTTAACCATCAAGATTGGGAGGAAAT 2140  
RESULT 4  
US-10-007-270-5  
; Sequence 5, Application US/10007270  
; Publication NO. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195

; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: US 09/183,972  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5

; LENGTH: 2244  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Human IPM 150 cDNA sequence, isoform C  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)-(2244)  
 ; OTHER INFORMATION: n is a, c, g, or t.  
 US-10-007-270-5

Alignment Scores:  
 Pred. No.: 0 Length: 2244  
 Score: 3323.00 Matches: 667  
 Percent Similarity: 95.56% Conservative: 0  
 Best Local Similarity: 95.56% Mismatches: 10  
 Query Match: 80.71% Indels: 23  
 DB: 13 Gaps: 1

US-10-007-270-2 (1-797) x US-10-007-270-5 (1-2244)

QY 1 MetTyrLeuGluThrArgAlaIlePheValPheThrIlePheLeuGlnValGlnGly 20  
 DB 151 ATGTATTGGAACTAGAGAGCTATTGTGTTTTTGGATTTTCTCCAAAGTTCAAGGA 210  
 QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
 DB 211 ACCAAAGATATCCATTAAACATATACCATCTGAACTTAAAGACATAGACAAATCCCCA 270  
 QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
 DB 271 AGAATGAAACCACTGAAAGTACTGAAATAATGTACAAATGTCAACATATGAGACGAATA 330  
 QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 DB 331 TTCGATTTGGCAAGNATCGAACAAAGATCCGATTTTCCCAACGGGGGTAAAGTC 390  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 DB 391 TGTCACACAGAAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTATAGATTGAGA 450  
 QY 101 ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 451 GTGTGTCCAGAGAGCATGGGAAGCATATCGATCTTTCTGGATCGCATCCCTGACACA 510  
 QY 121 GlyTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 511 GGGGAATATCAGAGCTGGGTGACATCTGCCAGCAGGAGACCTTCTGCTCTTTGACATT 570  
 QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgIleIleGln 160  
 DB 571 GGAAAAAATCTTCAGCAATTCAGAGACACCTGGATCTTCTCCAGCAGAGAAATAAAG 630  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 DB 631 AGAAGTTTCCCTGTACAGAAAAGATGAATATCTGCAGAGAGACATTGGGAGACCTGGT 690  
 QY 181 GluThrIleValIleSerThr----- 187  
 DB 691 GAACCAATTGTATTCAAC-AGCAATCTACATTTCAAGACTTGGGCGAGTATTCTAAGA 749  
 QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
 DB 750 AAACCTCAGAGAGCAATTCAGATGTGCCAAGCTCTCACTTGGGCTTTCCCTCTC 809  
 QY 200 ThrProAspAspThrLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219

DB 810 ACTCCTGATGACACCCCTCCTCAATGGAATTTCTCGAATAATACACTCAACGACACCAAGATG 869  
 QY 220 ProThrThrGluArgGluThrGluPheAlaValIleGluGlnArgValGluLeuSer 239  
 DB 870 CTTACACAGAAAGAGAAACAGAAATTCGCTGTGTGGAGGAGCAGGGGTGGAGCTCAGC 929  
 QY 240 ValSerLeuValAenGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
 DB 930 GTCTCTCTGTGTAAACCAAGAGTTCAAGGCAGAGCTGCTGACTCCAGTCCCATATTAC 989  
 QY 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGly 279  
 DB 990 CAGGAGCTAGCAGAAAGTCCCACTTCAGATCGAAAGATATTTAAGAACTTCCAGGA 1049  
 QY 280 PheLysLysIleHisValLeuGlyPheArgProLysGlyLysAspGlySerSerSer 299  
 DB 1050 TTCAAAAAAATCCATGTGTGTAGATTTAGACCAAGAAAGAAAGATGCTCAAGCTCC 1109  
 QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
 DB 1110 ACAGAGATGCAACTTACGGCCATCTTTAGAGACACAGTCAGAAAGCAAAAGCCCTGCA 1169  
 QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluValTyrHisGlyThr 339  
 DB 1170 AGTGACCTCTGCTCTTTGATTCCAAACAAATTTGAAAGTGAGGAAGTCTATCATGAACC 1229  
 QY 340 MetGluLysAspLysGlnProGluIleTyrLeuThrAlaThrAspLysLysArgLeuIle 359  
 DB 1230 ATGGAGAGACAAAGCAACCAAGAAATCTATCTCACAGCTACAGACCTCAAAAGCGTGATC 1289  
 QY 360 SerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
 DB 1290 AGCAAGCACTAGAGAGAGACAACTTTGGATGTGGGACAAATTCAGTTCATGATGAA 1349  
 QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
 DB 1350 ATTGCTGGATCACTGGCAGCCTTTGGTCTCTGACACCACTCAGAGTGCCCACTTTT 1409  
 QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProValGluProGlnLeu 419  
 DB 1410 GCTGTTATAACAGAGATGCTACTTTGAGTCAGAACTTCTCTGTTGAAACCCAGCTT 1469  
 QY 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProAlaMet 439  
 DB 1470 GAGACAGTGGACGAGCAGAGATGCTTACCTGACACTTCTTGGTCTCCACCTGCTATG 1529  
 QY 440 AlaSerThrSerLeuSerGluAlaProPhePheMetAlaSerSerIlePheSerLeu 459  
 DB 1530 GCCCT-ACCTCCCTGTGAGAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTG 1588  
 QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
 DB 1589 ACTGATCAAGGCACACACAGATACAAATGGCCACTGACCAACAATGCTAGTACAGGGCTC 1648  
 QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
 DB 1649 ACCATCCCAACAGATGATTATTCTGCAATCAGCCAACTGGCTCTGGGAATTTCAATCCA 1708  
 QY 500 ProAlaSerSerAspAspSerArgSerSerAlaGlyGlyLysAspMetValArgHisLeu 519  
 DB 1709 CTTGATCTTCAGATGACAGCCGATCAAGTCAGGTGGCGAAGGTATGGACAGACCTTA 1768  
 QY 520 AspGluSerAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539  
 DB 1769 GATGAATGGATCTGTCTGACACTCTGCCCATCTGAGGTACCGAGCTCAGCAATAT 1828  
 QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
 DB 1829 GTTCTGTCTCCAGATCAATTTCTTGAGGATACCACTCTCTGTCTCAGCTTACAGTATATC 1888  
 QY 560 ThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeu 579  
 DB 1889 ACCACTAGTTCTATGACCAATTCGCCCAAGGCCGAGAGCTGGTAGTGTCTTCTCAGTCTG 1948

QY 580 ArgValAlaAenMetAlaPheSerAsnAspLeuPheAenLysSerSerLeuGluTyrArg 599  
 Db 1949 CGTGTTCACATGGGCTTCTCCACGACCTGTTCAACAGAGCTATTGGAGTACCGA 2008  
 QY 600 AlaLeuGluGlnGlnPheThrGlnLeuValProTyrLeuArgSerAenLeuThrGly 619  
 Db 2009 GCTCTGGAGCAACAATTCACACAGCTGCTGGTTCATATCTACGTCCTTTCAGGA 2068  
 QY 620 PheLysGlnLeuGluLeuLeuAsnPheArgAsnGlySerValLeuValAenSerLysMet 639  
 Db 2069 TTTAGCAACTTGAATACTTAACTTCAGAAACGGAGTGTGATTGTGAATAGCAAAATG 2128  
 QY 640 LysPheAlaLysSerValProTyrAsnLeuThrLysValAlaValHisGlyValLeuGluAsp 659  
 Db 2129 AAGTTTGTCTAAGTCACTGGTCCGTATTAACCTCACCAGGCTGTGCACGGGGTCTTGGAGGAT 2188  
 QY 660 PheArgSerAlaAlaGlnGlnLeuHisLeuGluLeuAspSerTyrSerLeu 677  
 Db 2189 TTTGCTTCTGTCGAGCCCAACCACTCCATCTCGAAATAGACAGCTACTCTCTC 2242

## RESULT 5

US-10-007-270-8  
 ; Sequence 8, Application US/10007270  
 ; Publication No. US20020160954A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hageman, Gregory S.  
 ; APPLICANT: Kuehn, Markus H.  
 ; APPLICANT: University of Iowa Research Foundation  
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
 ; FILE REFERENCE: 020618-000120US  
 ; CURRENT APPLICATION NUMBER: US/10/007,270  
 ; CURRENT FILING DATE: 2001-11-08  
 ; PRIOR APPLICATION NUMBER: US 09/430,195  
 ; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: US 09/183,972  
 ; PRIOR FILING DATE: 1998-10-29  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 3668  
 ; TYPE: DNA  
 ; ORGANISM: Mus sp.  
 ; FEATURE:  
 ; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform A  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(3668)  
 ; OTHER INFORMATION: n is a, c, g, or t.  
 US-10-007-270-8

## Alignment Scores:

Pred. No.: 5,38e-260 Length: 3668  
 Score: 2548.50 Matches: 528  
 Percent Similarity: 75.12% Conservative: 79  
 Best Local Similarity: 65.35% Mismatches: 180  
 Query Match: 61.90% Indels: 21  
 DB: 13 Gaps: 9

US-10-007-270-2 (1-797) x US-10-007-270-8 (1-3668)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheThrPilePheLeuGlnValGlnGly 20  
 Db 196 ATGAATTTTCAAAATAAACAATGCTATCTTTGTTTGGGATTTTCTCCAAAGTTCAGGA 255  
 QY 21 ThrLysAspLysSerLysAenLysThrLysSerGluThrLysAspLysValLeuValAenSerPro 40  
 Db 256 ATCAAGATACCTCTATTAAATAATTACAGTCTCGAATTAATAACATAGACAAACCCCA 315  
 QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrValArgArgLys 60  
 Db 316 AGAATCGAAACAATTAAGAGTACTTCAACAGTGCACAAAGTGTCAACCATGAAACGATA 375

QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 Db 376 TTCGATTTCGCAAGCTTCGAACCAAAAGATCAGACATTTTCCCA---CCTGCTAACATC 432  
 QY 81 CysProGlnGluSerMetLysGlnLysLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 433 TGCCACAGGAATCCTTGAGACAGATTTTAGCAAGTCTTCAAGAAATATTATTAGACTGAGA 492  
 QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgLysPheLeuAspArgLysProAspThr 120  
 Db 493 GTATGTCAAGAGTCGTGTGGGAAGCATATCGTATCTTTCTGGACCGAATTCCTGACACA 552  
 QY 121 GlyGluTyrGlnAspTrpValSerLysCysGlnGlnGluThrPheCysLeuPheAspLys 140  
 Db 553 GAGGAATATCAAGACTGGGTGAGCTCTGCCAAGAAAGAAACCTTCTGCTCTTTTGACATT 612  
 QY 141 GlyLysAsnPheSerAsnSerGlnGlnHisLeuAspLeuGlnGlnArgLysGln 160  
 Db 613 GGGAAAAAATTCAGCAACTCCAGGAGCACCTAGATCTTCTTCAGCAGAGAAATAAAACAG 672  
 QY 161 ArgSerPheProAspArgLysAspGluLysSerAlaGluLysThrLeuGluProGly 180  
 Db 673 AGAAGCTTCTCTGGAGGAAGATGAGACAGCTCCATGGAGACACTGGAGCACCTACT 732  
 QY 181 GluThrIleValLysSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 Db 733 GAAGCCCTGTGTGTACCCACAGATGTTCCAGGATGTCCCTGGGCCCTTCCCACTTCT 792  
 QY 201 ProAspAspThrLeuAsnGlnLysLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
 Db 793 TCTGATGACACAGACCTCAAGGAGATTTCTCAGTGTCCCTCAGGACATTCACCAAGGCC 852  
 QY 221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGln 234  
 Db 853 ACAACAGAAAGTAAACAGAACCTATTCAAGGTCTGTAATTTCTCA-----TCAGAGGAG 906  
 QY 235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254  
 Db 907 AAGTGGAAATTGACATCTCTGCCCCAACCAACAGGTTCAGGCGAGAGCTCACCACCTCT 966  
 QY 255 GlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274  
 Db 967 GGGTCCACCATACTACCAGGAATCGTGGGCACAGTCCCACTGCAGTTGCCAAAGATATT 1026  
 QY 275 LysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysGluLys 294  
 Db 1027 AAGAAACTTCCAGGATTCGAGAAATCCGTGTATTAGGATTTAGACCAAGAAAGAAAGA 1086  
 QY 295 AspGlySerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314  
 Db 1087 GATGGTTCAAGCTCCACAGAAATACAGCTTATGGCCATCTTTAAGAGGGGACCATGCAGAA 1146  
 QY 315 AlaLysSerProAlaSerAspLeuSerPheAspSerAsnLysIleGluSerGluGlu 334  
 Db 1147 GCAAAAGCCCTGATAGTCATCTCTGTGATCCCAACAAATTTGAAGTGAAGA 1206  
 QY 335 ValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAsp 354  
 Db 1207 ATCCATCATGGAGTCAATA--GAACACAAACCAACAGAAACCTACCTCACAGCTACAGAC 1263  
 QY 355 LeuLysArgLeuLysSerLysAlaLeuGluGlnGlnSerLeuAspValGlyThrIle 374  
 Db 1264 CTCAAAAAATCATCATCAACTACTAGTAGAGACCTGCTCTTGGTAGAAGGGGAAATTT 1323  
 QY 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394  
 Db 1324 CCATTCCGTGATGAAGTTACTGGGACACTC-----TTCAGACCTGTCTCACTGAACCAT 1377  
 QY 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLysSerProGluLeuPro 414  
 Db 1378 CTGCCCAAGCCCTGCTGATGTACAGAGGATGCCATTGTGAGTCAGAACTTCCCTTC 1437  
 QY 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro----- 430



```
Db 1438 GTTGAGCTTAGGCTTGAGCGATGGACAGAGAGATCTGAGCTGCCTGGAAATCTCTCC 1497
Qy 431 ---AspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449
Db 1498 AAAGACAGTCTTGCTGCTCCACCTGATATCAGCCTCAATTTCCCGATCAGAAAATCTACCT 1557
Qy 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469
Db 1558 TCGTTT---ACACCTAGATCTCTCTCTAGATGCTCAAGCCCTCCCTCGATGACC 1614
Qy 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTrpSerAlaIle 489
Db 1615 ACTGCCCCAACAGCACTCATCCCAAGCCACTCTCCCACTATCTGATTTCTTACCATC 1674
Qy 490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArgSerSer 509
Db 1675 CGCCAATTGCTCTGGAATCGTCACATGGCGCTGCATCTCCATGACAGAGAGCTGATC 1734
Qy 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529
Db 1735 ACAACGACCCATGACACAACTCCGAGACCTAGATGGCATGGATGCTGACACGCCAGCC 1794
Qy 530 ProSerGluValProGluLeuSerGluTrpValSerValProAspHisPheLeuGluAsp 549
Db 1795 TTGTCAGAAATATCAGAACTCAGTGGATACGATTCTGCTCGGGTCAGTTCTTGAGATG 1854
Qy 550 ThrThrProValSerAlaLeuGlnTrpIleThrThrSerSerMetThrIleAlaProLys 569
Db 1855 ACCACACCCATCCCAACAGTAGGTTCATCCACCAGCTCCGAGACCATTCGCCACCAAG 1914
Qy 570 GlyArgGluLeuValValPhePheSerLeuArgValAlaAlaMetAlaPheSerAsnAsp 589
Db 1915 GCGCAGGAGCTAGTGGTATTCTTACGCTGGCGTGTGCTAACTACGCTTCCTCTATGAC 1974
Qy 590 LeuPheAsnLysSerSerLeuGluTrpArgAlaLeuGlnGlnPheThrGlnLeu 609
Db 1975 CTGTTCAACAGAGTCTCTGGAGTATCAGCCCTGGAAACAGCATTCACAGACCTGCTG 2034
Qy 610 ValProTrpLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg 629
Db 2035 GTTCCCTATCTACGATCGAATCTTACGGGATTTAAGCAACTGGAATATCTCAGCTTCAGA 2094
Qy 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTrpAsnLeu 649
Db 2095 AACCGAAGTGTATCGTGAACAGCAAGTGGCGTTGCAAGGGCGGTACCCCTACAACCTC 2154
Qy 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnHis 669
Db 2155 ACCAGGCGTGGCGGGTCTTGAGGATCTTCGATCCACCGCAGCTCAAGGCTCAAT 2214
Qy 670 LeuGluIleAspSerTrpSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689
Db 2215 CTGGAATCGAAAGCTACTCCCTCGACATTTGAACAGCTGATCAGCGGATCCCTGCAAA 2274
Qy 690 PheLeuAlaCysGlyValPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709
Db 2275 CTCCTAGACTGGCAAAATTTCCCAAGTGTGTAAAGAATGATGGACAGAGAGACAGAG 2334
Qy 710 CysArgCysLysProGlyTrpAspSerGlnIleSerLeuAspGlyLeuGluProGlyLeu 729
Db 2335 TGTCTGCTGACAGACGAGACATGAGACCAAGGACCTTCGACTACCAAGACCTCGAAGCTC 2394
Qy 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749
Db 2395 TGTCCCTCTGGA---AAGACTTGTGGCGCGCCGAGAACCAAGCACTCCATGACAGCCA 2451
Qy 750 ProAspHisSerGluAsnGlnAlaTrpLysThrSerValLysPhePheGlnAsnGln 769
Db 2452 CCAGATCACTTACAAACCAAGCTCAGGAACCTGGTGTAAAGCTA-----CGTCAG 2505
Qy 770 AsnAsnLysValIleSerLysArgAsnSerGluLeuThrValGluTrpGluGluPhe 789
```

```
Db 2506 CAAATAAGGTAGTCAAGAAAAGAAATTTCTAACTATCAGCTATAGGATTTGAGAAATTT 2565
Qy 790 AsnHisGlnAspTrpGluGlyAsn 797
Db 2566 GAAGACCAAGACTGGGAGGAAAT 2589
RESULT 6
US-10-007-270-10
; Sequence 10, Application US/10007270
; Publication No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE OF INVENTION: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPM 150 cDNA sequence, isoform D
US-10-007-270-10
Alignment Scores:
Pred. No.: 2,89e-132 Length: 1726
Score: 1342.50 Matches: 310
Percent Similarity: 44.96% Conservative: 51
Best Local Similarity: 38.61% Mismatches: 99
Query Match: 32.61% Indels: 343
DB: 13 Gaps: 9
US-10-007-270-2 (1-797) x US-10-007-270-10 (1-1726)
Qy 1 MetTyrLeuGluThrArgArgAlaIlePheValPheThrIlePheLeuGlnValGlnGly 20
Db 140 ATGAATTTCAATTAACATGCTATCTTTTGGATTTTCTCCAGTTTCAGGA 199
Qy 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
Db 199 ----- 199
Qy 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60
Db 199 ----- 199
Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80
Db 199 ----- 199
Qy 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
Db 200 -----ATCAA 205
Qy 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
Db 206 GTATGTCAGAAAGTCGTGGGAGCATATCGTATCTTTGGACCGAATTCCTGACACA 265
Qy 121 GlyGluTrpGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140
Db 266 GAGGAATATCAAGACTGGGTGAGCTCTGCCAAGAAAGAACCTCTGCTCTTTGACATT 325
Qy 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgIleLysGln 160
Db 326 GGGAAAAACTTCAGCACTCCCGAGGACCTAGATCTTCTTCAGCAGAGATAAAGACAG 385
```

161 ArgSerPheProAspArgLysAspGluLeuSerAlaGluLysThrLeuGlyGluProGly 180  
1177  
386 AGAAGCTTCCTGGGAGAAAGATGACACAGCCTCCATGGAGACACTGGAGCACCTACT 445  
181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
1177  
446 GAAGCCCTGGGTACCCACAGATGTTCCAGGATGTCCTGGGGCCATTCCCACTCTCT 505  
201 ProAspThrLeuLeuAsnGluLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
1177  
506 TCTGATGACACAGACCTCAAGGAGATTCTCAGTGTCCCTCAAGGACATTCAAAAGCCC 565  
221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGln 234  
1177  
566 ACAACAGAAAGTATAACAGAACCTATTTCAGTGTCTGATTTCTCA-----TCAGAGGAG 619  
235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254  
1177  
620 AAGGTGGAGTTTCAGCATCTCTCTGCCAAACCCACAGGTTCAAGGCAGAGCTCACCAACTCT 679  
255 GlnSerProTyrThrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274  
1177  
680 GGGTCACATACCTACAGGAACCTGGTGGACAGTCCCACTGCACTTGCAGGATTTT 739  
275 LysLysLeuProGlyPheLysIleHisValLeuGlyPheArgProLysLysGluLys 294  
1177  
740 AAGAACTTCAGGATTCGGAGAAATCCGTGTATTAGATTAGACCAAGAAAGAGAA 799  
295 AspGlySerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314  
1177  
800 GATGGTTCAAGCTCCACAGAAATACACTTATGGCCATCTTAAAGAGGGACCATTCAGAA 859  
315 AlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGlu 334  
1177  
860 GCAAAAGCCCTGATCATCTACTCTCTCTGATTCACACAAATTTGAAAGTGAAGA 919  
335 ValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAsp 354  
1177  
920 ATCCATCATGGAGTCATA--GAAGACAAACACCAACCAACCACTACCTCACAGCTACAGAC 976  
355 LeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIle 374  
1177  
977 CTCAAAATCATCATCACTACTAGATGGAGACCTGCTTGTAGAGGGAATAAT 1036  
375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394  
1177  
1037 CCATTGGTGATGAAGTTACTGGACACTC-----TTCAGACCTGTCTACTGAACCAT 1090  
395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414  
1177  
1091 CTGCCCCAAGCCCTTGTGTGATGTCACAGAGGATGCCACTTTGAGTCCAGAACTTCTTTC 1150  
415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTyr 434  
1177  
1151 GTTGAGCTAGGCTTGAGGAGTGAC----- 1177  
435 SerProProAlaMetAlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSer 454  
1177  
455 SerIlePheSerLeuThrAspGlnGlyThrAspThrMetAlaThrAspGlnThrMet 474  
1177  
475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494  
1177  
495 GlyIleSerHisProProAlaSerSerAspSerSerArgSerSerAlaGlyGlyGluAsp 514  
1177

515 MetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSerGluValPro 534  
1177  
535 GluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThrThrProValSer 554  
1177  
555 AlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuVal 574  
1177  
575 ValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSer 594  
1177  
595 SerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArg 614  
1177  
615 SerAsnLeuThrGlyPheLysGlnLeuGluLeuAsnPheArgAsnGlySerValIle 634  
1178  
635 ValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHis 654  
1195  
655 GlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHisLeuGluLeuAspSer 674  
1195  
675 TyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGly 694  
1196  
695 GluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysPro 714  
1238  
1238 AAATTGCTCCAGTGTGTAAAGATGAGTGGACAGAGGAAGCAGAGTGTCTGCTGCAGACAG 1297  
715 GlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThr 734  
1298  
1298 GGACATGAGAGCCAGGAGCCCTGGACTACAGACCCCTGAACCTCTGTCCCTCTGGA--- 1354  
735 LysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerGlu 754  
1355  
1355 AAGACTTGTGGCGCGCGGAGCAACAGCAACTCCATGCGAGGCCACACAGATCACTCTACA 1414  
755 AsnGlnAlaTyrLysThrSerValLysPheGlnAsnGlnGlnAsnAsnLysValIle 774  
1415  
1415 AACCAAGCTCAGGAACCTGGTGTAAAGGCTA-----CGTCAGCAAAATAAGGTAGTC 1468  
775 SerLysArgAsnSerGluLeuThrValGluTyrGluGluPheAsnHisGlnAspTyr 794  
1469  
1469 AAGAAAAGAAATTTAAACTATCAGTATCAGTATGAGATTGAAGACACGAGACTGG 1528  
795 GluGlyAsn 797  
1529  
1529 GAGGGAAT 1537

## RESULT 7

US-10-007-270-12  
; Sequence 12, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195

[illegible]

Qy	397	-----ThrSerPheAlaValAlIleThrGluAspAlaThrLeuSerPro	410
Db	1659	ACCCGCGCAGTGTCTCAGACTGCGTCTGCTGTGGCTCTCGAGAAAGGACTTCTGGATCT	1718
Qy	411	GluLeuProValGluProGlnLeuGluThrValAspGlyAlaGlu	456
Db	1719	CACCTG-----GTAGAGATGATGATTAGCCAATGTTGAGAGTCAAGATTTCTTCTTCT	1772
Qy	427	---HisGlyLeuProAspThrSerTTrpSerProProAlaMetAlaSerThr	442
Db	1773	ATTGATTCAATGCTTCAAGTTCATTCACTCAACCTGTGCAAAAGAAACAATACCATCC	1832
Qy	443	-----SerLeuSerGluAlaPro	450
Db	1833	ATGGAGACTCTGATGTGCTTAACTTCTTAACTTCAACCATCTGCACCTTCTCTATACCTTTT	1892
Qy	451	PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr	470
Db	1993	GGCTTGGACTCCTTGACCTCCAAAGTCAAAGACCAATTAAGAGTGAGCCCTTTCTCTGCCA	1952
Qy	471	AspGlnThrMet	474
Db	1953	GATGTCATCCATGGAAAAGAGTTAATATTGACGGTGGTTTAGTTCAGGGTCTGGGCAA	2012
Qy	475	LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu	494
Db	2013	AAGGTAGACTGATTACTTGGCCATGGAGTGAGACTTCATCA---GAGAAGCGCGCGAA	2069
Qy	495	GlyIleSerHisProProAlaSerSerAspAspSerArgSerSerXlaGlyGlyLeuAsp	514
Db	2070	CCACTGTCCAAAGCGGTGCTGAAGATGATGATTTCACTTTTGCAGCTGAGATTGAAGAC	2129
Qy	515	MetValArgHisLeu---AspGluMetAspLeuSerAsp	536
Db	2130	AAGAACTAGTTTGTGTGACAAATTTGGATTCACAGACCAATTAAGTAAGCACTCAAAA	2189
Qy	527	-----ThrProAlaProSerGluValPro	534
Db	2190	TATGAACATGATGACAGATCCACACACTTTCACAGAGAAAGAGCTCTTAGTGGCGCTGCT	2249
Qy	535	-----GluLeuSerGluTyrValSerValProAspHisAlaPhe	546
Db	2250	GTGCCCATCTTCGCAGATACTGCACTGATCTGCTGCTCTTAACCTTCCCAAGCACAATA	2309
Qy	547	LeuGlu	550
Db	2310	TCAGAGTACCTGGTGTGATGATTGCTCAGTTACCAAGCACCTCTTATCTGACATCT	2369
Qy	551	ThrProValSerAla	555
Db	2370	GTAGCAATCTCTGCCTCTACTGATAAATCAGATCAGGCAGATGCCATCTCTAAGGGAGGAT	2429
Qy	556	LeuGlnTyrIleThrThrSerSer	563
Db	2430	ATGGACAAATTAAGTCACTGATCATCCAACTAGTAATGTTTGACAGTGAGGTTTCAATGGTA	2489
Qy	564	-----MetThrIleAlaProIleGlyAlaGlu	572
Db	2490	AAGCCAGATATGCCAACTTTGTGGACTATATTGCCAGAATCAGAGAGAGTTTGGACAGA	2549
Qy	572	-----	572
Db	2550	ACTTCTTCCCTAGAGAAATTGTCAGAGACATATTGGCAAGTACACACAGAGTGTGAC	2609
Qy	572	-----	572
Db	2610	AGGCTCTGGTTATCTGTGACACAGTCTACCAATTGCCTCCCAACCAATCTCCACCCCTG	2669
Qy	572	-----	572
Db	2670	CTAGAGGATGAAGTAATTATGGGTGTACAGGATATTTTCGTATGAACATGGACCGGATAGGC	2729
Qy	572	-----	572

Db 2730 ACAGATTACTATCATCGCTGACCAAGTCCAAAGAGCAAAATGGCAAGGTGGTGTAGTTATGTC 2789  
QY 572 ----- 572  
Db 2790 GAAATGTCAACAAGTGTTCACCTCCACAGAGATGGTTAGTGGCTTGGCCACAGAAAGGA 2849  
QY 573 -----LeuValValPhePheSerLeuArg 580  
Db 2850 GGAGATGACTTGAGTTATACCAGACTTCAGGAGCTTTGGTGGTTTCTTCACGCCCTCCGA 2909  
QY 581 ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerLeuGluTyrArgAla 600  
Db 2910 GTGACTAACATGATGTTTTCAGAGATCTGTTTAAATAAACAACCTCTGGAGTATAAAGCC 2969  
QY 601 LeuGluGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
Db 2970 CTGAGCAAGATTCCTTGAATCTGCTGCTCCCTATCTCCAGTCAAAATCTCAGGGGTTTC 3029  
QY 621 LysGlnLeuGluLeuLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
Db 3030 CAGAACTTAGAAATCTCAATTCAGAAATGGCAGCATTTGGTGAACATCGAATGAAG 3089  
QY 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660  
Db 3090 TTTGCCAATTCGTCCCTCCTTAACGTCAACAATCGCGGTGTACATGATCTCTGGAAGACTTT 3149  
QY 661 ArgSerAlaAlaGlnGlnLeuHisLeuGluLeuAspSerTyrSerLeuAsnIleGlu 680  
Db 3150 TGTACCACCTGCCTCAATATACCATGAATCTGGCTATTGATAAATCTCTCTTGATGGAA 3209  
QY 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
Db 3210 TCAGGTGATGAAGCAACCTTCGAAGTTTCAGGCTGTAATGAATTTTCAGAGTGTCTG 3269  
QY 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGln--- 719  
Db 3270 GTCAACCCCTGGAGTGGAGAAAGTCAAGTGCCTGCTCCCTGGATACCTCAGGTGTGAA 3329  
QY 720 -----GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLys 735  
Db 3330 GAACGGCCCTCTCAGAGTCTCTGTGACCTACAGCTGACTCTGCTGATGATGGAAG 3389  
QY 736 GluCysGluValLeuGlnGlnGlyLysGlyAlaProCysArg 748  
Db 3390 ---TGTGACATTATGCTGGCGCACGGGGCCATTGTAGG 3425

## RESULT 9

US-10-007-270-14  
; Sequence 14, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 555  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Monkey IPM 150 cDNA (partial)  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Monkey species

## US-10-007-270-14

Alignment Scores:  
Pred. No.: 2,12e-84 Length: 555  
Score: 885.00 Matches: 167  
Percent Similarity: 95.65% Conservatives: 9  
Best Local Similarity: 90.76% Mismatches: 8  
Query Match: 21.50% Indels: 0  
DB: 13 Gaps: 0

## US-10-007-270-2 (1-797) x US-10-007-270-14 (1-555)

QY 73 PhePheProThrGlyValLysValCysProGlnGluSerMetLysGlnIleLeuAspSer 92  
Db 4 TTTCTTCCGACGGGGTTAAAGTCTGTCCACAGAAATCCATGAAACAGATTTAGCCAGT 63  
QY 93 LeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTyrGluAlaTyrArgIle 112  
Db 64 CTTCAAGCTTTATTATAGATTGAGAGTGTGTGAGAAAGCAGTATGGAAAGCATATCGGATC 123  
QY 113 PheLeuAspArgIleProAspThrGlyGluTyrGlnAspTyrValSerIleCysGlnGln 132  
Db 124 TTTCTGGATCGCATCCCTGTGACACAGGGGAATATCAGGACTGGTTCAGCTTCTGCCAGCAG 183  
QY 133 GluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSerGlnGluHisLeuAsp 152  
Db 184 GAGACCTTCTGCTCTTTGACATCGACAAACCTTCAGCAATTCAGGAGCAGCCTGGAT 243  
QY 153 LeuLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLysAspGluIleSerAla 172  
Db 244 CTTCTCCAGCAGAGAAATAAACAGAGAGTTCCTCTGAGAGAAAGATGAAGTATCTACA 303  
QY 173 GluLysThrLeuGlyGluProGlyGluThrIleValIleSerThrAspValAlaAsnVal 192  
Db 304 GAGAAGACATTTGGGAGAGCTAGTGAACCATTTGTGTTTCAACAGATGTTTGCAGCGTC 363  
QY 193 SerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsnGluIleLeuAspAsn 212  
Db 364 TCACCTGGGCTCTTCCCTGTGACTCCTGATGACACCTCTCAATGAATTTCTCGATTAAT 423  
QY 213 ThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGlu 232  
Db 424 GCATCTACAGCACACCAAGATGCTTACACAGAGAGAAACAGAACTCGCTGTGTCTGAG 483  
QY 233 GluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAla 252  
Db 484 GAGCAGAGGGTGGAGCTTCAGCATCTCTCTGATAAACAGAGAGTTCAGGCGAGAGCTCGCT 543  
QY 253 AspSerGlnSer 256  
Db 544 GACTCTCAGTCA 555

## RESULT 10

US-10-007-270-18  
; Sequence 18, Application US/10007270  
; Publication No. US20020160954A1  
; GENERAL INFORMATION:  
; APPLICANT: Hageman, Gregory S.  
; APPLICANT: Kuehn, Markus H.  
; APPLICANT: University of Iowa Research Foundation  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES  
; FILE REFERENCE: 020618-000120US  
; CURRENT APPLICATION NUMBER: US/10/007,270  
; CURRENT FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: US 09/430,195  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 09/183,972  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 2964  
; TYPE: DNA





```
QY 531 -----SerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGlu 548
Db 1964 CACATATCAGAGTACCTGCTGTTGATGATTACTCAGTACCAAGACCCCTCTTATACGT 2023
QY 549 AspThrProValSerAla
Db 2024 ACATCTGTAGCAATCTGCTCTACTGATAAATCAGATCAGGCAGATGCCATCCTAAGG 2083
QY 556 -----LeuGlnTyrIleThrThrSerSer
Db 2084 GAGGATATGGAAACAAATTAAGTACGATCCTCAACTATGAATGGTTTTCAGACGAGGTTTCA 2143
QY 564 -----MetThrIleAlaProLysGlyArgGlu----- 572
Db 2144 ATGGTAAGCCAGATATGCAAACTTTGGGACTATATTGCCAGATCAGAGAGGTTGG 2203
QY 572 -----
Db 2204 ACAAGAACTTCTCCCTAGAGAAATGTTCCAGAGACATATTGGCAAGTACACACAGAT 2263
QY 572 -----
Db 2264 GCTGACAGGCTCTGTTTATCTGTGACACAGTCTACCAATGCTCCCTCCACCAATCTCC 2323
QY 572 -----
Db 2324 ACCCTGCTAGAGGATGAAGTAATATTATGGGTGTACAGGATATTTCGTAGAACTGGACCG 2383
QY 572 -----
Db 2384 ATAGGCACAGATTACTATCAGCTGAGCAAGTCCAAAGAGCAAAATGGCAAGGTTGGTAGT 2443
QY 572 -----
Db 2444 TATGTGGAATGTCACAAAGTGTCTACTCCACAGAGATGGTTAGTGTGGCTTGGCCAC 2503
QY 573 -----LeuValValPhePheSer 578
Db 2504 GAAGGAGGAGATGACTTGATTATATCCAGACTTCAGGAGCTTTGGTGGTTTCTTCAGC 2563
QY 579 LeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyr 598
Db 2564 CTCGAGTGACTAAACATGATGTTTTCAGAGATCTGTTTATATAAACTCTCTTGAGTAT 2623
QY 599 ArgAlaLeuGluGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThr 618
Db 2624 AAAGCCCTGGAGCAAGATTCTTAGAATGCTGTGTTCCCTATCTCCAGTCAAACTCTCAG 2683
QY 619 GlyPheLysGluLeuIleLeuAsnPheArgAsnGlySerValIleValAsnSerLys 638
Db 2684 GGGTTCAGAACTTAGAAATCTCAACTTCAGAAATGGCAGATTTGGTGAACAGTCGA 2743
QY 639 MetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGlu 658
Db 2744 ATGAAGTTTGGCAATCTGCTCCCTCTCAAGCTCAACAATGGGTGTACATGATCTGGAA 2803
QY 659 AspPheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsn 678
Db 2804 GACTTTTGACCACTGCCTTACAAATCCATGAACTTGGCTATTGATGAATACTCTCTTGAAT 2863
QY 679 IleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGln 698
Db 2864 GTGGATCAGGTGATGAGCCCAACCTTCCAAATTTCCAGGCTGTGAATGAATTTTCAGAA 2923
QY 699 -CysValLysAsn-GluArgThrGluGluAlaGluCysArg 711
Db 2924 GTGCTGTGTCACCCCTGGAGTGGAGAAACAAAGTGCAGA 2964
```

RESULT 11

US-10-007-270-23

; Sequence 23, Application US/10007270

; Publication No. US20020160954A1

## GENERAL INFORMATION:

```
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; TITLE OF INVENTION: University of Iowa Research Foundation
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4204
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Mouse IPM 200 cDNA sequence (partial)
; NAME/KEY: misc feature
; LOCATION: (1)-(4204)
; OTHER INFORMATION: n is a, c, g, or t.
; US-10-007-270-23
```

## Alignment Scores:

Pred. No.:	2,598-78	Length:	4204
Score:	841.00	Matches:	261
Percent Similarity:	41.20%	Conservative:	123
Best Local Similarity:	28.00%	Mismatches:	238
Query Match:	20.43%	Indels:	310
DB:	13	Gaps:	34

US-10-007-270-2 (1-797) x US-10-007-270-23 (1-4204)

```
QY 96 TyrTyrArgLeuArgValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAsp 115
Db 21 TATTTTAAAGCCGAGTGTGGAGAGCCATCTGGAAAGCCCTTCAGGACGTTTTCGGAT 80
QY 116 ArgIleProAspThrGlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPhe 135
Db 81 CGACTTCTGGGCGTGCATGAATATCGTCACTGATGAATTTATGTGAGGATGGAGTCACA 140
QY 136 CysLeuPheAspIleCysLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGln 155
Db 141 AGTGATTTTGAATGGCGCCCATTTTATGTCAGTCTGTGGAACATAGAAACCTATATCATG 200
QY 156 GlnArgIle-----LysGlnArgSerPheProAspArgLysAspGluIleSerAla 172
Db 201 AAGAACTGGCTTACACAGGAGGAGCTGAGAGCAGCTCTCGAAGGATCAG---TCCTGT 257
QY 173 GluLysThrLeuGlyGluPro-----GlyGluThrIleValIleSerThrAspVal 189
Db 258 GGGCCTGAGTTGTCTTCCAGTTCCTATTGTTGAGACC-----TCAACACTGCACA 308
QY 190 AlaAsnValSerLeuGlyProPhePro-----LeuThrPro 201
Db 309 GGTGCTGTCTCCAGTCTCTCTATCCAGGGTGGTTCGGAGAGCAGCCAGCGTCACCG 368
QY 202 AspAspThrLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetProThr 221
Db 369 CAGGAGATATCAGCAATGAATTT---GAGAAATGTGACAGAGGAGCCCAACACGAGCT 425
QY 222 ThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSerValSer 241
Db 426 GCTGAACAGATTGCGGAATTC-----AGATCCAA 455
QY 242 LeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGlu 261
Db 456 CTTCCTGGGAAGGATACAGTGAAGAACTCCGGATCCCTCCAGCGCCCTCTACCGGCTC 515
QY 262 LeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLys 281
```



QY 737 CysGluValLeuGlnGlyLysGlyAlaProCysArg 748  
 Db 2688 TGTGACATTATGCTGGCATGGAGCCATTGTGTAGA 2723

## RESULT 12

US-10-198-846-12589  
 ; Sequence 12589, Application US/10198846  
 ; Publication No. US20030099974A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lillie, James  
 ; APPLICANT: Xu, Yongyao  
 ; APPLICANT: Wang, Youzhen  
 ; APPLICANT: Steinmann, Kathleen  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 ; FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; THERAPY OF BREAST CANCER  
 ; FILE REFERENCE: MRI-049  
 ; CURRENT APPLICATION NUMBER: US/10/198,846  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/306,220  
 ; PRIOR FILING DATE: 2001-07-18  
 ; NUMBER OF SEQ ID NOS: 14084  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12589  
 ; LENGTH: 2026  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 1, 2026  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-10-198-846-12589

Alignment Scores:  
 Pred. No.: 4,558-10 Length: 2026  
 Score: 194.50 Matches: 85  
 Percent Similarity: 40.34% Conservative: 59  
 Best Local Similarity: 23.81% Mismatches: 146  
 Query Match: 4.72% Indels: 67  
 Db: 14 Gaps: 15

US-10-007-270-2 (1-797) x US-10-198-846-12589 (1-2026)

QY 367 GlnSerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAla 386  
 Db 285 CAGGACAGGAGTGTCACTGTGCCCCCGCCAGCAACAGCAGTTCAGGTTCAGTGCACCC 344  
 QY 387 PheGlyProAspThrGlnSerGluLeuProThrSerPheAlaValIle----- 402  
 Db 345 TGGGACAGGAGTGTCACTCG---GTCCAGTCAACAGGCGAGCCCTGGGCTCCACCAACC 401  
 QY 403 -----ThrGluAspAlaThrLeuSerProGluLeuProPro-----ValGlu 416  
 Db 402 CCGCCAGCCAGAGTGTCACTCAGCCCGGACACAGCCAGCCCGGCTCCACCGCC 461  
 QY 417 ProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThr----- 432  
 Db 462 CCCCCAGCCAGCGGTGTCACTCGGCC-----CCGACACAGCCAGCCCGCCCGC 509  
 QY 433 ---SerTyrSerProAlaMetAlaSerThrSerLeuSerGluAla-----ProPro 449  
 Db 510 GGCTCAGCCGCCCGCCAGCCAGCGTGTCACTCGCCCGGACACAGCCAGCCCGCCCGC 569  
 QY 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469  
 Db 570 GGCTCAGCCGCCCGCCAGCCAGCGTGTCACTCGCCCGGACACAGCCAGCCCGCCCGC 605  
 QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSer-----AspTyr 486  
 Db 606 GCCCCGACACAGCCCGCCCGGCTCCACCGCCCGGACAGCCAGCGTGTGTACCTCG 665  
 QY 487 SerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro-----AlaSerSer 503

Db 666 GCCCGGACACAGCCCGCTTGGCTCCACCGCCCTCCAGTCCCAATGTGTCACTCG 725  
 QY 504 AspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAsp 523  
 Db 726 GCCTCAGGCTGTGCATCAGGCTCAGCTTCTACTCTGTGTGCACACGCGACCTCTCCAGG 785  
 QY 524 LeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrValSerValPro 543  
 Db 786 GCTACCAACACCCAGCCAGCAGCAGCTCCA-----TTCTCAATTGCC 830  
 QY 544 AspHisPheLeuGluAspThrThrProVal----- 553  
 Db 831 AGCCACCACTCTGATCTCTATACCACTTGTGCCAGCCATAGCACCAAGATGATGCCAGT 890  
 QY 554 -----SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLys 569  
 Db 891 AGCACTCACCATAGCAGGTACTCTCTCTCTTTTCTCTCTTTCATTTCAATTTCAACTTAA 950  
 QY 570 GlyArgGluLeuValValPhePhe-----SerLeuArgValAlaAsnMetAlaPheSer 587  
 Db 951 TTGCTACTGGGTCTCTTTCTTTTCTCTCTTTCATTTCAATTTCAACTTAACTTAA 1010  
 QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln 607  
 Db 1011 TCCTCTCTGGAAGATCCCAAGCAGCAGTACTACCAAGAGCTGCAGAGAGACATTTCTGAA 1070  
 QY 608 LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuLysLeuLeu 627  
 Db 1071 ATGTTTTCAGATTATTAACAAGG-----GTTTTCTGGGCTCTCCATATTAA 1124  
 QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647  
 Db 1125 TTCAGGCCAGGATCTGTGTGTGTACATTTGACTCTGGCTTCCGAGAAGT----- 1175  
 QY 648 AsnLeuThrLysAlaValHisGlyVal-----LeuGluAspPheArgSerAlaAla 664  
 Db 1176 -----ACCATCAATGTCCAGCTGGAGACACAGTTCATCATATAAACGGAAGCA 1229  
 QY 665 AlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluPro 681  
 Db 1230 GCCTCTCGATATAACCTGACGATCTCAGACGTCAGCGTGTGTGTGTGTGCA 1280

## RESULT 13

US-09-964-824A-105  
 ; Sequence 105, Application US/09964824A  
 ; Patent No. US20020102531A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Horrigan, Stephen  
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
 ; FILE REFERENCE: 689290-73  
 ; CURRENT APPLICATION NUMBER: US/09/964,824A  
 ; CURRENT FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/236,033  
 ; PRIOR FILING DATE: 2000-09-28  
 ; PRIOR APPLICATION NUMBER: US/60/236,032  
 ; PRIOR FILING DATE: 2000-09-28  
 ; PRIOR APPLICATION NUMBER: US/60/236,028  
 ; PRIOR FILING DATE: 2000-09-28  
 ; NUMBER OF SEQ ID NOS: 583  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 105  
 ; LENGTH: 4139  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-964-824A-105

Alignment Scores:  
 Pred. No.: 4,86e-09 Length: 4139  
 Score: 189.50 Matches: 91  
 Percent Similarity: 40.79% Conservative: 53  
 Best Local Similarity: 25.78% Mismatches: 132

```
Query Match: 4.60% Indels: 77
DB: 9 Gaps: 18
US-10-007-270-2 (1-797) x US-09-964-824A-105 (1-4139)

Qy 385 ProAlaPheGly-----ProAspThrGlnSerGluLeuProThrSerPheAla 400
Db 2513 CCAGCCACGGTGTACCTCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2569
Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuPro-----ValGlu 416
Db 2570 CCCCAGCCACCGGTGTACCTCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2629
Qy 417 ProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThr 432
Db 2630 CCCCAGCCACCGGTGTACCTCGGCC---CCGGACACACAGGCGGCCGCCG 2677
Qy 433 ---SerTrpSerProProAlaMetAlaSerThrSerLeu-----ACC 2845
Db 2678 GGCTCCACCGGCCCGGCTCCACCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2905
Qy 445 ---SerGluAlaProProPheMetAlaSerSerIlePheSerLeuThrAsp----- 461
Db 2738 GGCTCCACCGGCCCGGCTCCACCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2788
Qy 462 ---GlnGlyThrThrAsp-----ThrMetAlaThrAspGlnThr 473
Db 2789 CCGGCCCGGGCTCCACCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2845
Qy 474 MetLeuValProGlyLeuThrIleProThrSer-----AspTyrSerAlaIleSer 490
Db 2846 AGGCCCGGCCCGGGCTCCACCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2905
Qy 491 GlnLeuAlaLeuGlyIleSerHisProPro-----AlaSerSerAspSerArg 507
Db 2906 AGGCCCGGCCCGGGCTCCACCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2965
Qy 508 SerSerAlaGlyGlyAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527
Db 2966 GCATCAGGCTCAGCTTCTACTCTGTGTGTCACACAGGACCTCTCGAGGGGTACCAACAC 3025
Qy 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547
Db 3026 CCAGCCAGCAGACATCCCA-----TTCTCAATCCACGACCACTCT 3070
Qy 548 GluAspThrThrProVal----- 553
Db 3071 GATACCTCTACCCCTTGCAGCATAGCACCAAGACTGATGCCAGTACCTACCAT 3130
Qy 554 SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeu 573
Db 3131 AGCTCGATACCTCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 3190
Qy 574 ValValPhePhe-----SerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591
Db 3191 GTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3250
Qy 592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValPro 611
Db 3251 GATCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3310
Qy 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGly 631
Db 3311 ATTATATAACAGGG-----GGTTTCTGGGCTCTTCCATATATTAAGTTCAGCCAGGA 3364
Qy 632 SerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLys 651
Db 3365 TCTGTGGTGTACAAATGACTCTGGCTTCCGAGAGGT-----ACCATC 3409
Qy 652 AlaValHisGlyVal-----LeuGluAspPheArgSerAlaAlaGlnGlnLeu 668
Db 3410 AATGTCACGACGCTGGAGACACAGTTCATAGTATAAAACGAGCAGCCTCTCGATAT 3469
```

```
Qy 669 HisLeuGluIleAspSerTyrSerLeuAsnIleGluPro 681
Db 3470 AACCTGACGATCTCAGACGTCAGCGTGTGATGTGCCA 3508
```

## RESULT 14

```
US-09-964-824A-578
; Sequence 578: Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 578
; LENGTH: 4139
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-578

Alignment Scores:
Pred. No.: 4,866-09 Length: 4139
Score: 189.50 Matches: 91
Percent Similarity: 40.79% Conservative: 53
Best Local Similarity: 25.78% Mismatches: 132
Query Match: 4.60% Indels: 77
DB: 9 Gaps: 18

US-10-007-270-2 (1-797) x US-09-964-824A-578 (1-4139)

Qy 385 ProAlaPheGly-----ProAspThrGlnSerGluLeuProThrSerPheAla 400
Db 2513 CCAGCCACGGTGTACCTCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2569
Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuPro-----ValGlu 416
Db 2570 CCCCAGCCACCGGTGTACCTCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2629
Qy 417 ProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThr 432
Db 2630 CCCCAGCCACCGGTGTACCTCGGCC---CCGGACACACAGGCGGCCGCCG 2677
Qy 433 ---SerTrpSerProProAlaMetAlaSerThrSerLeu-----ACC 444
Db 2678 GGCTCCACCGGCCCGGCTCCACCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2737
Qy 445 ---SerGluAlaProProPheMetAlaSerSerIlePheSerLeuThrAsp----- 461
Db 2738 GGCTCCACCGGCCCGGCTCCACCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2788
Qy 462 ---GlnGlyThrThrAsp-----ThrMetAlaThrAspGlnThr 473
Db 2789 CCGGCCCGGGCTCCACCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2845
Qy 474 MetLeuValProGlyLeuThrIleProThrSer-----AspTyrSerAlaIleSer 490
Db 2846 AGGCCCGGCCCGGGCTCCACCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2905
Qy 491 GlnLeuAlaLeuGlyIleSerHisProPro-----AlaSerSerAspSerArg 507
Db 2906 AGGCCCGGCCCGGGCTCCACCGGCCCGGACACACAGG---CCGGCCCGGGCTCCACGCC 2965
Qy 508 SerSerAlaGlyGlyAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527
Db 2966 GCATCAGGCTCAGCTTCTACTCTGTGTGTCACACAGGACCTCTCGAGGGGTACCAACAC 3025
```

Db 2966 GCATCAGCTCAGCTTCTCTCGTGCACAAACGGACCTCTGCCAGGGCTACCAAC 3025  
Qy 528 ProLapSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547  
Db 3026 CCAGCCAGCAGAGCACTCCA-----TTCTCAATTCCAGCCCACTCT 3070  
Qy 548 GluAspThrProVal-----553  
Db 3071 GATACCTCTACCACTTCCAGCTGCAGCAATAGCAGCACTGATGCCAGTACATCACCAT 3130  
Qy 554 SerAlaLeuGlnTyrIleThrSerMetThrIleAlaProLysGlyArgGluLeu 573  
Db 3131 AGCTCGGTACCTCTCTCACTCTCTCAATCAGCAGCACTTCTCCAGTGTCTACTGGG 3190  
Qy 574 ValValPhePhe-----SerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591  
Db 3191 GTCTCTTTCTTTCTCTCTCTTTTTCACATTTCAAACTCCAGTTTAAATCTCTCTGGAA 3250  
Qy 592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnPheThrGlnLeuValPro 611  
Db 3251 GATCCAGCAGCAGTACTACCAAGAGCTGCAGAGACATTTCTGAAATGTTTTCAG 3310  
Qy 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluLeuLeuAsnPheArgAsnGly 631  
Db 3311 ATTTATAAACAAAGG-----GGTTTCTGGGCTCTCTCAATATTAAAGTTTCAGGCCAGGA 3364  
Qy 632 SerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLys 651  
Db 3365 TCTGTGGTGATCAATGACTCTGGCTTCGAGAGGT-----ACCATC 3409  
Qy 652 AlaValHisGlyVal-----LeuGluAspPheArgSerAlaAlaGlnGlnLeu 668  
Db 3410 AATGTCCAGCAGTGGAGACACAGTTCATCAGTATATAAACGGAAGCAGCTCTCGATAT 3469  
Qy 669 HisLeuGluIleAspSerTyrSerLeuAsnIleGluPro 681  
Db 3470 AACCTGAGATCTCAGACGTCAGCGTGAGTGATGTGCCA 3508

## RESULT 15

US-09-864-864-334  
; Sequence 334, Application US/09864864  
; Patent No. US20020102679A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Dillon, David C.  
; APPLICANT: Secret, Heather  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steve P.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Carter, Darrick  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.523  
; CURRENT APPLICATION NUMBER: US/09/864,864  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 341  
; SOFTWARE: Corixa Invention Disclosure Database  
; SEQ ID NO 334  
; LENGTH: 4139

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-864-864-334

Alignment Scores:  
Pred. No.: 4,869-09 Length: 4139  
Score: 189.50 Matches: 91  
Percent Similarity: 40.79% Conservative: 53  
Best Local Similarity: 25.78% Mismatches: 132  
Query Match: 4.60% Indels: 77

DB: 9 Gaps: 18  
US-10-007-270-2 (1-797) x US-09-864-864-334 (1-4139)  
Qy 385 ProAlaPheGly-----ProAspThrGlnSerGluLeuProThrSerPheAla 400  
Db 2513 CCAGCCAGCAGGTGTCACTCGGCCCGGACACACAGG---CCGGCCCCGGGTCCACCGCC 2569  
Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProPro-----ValGlu 416  
Db 2570 CCCCCAGCCACGAGTGTCACTCGGCCCGGACACACAGGCGCCGGGTCCACCGCC 2629  
Qy 417 ProGlnLeuGluThrValAspGlyValGluHisGlyLeuProAspThr-----432  
Db 2630 CCCCCAGCCACGAGTGTCACTCGGCC-----CCGGACACACAGGCGGCCCGC 2677  
Qy 433 ---SerTrpSerProAlaMetAlaSerThrSerLeu-----444  
Db 2678 GGTCTCACCGCCCGCCCGGACCGGTCACCTCGGCCCGGACACACAGGCGGCCCGC 2737  
Qy 445 ---SerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAsp-----461  
Db 2738 GGTCTCACCGCCCGCCCGC-----GCCACGGTGTCACTCGGCCCGGACACACAGG 2788  
Qy 462 ---GlnGlyThrThrAsp-----ThrMetAlaThrAspGlnThr 473  
Db 2789 CCGGCCCGCGGTCTCCACCGCCCGGACCGGTGTCACTCGGCCCGGAC---ACC 2845  
Qy 474 MetLeuValProGlyLeuThrIleProThrSer-----AspTyrSerAlaIleSer 490  
Db 2846 AGCGCGCCCGGGTCCACCGCCCGGACCGCCCGGACCGGTGTCACTCGGCCCGGACAC 2905  
Qy 491 GlnLeuAlaLeuGlyIleSerHisProPro-----AlaSerSerAspSerArg 507  
Db 2906 AGGCCCGCTTGGGTCTCCACCGCCCGGACCGGTGTCACTCGGCCCGGAC---2965  
Qy 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527  
Db 2966 GCATCAGCTCAGCTTCT 3025  
Qy 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547  
Db 3026 CCAGCCAGCAGAGCACTCCA-----TTCTCAATTCAGCCCACTCT 3070  
Qy 548 GluAspThrThrProVal-----553  
Db 3071 GATACCTCTACCACTTCCAGCCATAGCAGCACTGATGCCAGTACCATCACCAT 3130  
Qy 554 SerAlaLeuGlnTyrIleThrSerMetThrIleAlaProLysGlyArgGluLeu 573  
Db 3131 AGCTCGGTACCT 3190  
Qy 574 ValValPhePhe-----SerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591  
Db 3191 GTCTCTTTCTTTCTCTCTCTTTTTCACATTTCAAACTCCAGTTTAAATCTCTCTGGAA 3250  
Qy 592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnPheThrGlnLeuValPro 611  
Db 3251 GATCCAGCAGCAGTACTACCAAGAGCTGCAGAGACATTTCTGAAATGTTTTCAG 3310  
Qy 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluLeuLeuAsnPheArgAsnGly 631  
Db 3311 ATTTATAAACAAAGG-----GGTTTCTGGGCTCTCTCAATATTAAAGTTTCAGGCCAGGA 3364  
Qy 632 SerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLys 651  
Db 3365 TCTGTGGTGATCAATGACTCTGGCTTCGAGAGGT-----ACCATC 3409  
Qy 652 AlaValHisGlyVal-----LeuGluAspPheArgSerAlaAlaGlnGlnLeu 668  
Db 3410 AATGTCCAGCAGTGGAGACACAGTTCATCAGTATATAAACGGAAGCAGCTCTCGATAT 3469  
Qy 669 HisLeuGluIleAspSerTyrSerLeuAsnIleGluPro 681

Db 3470 AACCTGACGATCTCAGACGTCAGCGTGAGTGAGTGATGTGCCA 3508  
:::|||||:::|||||:::|||||:::|||||:::|||||

Search completed: March 2, 2004, 00:55:48  
Job time : 790 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2004, 20:33:11 ; Search time 146 Seconds

(without alignments)  
3029.424 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117  
Sequence: 1 MILETTRAIKVFVIFLQVQ.....NSLLTVYEFNQHDEGN 797

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US10007270/runat\_25022004\_164208\_27225/app\_query.fasta\_1.967  
-DB=Issued Patents NA -QFMT=fastcap -SUFFIX=xni -MINMATCH=0.1 -LOOPGL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10007270 -CGN 1\_69 @runat\_25022004\_164208\_27225 -NCPUS=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTCUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	157	3.8	19307	3	US-08-836-022A-10
C 2	157	3.8	19307	3	US-08-836-022A-10
C 3	146	3.5	8982	2	US-08-976-255-5
4	145.5	3.5	6192	2	US-08-479-537A-1
5	145.5	3.5	6192	3	US-09-083-116-1
6	145.5	3.5	6192	4	US-09-134-916A-1
7	145	3.5	8224	6	5180808-1
8	144.5	3.5	3104	4	US-09-418-780A-2
9	144.5	3.5	3106	4	US-09-392-714-4
10	141.5	3.4	6407	2	US-08-616-844-7
11	141.5	3.4	6407	2	US-08-599-854-7
12	141.5	3.4	6407	3	US-08-944-868A-7

13	141.5	3.4	6407	3	US-08-944-423A-7	Sequence 7, Appli
14	141.5	3.4	6407	3	US-08-944-496-7	Sequence 7, Appli
C 15	138	3.4	580073	4	US-08-545-528D-1	Sequence 1, Appli
16	137.5	3.3	2156	1	US-08-178-477B-31	Sequence 31, Appli
17	137.5	3.3	2156	4	US-09-304-121-1	Sequence 1, Appli
18	137.5	3.3	2156	4	US-09-023-655-1111	Sequence 1111, Ap
19	137.5	3.3	2458	4	US-09-513-783A-175	Sequence 175, App
C 20	135.5	3.3	2835	4	US-09-134-001C-1515	Sequence 1515, Ap
C 21	135.5	3.3	3561	4	US-09-134-001C-1685	Sequence 1685, Ap
22	135.5	3.3	4928	4	US-09-620-312D-329	Sequence 329, App
23	135.5	3.3	6414	4	US-09-134-001C-1626	Sequence 1626, Ap
C 24	135.5	3.3	13377	4	US-09-484-970B-60	Sequence 60, Appli
C 25	134.5	3.3	8312	4	US-09-620-312D-1048	Sequence 1048, Ap
26	134	3.3	13473	5	PCT-US96-03916-1	Sequence 1, Appli
27	134	3.3	18912	5	PCT-US96-03916-59	Sequence 279, Appl
28	131.5	3.2	3073	4	US-09-620-312D-279	Sequence 279, App
29	131	3.2	4822	4	US-09-484-970B-106	Sequence 106, App
30	130.5	3.2	5494	3	US-08-910-864-10	Sequence 10, Appli
31	130.5	3.2	5510	1	US-08-123-161A-7	Sequence 7, Appli
32	130.5	3.2	5510	1	US-08-483-278-7	Sequence 7, Appli
33	130.5	3.2	5645	4	US-09-023-655-1319	Sequence 1319, Ap
34	130.5	3.2	5681	4	US-09-919-172-58	Sequence 58, Appl
35	130	3.2	3573	4	US-09-107-532A-3492	Sequence 3492, Ap
C 36	129	3.1	3540	4	US-09-976-594-888	Sequence 888, App
C 37	128.5	3.1	1830121	4	US-08-557-884-1	Sequence 1, Appli
C 38	128.5	3.1	1830121	4	US-09-643-990A-1	Sequence 1, Appli
39	128	3.1	5952	4	US-09-687-875A-1	Sequence 134, App
40	127.5	3.1	4323	4	US-09-620-312D-134	Sequence 23, Appli
41	127.5	3.1	5933	4	US-09-919-172-23	Sequence 2, Appli
42	127	3.1	9626	4	US-09-150-867-2	Sequence 30, Appli
43	126.5	3.1	14770	4	US-09-220-132-30	Sequence 39, Appli
44	126	3.1	4522	4	US-08-956-171E-39	Sequence 5, Appli
45	126	3.1	8789	1	US-08-328-254-5	

#### ALIGNMENTS

RESULT 1  
US-08-836-022A-10/c  
; Sequence 10, Application US/08836022A  
; Patent No. 6001557  
; GENERAL INFORMATION:  
; APPLICANT: Trustees of the University of Pennsylvania  
; APPLICANT: Wilson, James M.  
; APPLICANT: Fisher, Krishna J.  
; APPLICANT: Chen, Shu-Jen  
; APPLICANT: Weitzman, Matthew  
; TITLE OF INVENTION: Improved Adenovirus Virus and  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr, P O Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,022A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/331,381  
; FILING DATE: 28-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: GNPVN.008PCT  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-540-9200  
 ; TELEFAX: 215-540-5818  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 19307 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: cDNA  
 ; US-08-836-022A-10

## Alignment Scores:

Pred. No.: 0, 000161 Length: 19307  
 Score: 157.00 Matches: 173  
 Score: 35.60% Conservative: 151  
 Best Local Similarity: 19.01% Mismatches: 318  
 Query Match: 3.81% Indels: 268  
 DB: 3 Gaps: 44

US-10-007-270-2 (1-797) x US-08-836-022A-10 (1-19307)

QY 14 llePheLeuGlnValGlnGlyThrLysAspIleSerIleAenIleTyrHis---SerGlu 32  
 DB 8368 CTTTAAAGCAAGAGAGCTCTCTTAAGAAATATAAAGACAAATTTGCAACAAATCTCAGGT 8309  
 QY 33 ThrLysAspIleAspAsnProArgAenGluThrThrGluSerThrGluLysMetTyr 52  
 DB 8308 CGGATTGATATATTCACAAGNAGACAGCAGCCTTGCAAGTGCACCTCCATGGAA 8249  
 QY 53 LysMetSerThr-----MetArg 59  
 DB 8248 AAGGTGAAGTACAGGAAGCGGTGGCACAGATGGATTTCAGGGGAAAAAATTCATAGA 8189  
 QY 60 llePheAspLeuAlaLysHisArgThrLysArgSerAla-----PhePhePro 75  
 DB 8188 ATGTACAAGGACAGCAAGGGGAGATCGACAGATCAGTTGAAAATGGCGACATTTTCAT 8129  
 QY 76 ThrGlyValLysValCysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAla 95  
 DB 8128 TATGATATGAAGTA-----TTTAATCAATGGCTGAATGAAGTTGAACAG 8084  
 QY 96 TyrTyrArgLeuArgValCysGlnGluAlaValTrpGlu-----AlaTyrArgIlePhe 113  
 DB 8083 TTTTTCAAA--AAGACACAAAATCCTGAAAACCTGGGAACATGCTAAATACAAATGGTAT 8027  
 QY 114 LeuAspArgIleProAsp-----119  
 DB 8026 CTTAAGGAACTCCAGATGGCATTTGGGCGCGCTCAGCTGTTTCAGAACACTGAATGCA 7967  
 QY 120 ThrGlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAsp 139  
 DB 7966 ACTGGGGAA-----GAAATAATTCAACAG-----7943  
 QY 140 lleGlyLysAsnPheSerAsnSerClnGluHisLeuAspLeuLeuGlnArgIleLys 159  
 DB 7942 -----TCITCAAAAACAGATGCAATATTCACAGAAAATATAGGA 7901  
 QY 160 Gln-----ArgSerPheProAspArgLysAspGluIle 170  
 DB 7900 ACCTTGAGTCTCGGTGGCAGCAGATCTGCAAGAGCTGGCAGAAAGGAGAGAGGATT 7841  
 QY 171 SerAlaGluLysThrLeu-----GlyGluProGlyGluThrIleValle 185  
 DB 7840 GAAGAACAAAAGAAATGTTCTGTGCAAGATTTCAAGAGATTTAAATGAATTTGTTTGG 7781  
 QY 186 SerThrAspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeu 205  
 DB 7780 CTGGAGAGACAGATAACATTCCTTACTTACTCATT-----GGAGATGACAGCAG 7730  
 QY 206 LeuAsnGluIleLeuAspAsnThrLysAsnAspThrLysMetProThrThrGluArgGlu 225  
 DB 7729 CTAAGAAGAA-----CAACTTGAACAAGTCAAGTTACTGGCAGAGAGATGGCC 7682

QY 226 ThrGluPheAlaValLeuGluGlnArgValGluLeuSerValSerLeuValAsnGln 245  
 DB 7681 CTGCGCCAGGGAAATCTTAAACAATTAATAAGAACAGGAGAGCTACTTGTAAAGTCT 7622  
 QY 246 LysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLys 265  
 DB 7621 CCATAAGGCCAGAGAGCAAGATAAA-----CTTGAAGAAGAGCTCAACAG 7574  
 QY 266 SerGlnLeuGlnMetGlnLysIlePheLysLysLeuPro-----GlyPheLysLys 282  
 DB 7573 ACAAAATCTCCAGTGGATAAAGGTCTCCAGAGCTTTACCTGAGAAAACAAGGAGAGCTTGAG 7514  
 QY 283 IleHisValLeuGlyPheArgProLysLysAspGlySerSerSerThrGluMet 302  
 DB 7513 GTTCACCTTAAAGATTTTAGGAGCTTGAAGAGCAG-----CTGGATCACCTG 7466  
 QY 303 GlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeu 322  
 DB 7465 CTTCTGTGGTCTCTCTATTAAGAACCAAGCTTGAATTTATACCAACCAAGTCAGGCA 7406  
 QY 323 LeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThrMetGlu 342  
 DB 7405 GGACCGTTTGATTAAGAGATT-----GAAGTAACAGTTCACGGT-----7364  
 QY 343 AspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuLysLysAla 362  
 DB 7363 -----AAACAA-----GCGGATGTGAAAGGCTTTTGTGGAAGGG 7328  
 QY 363 -----LeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 380  
 DB 7327 CAGCATTTGTATAGGAAAA-----7307  
 QY 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
 DB 7306 -----CCAAGCACTCAG-----7295  
 QY 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeuGlu 420  
 DB 7294 -----CCAGTGAAGAGGAAGTAGAA 7274  
 QY 421 ThrVal-----AspGlyAlaGluHisGlyLeu-----429  
 DB 7273 GATCTAGAGTCTAGTGGAGGCTGTAAACCAATTTACTTCGGGAGCTGAGGACAAGCAG 7214  
 QY 430 ProAspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449  
 DB 7213 CCGTACCGTGCC-----CCTGCACTGAGCACTACTGGAGCCTCT-----7175  
 QY 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469  
 DB 7174 -----GCCAGTCAGACTGTTACTCTA-----GTGACACAATCTGTGTT 7136  
 QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIle 489  
 DB 7135 ACTAAGAACT--GTCATCTCCAACTAGAAATGCCATCTCT-----7094  
 QY 490 SerGlnLeuAlaLeuGlyLysSerHisProProAlaSerSerAspAspSerArgSerSer 509  
 DB 7093 -----TTGCTGTGGAGTA-----CCTGCACTGGCAGACTCAACGAGCTGG 7049  
 QY 510 AlaGlyGlyLysMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529  
 DB 7048 ACAGAACTTACAGACTGGCTGTCTCTGTTGATCGAGTTATAAATACAGAGAGTGATG 6989  
 QY 530 ProSerGluValProGluLeuSerGluTyrVal-----SerValProAsp 544  
 DB 6988 GTGGGTGATCTGGAACATCAATGAATGAATGATCAAAACAGAGCAACACTGCAAGAT 6929  
 QY 545 HisPheLeuAspThrThrProValSerAlaLeuGlnTyrIleThrSerSerMet 564  
 DB 6928 -----TTGGAACAGAGAGCGCC-----CAATTGGAAGAACTCATCTACTCTCCAG 6881  
 QY 565 ThrIleAlaProLys-----GlyArgGluLeuValValPhePheSerLeuArgValAla 582

```
Db 6880 AATTTGAAAACAAACACCAAGCAATCAGAGAGCTAGACATCATCTACTGATCGAATTGAA 6821
Qy 583 AsnMetAlaPheSer-
Db 6820 AGAATTCAGATTCAGTGGGATGAGTTTCAAGAACAGCTGCAGAACAGGAGACACAGTTG 6761
Qy 588 AsnAspLeuPheAsnLeuSerSerLeuGluTyrArgAlaLeuGluGlnPheThrGln 607
Db 6760 AATGAAATGTTA---AAGATTCAACAATAGTGGTGAAGCTAAGGAAGACCGCAACAG 6704
Qy 608 LeuLeu-
Db 6703 GTCATAGCAGAGCTCAGAGGCAAGCTTCACTCATCGAAGAGTCTCTCACACAGTAGAT 6644
Qy 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeu---GluLeuAsnPheArgAsn 630
Db 6643 GCATTCGAAGAGATCACAGAACCAAGCAGGTGGCCAAAGACCTCCGTCACACGCGAG 6584
Qy 631 GlySerValIleVal-AsnSerLysMetLysPheAlaLysSerValProTyrAsn 648
Db 6583 ATAAGTGTAGACGTGGCAATGATTTGGCACTGAACTTCTCTCGGACTATTCTGCTGAT 6524
Qy 649 LeuThrLysAlaValHisGlyValLeuGluAspPhe-
Db 6523 GATACAGAAAGTACACATGATACAGAGATATCAATCTTCTGGGAAACATTCAT 6464
Qy 661 -ArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyr 675
Db 6463 AAAGAGTAAGTGACAGAGCTGCTTTGGAGAAACTATAGATTACTGCAGCAGTTC 6404
Qy 676 SerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGlu 695
Db 6403 CCTCTGGACCTGGAG-----AAGTTCTTCTCGGATTACG 6368
Qy 696 PheAlaGlnCysValLysAsn-----Glu 703
Db 6367 GAAGCAGAAACAACTGCCAATCTGTCTACAGACGCTCCCGTAGAGAGAGCTCCTAGAA 6308
Qy 704 ArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAsp 723
Db 6307 GACTCCAGGGGAGTCAGAGAGCTGATGAACCATCGGACAGATCTCCAGGAGAAATTGAA 6248
Qy 724 -----GlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740
Db 6247 ACTCACACAGATATCTATCAACAATCTTGATGAAATGGCCAAAATCCCTGAGATCCCTG 6188
Qy 741 GlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThr 760
Db 6187 GAAGTTCGGATGAGACACCCCTGTTACAAAGACGTTTGGATAACATGAATTTCAAGTGG 6128
Qy 761 Ser-----ValLysLysPheGlnAsnGlnGlnAsnAsnLysValIleSerLysArgAsn 778
Db 6127 AGTGAACCTTCAGAAAAGTCTCTCAACATAGTACGTCCTTGGAGCAAGTCTCTGACCAG 6068
Qy 779 SerGluLeuLeuThrValGluTyrGluGlu 788
Db 6067 TGGAGCGCTTTCGATCTTCTCTTCAGGAA 6038
```

## RESULT 2

US-09-427-048A-10/c

Sequence 10, Application US/09427048A

Patent No. 6203975

GENERAL INFORMATION:

APPLICANT: Trustees of the University of Pennsylvania

Wilson, James M.

Fisher, Krishna J.

Chen, Shu-Jen

Weitzman, Matthew

TITLE OF INVENTION: Improved Adenovirus Virus and

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

```
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/427,048A
FILING DATE: 21-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,022
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNPVN.008PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-427-048A-10
```

## Alignment Scores:

Pred. No.:	0.000161	Length:	19307
Score:	157.00	Matches:	173
Percent Similarity:	35.60%	Conservative:	151
Best Local Similarity:	19.01%	Mismatches:	318
Query Match:	3.81%	Indels:	268
DB:	3	Gaps:	44

US-10-007-270-2 (1-797) x US-09-427-048A-10 (1-19307)

Qy	14	IlePheLeuGlnValGlnGlyThrLysAspIleSerIleAsnIleTyrHis	---SerGlu 32
Db	8368	CTTTTAAACCAAGAGAGCTCTTAAAGATATAAAGACAATTTCCACAAATCTCAGT	8309
Qy	33	ThrLysAspIleAspAsnProProArgAsnGluThrThrGluSerThrGluLysMetTyr	52
Db	8308	CGGATTGATATTATTACAAAGAAAGACAGCAGCGCTTTGCAAAAGTCCACCTCCATGAA	8249
Qy	53	LysMetSerThr-	---MetArg 59
Db	8248	AAAGTGAAGTACACAGAACCCGTGGCACAGATGGATTTCCAGGGGGAAAACTTCATAGA	8189
Qy	60	IlePheAspLeuAlaLysHisArgThrLysArgSerAla-	---PhePhePro 75
Db	8188	ATGTACAAAGAACCAAGGGCGATTCCACAGATCAGTTGAAAAATGGGACACTTCAT	8129
Qy	76	ThrGlyValLysValCysProGlnGlnSerMetLysGlnIleLeuAspSerLeuGlnAla	95
Db	8128	TATGATATGAAGGTA-----TTTATCAATGGCTGAATGAAGTTGAACAG	8084
Qy	96	TyTyrArgLeuArgValCysGlnGluAlaValTyrGlu-	---AlaTyrArgIlePhe 113
Db	8083	TTTTTCAAA---AAGACACAAAAATCTCGAAACTGGGAACATGCTAAATACAAATGGTAT	8027
Qy	114	LeuAspArgIleProAsp-	----- 119
Db	8026	CTTAAAGGAACCTCCAGATGGCATTTGGCAGCGCTCAAGCTGTTGTGAGAACACTGAATCA	7967

QY 120 ThrGlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAsp 139  
DB 7966 ACTGGGAA-----GAAATAATCAACAG----- 7943  
QY 140 IleGlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnArgIleLys 159  
DB 7942 -----TCTTCAAAACAGATGTCATATTTCTACAGAAATAATAGGA 7901  
QY 160 Gln-----ArgSerPheProAspArgLysAspGluIle 170  
DB 7900 AGCTTGAGTCTGGGTGGCAGACATCTGCAAGAGCTGGCAGAAAGAGAGAGATT 7841  
QY 171 SerAlaGluLysThrLeu-----GlyGluProGlyGluThrIleValIle 185  
DB 7840 GAAGAACAAAGATGCTGTGCAGAAATTCACAGAGATTAAATGAATTTGTTGG 7781  
QY 186 SerThrAspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeu 205  
DB 7780 CTGGAAGAGCAGATAACATTGCTATTACTCCACTT-----GGAGATGACAGCAG 7730  
QY 206 LeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGluArgGlu 225  
DB 7729 CTAAAGAA-----CACTTGAAACAGTCAAGTTACTGGCAGAGAGATTGCC 7682  
QY 226 ThrGluPheAlaValLeuGluGlnArgValGluLeuSerValSerLeuValAsnGln 245  
DB 7681 CTGCGCCAGGGAATCTTAAACAAATTAATGAACAGGAGCAGTACTTGTAAAGTCT 7622  
QY 246 LysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLys 265  
DB 7621 CCATAGCGCAGAGACAGAGATAA-----CTTGAAAGAGAGCTCAAAACAG 7574  
QY 266 SerGlnLeuGlnMetGlnLysIlePheLysLysLeuPro-----GlyPheLysLys 282  
DB 7573 ACAATCTCCAGTGATAGAGTCTCCAGAGCTTTACCTGAGAACAAAGGAGAGCTTGAG 7514  
QY 283 IleHisValLeuGlyPheArgProLysGlyLysAspGlySerSerThrGluMet 302  
DB 7513 GTTCACTTAAAGATTTTAGCAGCTTGAGAGCAG-----CTGATCACCTG 7466  
QY 303 GlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeu 322  
DB 7465 CTTCTGTGGTCTCCTTATAGAACCCAGTGGAAATTTATACCAACCAAGTCAGGCA 7406  
QY 323 LeuSerPheAspSerAsnLysIleGluSerGluValTyrHisGlyThrMetGluGlu 342  
DB 7405 GGACGGTTTGACATAAAGAGATT-----GAAGTAACAGATTCACGCT----- 7364  
QY 343 AspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIleSerLysAla 362  
DB 7363 ---AAACAA-----CGGATGTGGAAGCGCTTTTGTCAAAAGGG 7328  
QY 363 -----LeuGluGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380  
DB 7327 CAGCATTGTATAGGAAAA----- 7307  
QY 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
DB 7306 -----CCAGCACTCAG----- 7295  
QY 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeuGlu 420  
DB 7294 -----CCAGTGAAGAGGAAGTTAGAA 7274  
QY 421 ThrVal-----AspGlyAlaGluHisGlyLeu----- 429  
DB 7273 GATCTGAGTCTGAGTGGGAGGCTTAAACCACTTACTTCGGAGCTGAGGACAAAGCAG 7214  
QY 430 ProAspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449  
DB 7213 CTTGACCGGCC-----CCTGGACTGAGCACTACTGGAGCCTCT----- 7175  
QY 450 PhePheMetAlaSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469

DB 7174 -----GCCAGTCAGACTGTTACTCTA-----GTGACACAATCTGGTT 7136  
QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIle 489  
DB 7135 ACTAAGGAACT---GTCATCTCCAAACTAGAAATGCCATCTCT----- 7094  
QY 490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArgSerSer 509  
DB 7093 -----TTCTCTTTGAGGTA-----CTGCACTGGCAGACTTCAACCAAGCTGG 7049  
QY 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529  
DB 7048 ACAGAACTTACAGACTGGCTGCTCTGCTGTATCGAGTTATAAATCAACAGAGTGATG 6989  
QY 530 ProSerGluValProGluLeuSerGluTyrVal-----SerValProAsp 544  
DB 6988 GTGGGTGATCTGGAAGACATCAATGAATGATCATCAACAGAGCAACACTGCAAGAT 6929  
QY 545 HisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMet 564  
DB 6928 -----TTGGAACAGAGACGCCCC-----CAATTGGAAGAACTCATCTGCTGCCAG 6881  
QY 565 ThrIleAlaProLys-----GlyArgGluLeuValValPhePheSerLeuArgValAla 582  
DB 6880 AATTGAAAAACAAACCCAGCAATCAAGAAGCTAGAACAACTACTGATCAATTTGAA 6821  
QY 583 AsnMetAlaPheSer----- 587  
DB 6820 AGAATTCAGATTCAGTGGGATGAGGTTCAAGAACAGCTGCAGAACAGGAGACACAGTTG 6761  
QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln 607  
DB 6760 AATGAAATCTTA---AAGGATTCAACACAATCGCTGGAAGCTTAAGAAAGAACCCGACAG 6704  
QY 608 LeuLeu----- 611  
DB 6703 GTCATAGGACAGCTCAGAGGCAAGCTTGACTCATGAAAGAAAGGTCCTCACAGTAGAT 6644  
QY 612 TyrLeuArgSerAsnLeuThrGlyPheLysGlnLeu---GluIleLeuAsnPheArgAsn 630  
DB 6643 GCAATCCAAAGAAAGATCACAGAAACCAAGCAGTTGGCCAAAGACCTCGTCAACGGCAG 6584  
QY 631 GlySerValIleVal-----AsnSerLysMetLysPheAlaLysSerValProTyrAsn 648  
DB 6583 ATAAGTGTAGCTGGCAAAATGATTGGCAGCTGAAACTTCTTCGGGACTATTCTGCTGAT 6524  
QY 649 LeuThrLysAlaValHisGlyValLeuGluAspPhe----- 660  
DB 6523 GATACCGAAAGATACATGATATAACAGAGATATCAATACTTCTTGGGAAACATTCAT 6464  
QY 661 -----ArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyr 675  
DB 6463 AAAAGAGTAAGTGAGCAAGAGCGCTGTTTGAAGAAACTCATAGATTACTGCGAGCAGTTC 6404  
QY 676 SerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGlu 695  
DB 6403 CCTCGACCTGGAG-----AAGTTCTTCTCTGGATTACG 6368  
QY 696 PheAlaGlnCysValLysAsn-----Glu 703  
DB 6367 GAAGCAGAAACAACTGCCAATGTCTACAGAGCGCTTCCCGTAAGGAGAGCTCTCTAGAA 6308  
QY 704 ArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAsp 723  
DB 6307 GACTCCAGGGAGTCCAGAGAGCTGATGAACCACTGCAAGATCTCCAAGGAGAAATTTGAA 6248  
QY 724 -----GlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740  
DB 6247 ACTCACACAGATATCTATCACAACTTTGTATGAATAATGGCCAAATAATCTGAGATCCCTG 6188  
QY 741 GlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThr 760

Db 6187 GAAGGTCGATGAAGACCCCTGTTACAAAGACGTTTGGATACATGAATTTCAAGTGG 6128  
QY 761 Ser-----ValLysLysPheGlnAsnGlnGlnAsnLysValLleSerLysArgAsn 778  
Db 6127 AGTGAACCTCAGAAAGAGTCTCTCAACATTAGGTGCTCCCATTTGGAAAGCAAGTTCTGACAG 6068  
QY 779 SerGluLeuThrValGluLysGluGlu 788  
Db 6067 TGGAGCGTTTGATCTCTTCTTCAGGAA 6038  
RESULT 3  
US-08-976-255-5  
; Sequence 5, Application US/08976255  
; Patent No. 6136581  
; GENERAL INFORMATION:  
; APPLICANT: Jono, Keith E.  
; APPLICANT: Plowman, Gregory  
; TITLE OF INVENTION: KINASE GENES AND USES  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/976.255  
; FILING DATE: No. 6136581ember 21, 1997  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 60/031,675  
; FILING DATE: No. 6136581ember 22, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 229/182  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 982 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-976-255-5  
Alignment Scores:  
Pred. No.: 0.000616 Length: 8982  
Score: 146.00 Matches: 175  
Percent Similarity: 32.72% Conservative: 109  
Best Local Similarity: 20.16% Mismatches: 302  
Query Match: 3.55% Indels: 283  
DB: 3 Gaps: 38  
US-10-007-270-2 (1-797) x US-08-976-255-5 (1-8982)  
QY 40 ProArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArg 59  
Db 2203 CCCTTCACATATATTATGATGTGGACAAATCGAGATTGGCCAGTCCACCAAAA 2262  
QY 60 IlePheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLys 79  
Db 2263 ATATTCGACTTAATGGAATTAACGGAGTTCAACGGCGACTTTAAACCTGCCACTTTAAGT 2322

QY 80 ValCys-----ProGlnGluSerMetLysGlnLleLeuAspSerLeuGlnAlaTyr 96  
Db 2323 TCCAGTTGGATAAACCCCAAGAGTCAGTC----- 2352  
QY 97 TyrArgLeuArgValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArg 116  
Db 2352 ----- 2352  
QY 117 IleProAspThrGlyGluTyrGlnAspTrpVal-----SerIleCysGlnGlnGluThr 134  
Db 2353 -----ATAACAGGCCACTTTTGAGAAAGAAAAGCCCGCTAAGATTTTTCACAGTCAGCCT 2406  
QY 135 PheCysLeuPheAsp----- 139  
Db 2407 CTCCTGCCTATCAGATAATCTTATGACCACCAAGATAATTTTGTATTCATTGATGTTCAAGAA 2466  
QY 140 IleGlyLysAsnPhe-----SerAsnSer 147  
Db 2467 TTGTCAGAAAACCTTTTATTTCTTCAAGAGAAAACCTTACTTAAAGGGCTCATTTGTCACG 2526  
QY 148 GlnGluHisLeuAspLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
Db 2527 AAAGAACACATAAATGATCTTCAGACAGAACTTAAGATGCTGTTTACTGAGAGCTATG 2586  
QY 168 AspGluIleSerAlaGluLysThrLeu-----GlyGluPro 179  
Db 2587 TTAGAAACGTCATGTAGAAACTCTTTAGACTACTGAGCTTCAGTTTGTGTAATAAGCA 2646  
QY 180 GlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeu 199  
Db 2647 GGC-----TTGCTCTTGTTCAGGAAAACGTAAGC-----ACA 2679  
QY 200 ThrProAspAspThr-----LeuLeuAsnGluIleLeuAspAsnThrLeuAsn--- 215  
Db 2680 AAGGTGACGATACAGATGCTGCTACAGTGACACTTTGAGCACCTCATTCAGTCT 2739  
QY 216 -----AspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGluGlu 233  
Db 2740 TCCCGGAAGTGCAGGTACCTCTTACCTCTTCTGAAACAGAAAGAACCCCGCTCGGTA 2799  
QY 234 GlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAsp 253  
Db 2800 CCCCAGACTCACTCCCAACACAGGAGAAACCCAGCCCGCTGTTAGATGTTATTGTC 2859  
QY 254 SerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIle 273  
Db 2860 CCGGAGGACTCTTCCACAGGACATCAGTCCACAGCTGTGACTGTCCCGTTGAAAT 2919  
QY 274 PheLysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysGlu 293  
Db 2920 -----CTCTCAACTGATGCCAGAACCCACAGCCTGGATAACAGG---TCCAGAGAC 2967  
QY 294 LysAspGlySerSerThrThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAla 313  
Db 2968 TCTCTCGGAGAGTGAGGAGACCTCGGACTCAC-----GAAAGTACTCTGTT 3018  
QY 314 GluAlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGlu---Ser 332  
Db 3019 CTGTGTGATGATCATCTTCCAGCAGGCTGAGTGTAGGAGTAGTCTCCCGGAACCTGGA 3078  
QY 333 GluGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAla 352  
Db 3079 CAGGAATTCACATAAACCAATTTTCGAGAGACCATCATCAGTCTAT----- 3123  
QY 353 ThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGly 372  
Db 3124 -----CCCGCGCTAGAGAAAACCTTAGAGCTGTGGAGACTTTAAATCAGCTC 3171  
QY 373 ThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGln 392  
Db 3172 AATTCTAAGACGACGAAAGAACAGCGGCTTGTGTCTGCTCTCTCTCTCGGACTCA--- 3228

393 SerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu 412  
3229 -----ACCGTACGAGACGCTCTCGGAGGAC---AGCTTGTACGACCCCTTC 3273  
413 ProProValGluProGlnLeuGluThrValAspGlyAlaGlu----- 426  
3274 CCAGCTCTGAGCCGCTCCCTGGAACCCCGGACTCTCTGAGTCAAGTGGATGCCAGAA 3333  
426 ----- 426  
3334 GCGCTACTGGACTCTTTAGGATCTCACACTCCCAAGAACTAGTCCCGCCGATAAGCG 3393  
427 -----HisGlyLeuProAspThrSerTrpSer---ProProAla 438  
3394 GCAGACAGTGGCTACGAACACAGACACTTGGAGTCTCCGAGTGGACCTTCATCCCGCT 3453  
439 MetAlaSerThrSerLeuSerGlu-AlaProProPhePheMetAlaSerIlePheSe 458  
3454 CCGAGGGCAGCCGAGACTCAGAACCCAGCCAGCGGCGATGGCGCCACAGCGGTCTG 3513  
458 rLeuThrAspGlnGlyThr----- 464  
3514 CTCCCAACCCGCTCATGTCTCATCTCAGATCCGCGGATGTCACAGAGGCACAGAAGTG 3573  
465 -----ThrAspThrMetAlaThrAspGlu 472  
3574 ACCCTGAGACGTTACAGCTGGCTCCAGGGTTCATACCGAGACTCTCGCTACTCTCA 3633  
472 nThrMet---LeuValProGlyLeuThrIleProThrSerAspThrSerAlaIleSerGlu 491  
3634 GACAATGACTCTGAGCCCGAGAAAGGTCTGAGGAGGTCCCGGGA-ACCTCCCATCCG 3692  
491 nLeuAlaLeuGlyIleSerHisPro-----ProAla 501  
3693 CTGTGTGTGTACAGAGCAGCCCTACCCGAGCAGTCTCCCGGCAAGTCTCTGC 3752  
501 aserSerAsp-----AspSerArgSerSerAlaGlyGluAspMetValArgHi 518  
3753 TCCCGAGATAGTCTCCGGAAGCCAGAAAGCCAGCCAGCAGATGAAAGTTCTGTCTGC 3812  
518 sLeu-----AspGluMetAspLeuSerAspThrProAlaProSerGlu-----Va 533  
3813 TTTCACAACTCCATGACCTGGATTAAGACCCAGCCGCGGAGCCAGCAGACTGTGT 3872  
533 ProGlu-----LeuSerGlu 538  
3873 TCCCGAGGAGTGCATCCCGAGAGACAGGAGCAGCAGTCTCCGAGTGTGCTGAATGC 3932  
538 uThrValSerValProAspHisPhe---LeuGluAspThrThrProValSer----- 554  
3933 AGAATTTAGCGCGGATGACTTCGAGACAGCAGCAGTCCGCTCCCTGACCTCGCTTC 3992  
555 -----AlaLeuGlnTrpIleThr----- 561  
3993 CACGGGGACCAACAGCAAGTCTCTTGCCTACACCAATTCGCTGGAGCAAGTCCCT 4052  
562 SerSerMetThrIleAlaProLysGlyArgGluLeuVal-----PhePh 577  
4033 GTCCAGCCACTCCGAGGCGCCGAGTTGAAGAGCCGAGCAGTCAAGAGGAAGTACCTGGG 4112  
577 eSerLeuArgValAlaAsnMetAla---PheSerAsnAsp----- 589  
4113 GAACTCGGGGTTCAGGGATGCTCGACTCTCAGAGGACGGGATGGATGCAGACGAGGA 4172  
590 -----LeuPheAsnLysSerSerLeuGlu 597  
4173 GGACGAAACACGACGACTCGGACGAGGACCTCGGGCCCTCAACCTGCATACCTCAG 4232  
597 uThrArgAlaLeuGluGlnPheThrGlnLeuValProThrLeuArgSerAsnLe 617  
4233 CTCCGAGTGGAGGAGGAG-----ACCAGACCCCGTGCCTCATCTCCTCAGCAAGA 4286  
617 uThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSe 637

4287 GGACGAGGACCACTCGCGAGTCTGTGAAG----- 4317  
637 rLysMetLysPheAlaLysSerValProThrAsnLeuThrLysAlaValHisGlyValle 657  
4318 -----CCACAGCGGCAATGCCCGACCACTGCC----- 4350  
657 uGluAspPhe---ArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSerTrpSe 676  
4351 -GAGGACTCGAAGAGGAAAGAGGACGTCAGCTTTTCGATGATGTCCACAGTCTACCT 4409  
676 rLeuAsnIleGlu---ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyG1 695  
4410 GTTTCACGAGGAGACCCCAACCAAGAGCTGGGGCCCTGTGAGGAGGAGCGCTGCGGCC 4469  
695 u-----PheAlaGlnCysValLysAs 702  
4470 GGACCTGAGCGGCCAGCCCGCTCAGGCTCTCCCTACTGAGCAGGTGATCACTCACTC 4529  
702 nGluArgThrGluGluAlaGlu 709  
4530 CGAAGCTCCACGAGCAAGAA 4551  
RESULT 4  
US-08-479-537A-1  
; Sequence 1, Application US/08479537A  
; Patent No. 5861381  
; GENERAL INFORMATION:  
; APPLICANT: CHAMBER, Pierre  
; APPLICANT: KIENY, Marie-Paule  
; APPLICANT: LATHE, Richard  
; APPLICANT: HAREUVENI, Mara  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE  
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22131-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,537A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 90/13101  
; FILING DATE: 23-OCT-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR91/00835  
; FILING DATE: 23-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/039,320  
; FILING DATE: 04-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/403,576  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 017753-025  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6192 base pairs



```

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 58..120
FEATURE:
NAME/KEY: repeat_region
LOCATION: 439..5239
OTHER INFORMATION: /note= "The nucleotides spanning
OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
OTHER INFORMATION: The number of such repeats varies from 1 to 80."
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 121..6166
FEATURE:
NAME/KEY: repeat_region
LOCATION: 457
OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
FEATURE:
NAME/KEY: repeat_region
LOCATION: 487
OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
FEATURE:
NAME/KEY: repeat_region
LOCATION: 496
OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-08-479-537A-1

Alignment Scores:
Pred. No.: 0.000361 Length: 6192
Score: 145.50 Matches: 74
Percent Similarity: 38.11% Conservative: 51
Best Local Similarity: 22.56% Mismatches: 144
Query Match: 3.53% Indels: 59
DB: 2 Gaps: 13

US-10-007-270-2 (1-797) x US-08-479-537A-1 (1-6192)
Qy 389 ProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeu 408
Db 4921 CCGGACNNAGG---CCGNNCCGGGTCCACCGCCCNNGCCCGGTCACCTCG 4977
Qy 409 SerProGluLeuProPro-----ValGluProGlnLeuGluThrValAspGly 424
Db 4978 GCCCGGACNNAGGCGGNNCCGGGTCCACCGCCCNNGCCCGGTCACCTCG 5037
Qy 425 AlaGluHisGlyLeuProAspThr---SerTrpSerProAlaMetAlaSerThrSer 443
Db 5038 GCCCGGACNNAGGCGGNNCCGGGTCCACCGCCCNNGCCCGGTCACCTCG 5097
Qy 444 LeuSerGluAlaProProPheMetAlaSerSerIlePheSerLeuThrAspGlnGly 463
Db 5098 GCCCGGACNNAGGCGG---NNNCCGGG 5124
Qy 464 ThrThrAspThrMetAlaThrAspGlnThrMetLeu-----ValProGly 478
Db 5125 TCCACCGCCCNNGCCCGGTCACCTCGGCGCCGACNNAGGCGGNNCCGGG 5184
Qy 479 LeuThrIleProThrSer-----AspTyrSerAlaIleSerGlnLeuAlaLeuGly 495
Db 5185 TCCACCGCCCNNGCCCGGTCACCTCGGCGGACNNAGGCGGNNCCGGG 5244
Qy 496 IleSerHisProPro-----AlaSerSerAspAspSerArgSerArgAlaGlyGly 512
Db 5185 TCCACCGCCCNNGCCCGGTCACCTCGGCGGACNNAGGCGGNNCCGGG 5244

```

```

Db 5245 TCCACCGCCCNNGCCCGGTCACCTCGGCGGTCACCTCGGCGGTCACCTCGGCGGTCAGCT 5304
Qy 513 GluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSerGlu 532
Db 5305 TCTACTCTGTGTGCACAAACCGGCTCTGCGAGGGTACCACAAACCGGAGAGG 5364
Qy 533 ValProGluLeuSerGluThrValSerValProAspHisPheLeuGluAspThrThrPro 552
Db 5365 ACTCCACCC-----AGCATTCACGACCACTCTCTGATGATCTCTTCTTTTC 5409
Qy 553 Val-----SerAlaLeuGlnTyr 558
Db 5410 CTGCGCAGCATAGCACCAGACTGATGCGAGTACCTACCTACCATAGCAGGTACCTCT 5469
Qy 559 IleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePhe--- 577
Db 5470 CTCACCTCTCAATCACGACCTCTCTCCCGAGTTGTCTACTGGGGTCTCTTTCTTTTC 5529
Qy 578 ---SerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeu 596
Db 5530 CTGCTCTTTTTCACATTTCAAACCTCCAGTTTAATCTCTCTGGAAGATCCGACCGAC 5589
Qy 597 GluTyrArgAlaLeuGluGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsn 616
Db 5590 TACTACCAAGAGCTGCAGAGACATTTCTGAATGTTTTTGCAGATTTATAACAAGGG 5649
Qy 617 LeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsn 636
Db 5650 -----GGTTTTCTGGGCTCTCCAAATTAAGTTCAGCCAGAAATCTGTGTGTGTACNA 5703
Qy 637 SerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyVal 656
Db 5704 TTGACTCTGGCCTTCGAGAGGT-----ACCATCAATGTCCACGACGTG 5748
Qy 657 -----LeuGluAspPheArgSerAlaAlaGlnGlnLeuHisLeuGluLeuAsp 673
Db 5749 GAGACACAGCTTCAATCAGTATAAAAGGAGCGCTCTCGATATACCTGACGATCTCA 5808
Qy 674 SerTyrSerLeuAsnIleGluPro 681
Db 5809 GACGTCAGCGTGAGTCATGTGCCA 5832

RESULT 5
US-09-083-116-1
; Sequence 1, Application US/09083116
; Patent No. 6203795
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENT, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083.116
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,537
; FILING DATE:

```

PRIOR APPLICATION DATA: WO PCT/FR91/00835  
APPLICATION NUMBER: WO PCT/FR91/00835  
FILING DATE: 23-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/039,320  
FILING DATE: 04-APR-1993  
PRIOR APPLICATION DATA: US 08/403,576  
APPLICATION NUMBER: US 08/403,576  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 017753-025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 1:

Alignment Scores:		
Pred. No.:	0.000361	Length:
Score:	145.50	Matches:
Percent Similarity:	38.11%	Conservative:
Best Local Similarity:	22.56%	Mismatches:
Query Match:	3.53%	Indels:
DB:	3	Gaps:
		13
		6592

US-10-007-270-2 (1-797) x US-09-083-116-1 (1-6192)

389	ProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeu	408
	:::	
4921	CGGACNNAGG---CCGNNCCGGGTCCACGCCCCNNNGCCACGGGTCACTCG	4977
	:::	
409	SerProGluLeuProPro-----ValGluProGlnLeuGluThrValAspGly	424
	:::	
4978	GCCCGGACNNAGGCCGNNCCGGGTCCACGCCCCNNNGCCACGGGTCACTCG	5037
	:::	

Qy	425	AlaGluHisGlyLeuProAspThr	-----SerTyrSerProAlaMetAlaSerThrSer	443
Db	5038	GGCCCGGACNNNAGCGCGNNNCGGGCTCCACGGCCCCNNNGCCACCGGTGTCACTCTCG	5097	
Qy	444	LeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGly	463	
Db	5098	GGCCCGGACNNNAGCGCG	5124	
Qy	464	ThrThrAspThrMetAlaThrAspGlnThrMetLeu	-----ValProGly	478
Db	5125	TCCACCGCGCCNNNCGCCACCGGTGTCACTCGGCCCGCGGACNNNAGCGCGNNNCGGGC	5184	
Qy	479	LeuThrIleProThrSer	-----AspTyrSerAlaIleSerGlnLeuAlaLeuGly	495
Db	5185	TCCACCGCGCCNNNCGCCACCGGTGTCACTCGGCCCGCGGACNNNAGCGCGNNNTGGGC	5244	
Qy	496	IleSerHisProPro	-----AlaSerSerAspSerAspSerSerAlaGlyGly	512
Db	5245	TCCACCGCGCCCTCCAGTCACCAATGTCACTCGGCCCTCAGGTCTCTCATCAGCTCAGCT	5304	
Qy	513	GluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSerGlu	532	
Db	5305	TCTACTCTGGTGACACACCGGACCTCTGCAGGGCTACACACCCACCCACGACAGAGC	5364	
Qy	533	ValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThrPro	552	
Db	5365	ACTCCACCC	-----AGCATTCGCACGCCACTCTCTGATACTCTCACTCACC	5409
Qy	553	Val	-----SerAlaLeuGlnTyr	558
Db	5410	CTTGCAGCGCATAGCACCAAGACTGATGCCAGTAGCACTCACCATAGCAGGTACCTCT	5469	
Qy	559	IleThrThrSerSerMetThrIleAlaProGlyGlyArgGluLeuValValPhePhe	577	
Db	5470	CTCACCTCTCCAAATCACAGCACTTCTCCGCCAGTTGTCTACTGGGTCTCTTTCTTTTTC	5529	
Qy	578	---SerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeu	596	
Db	5530	CTGCTCTTTTCACATTTCAACCTCCAGTTTAATCTCTCTGGAAGATCCGACCCGAC	5589	
Qy	597	GluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsn	616	
Db	5590	TACTACCAAGAGCTGCAGAGAGACATTTCTGAAATGTTTTTCGAGAATTAATAACAAGGG	5649	
Qy	617	LeuThrGlyPheLysGlnLeuGluLeuLeuAsnPheArgAsnGlySerValIleValAsn	636	
Db	5650	-----GGTTTTCTGGGCTCTCCAAATATAGTTCAGGCCAGAAATCTGTGGTGGTACAA	5703	
Qy	637	SerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyVal	656	
Db	5704	TTGACTCTGGCTCTCCGAGAAGT	-----ACCATCAATCTCCACGACGTG	5748
Qy	657	-----LeuGluAspPheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAsp	673	
Db	5749	GAGACACAGTTCATCAGTATATAACGGGAAGCAGCGCTCTCGATATAACCTGACGATCTCA	5808	
Qy	674	SerTyrSerLeuAsnIleGluPro	681	
Db	5809	GACGTGACGGTGAGTCATGTGCCA	5832	

RESULT 6  
 US-09-134-916A-1  
 ; Sequence 1, Application US/09134916A  
 ; Patent No. 6328956  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHAMON, Pierre  
 ; APPLICANT: KIENY, Marie-Paule  
 ; APPLICANT: LAYE, Richard  
 ; APPLICANT: HAREUVENI, Mara  
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE  
 ; TREATMENT OR PREVENTION OF A MALIGNANT TUMOR  
 ; NUMBER OF SEQUENCES: 5



```

QY 657 -----LeuGluAspPheArgSerAlaAlaGlnGlnLeuHisLeuGluLeuLeu 673
Db 5749 GAGACACAGTTCATCAGTATAAACGGAAGCAGCGCTCTCGATATAACCTGACGATCTCA 5808
QY 674 SerTyrSerLeuAsnIleGluPro 681
Db 5809 GACGTCAGCGTGAGTCATGTGCCA 5832

RESULT 7
5180808-1
; Patient No. 5180808
; APPLICANT: RUOSLAHTI, ERKKI I.
; TITLE OF INVENTION: VERSICAN CORE PROTEIN, NUCLEIC ACID
; SEQUENCES ENCODING THE SAME, NUCLEIC ACID PROBES, ANTI-VERSICAN
; ANTIBODIES, AND METHODS OF DETECTING THE SAME
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/441,179
; FILING DATE: 27-NOV-1989
; SEQ ID NO.1:
; LENGTH: 8224
5180808-1

Alignment Scores:
Pred. No.: 0.000673 Length: 8224
Score: 145.00 Matches: 185
Percent Similarity: 31.30% Conservative: 128
Best Local Similarity: 18.50% Mismatches: 342
Query Match: 3.52% Indels: 346
DB: Gaps: 43

US-10-007-270-2 (1-797) x 5180808-1 (1-8224)

QY 40 ProArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArg 59
Db 4377 CCTCAAAATCAGACTCTCAGGTGGGAGGAATATC---CAGACTAGTAGACCAACACC 4433
QY 60 IlePheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLys 79
Db 4434 ATAACTGAACAAGACTCTAACAAGAATTCTTCAACAGCAGAAATT----- 4478
QY 80 ValCysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeu 99
Db 4479 -----AAGAAACAAACACCTCATCTAGTATTTCTGGCTAGAGCTTATGTTT 4529
QY 100 ArgValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAsp 119
Db 4530 GAAATGGCCAAAGAATTGTTATACATCAGCACCACAAACCATCTGACTTGTATTATGAACCT 4589
QY 120 ThrGlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAsp 139
Db 4590 TCTGGAGAAGGATCTGGAGAAGTG-----GAT 4616
QY 140 IleGlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLys 159
Db 4617 ATGTGTATTCATTT-----CACACTTCGCAACTACTCAGCAGCAACACAGA 4661
QY 160 GlnArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluPro 179
Db 4662 CAAGAAAGCAGCACCACCAATTTGTTCTGATGGTCCCTGGAAACATCCTCAGGTGCCA 4721
QY 180 GlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeu 199
Db 4722 AGCGTAAAGCTGTTACTCTGATGGATTCCTCAACAGATTTTCAGTG---ATGCTGCCTCTT 4778
QY 200 -----ThrProAspAspThrLeuLeuAsn----- 207
Db 4779 CATTCAAGCAGACAAAGACTCCCTGATCCAACTAGCACACTCTCAATACAGTGTC 4838
QY 208 -----GluIleLeuAspAsnThr 213
Db 4839 TATGAGAGGTCACAGACGGTAGTTTCCAGACCGGTTTTCAGGGGATTCGAGGATTCACCC 4898

```

```

QY 214 LeuAsnAspThrLysMetProThrThrGlu----- 223
Db 4899 TTAACCTAACAGAAAAAACCCACTCTGAAAATATTATCATAGACCTGGCAAGAGGAC 4958
QY 224 ArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSerValSerLeuVal 243
Db 4959 AAGGATTTAATATTGACAATTACAGAGAGTACCATTCTTGAAATTTACCTGAGCTGACA 5018
QY 244 AsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAla 263
Db 5019 TCGGATAAAAAATACTATCATAGATATTGATCATATAACCTGTGATGAAGACATTTCT 5078
QY 264 GlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIle 283
Db 5079 GGA-----ATGCAACACAGATATAGATACAGAGGTACCATCA----- 5114
QY 284 HisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSerThrGluMetGln 303
Db 5115 -----GAACCCACATGACAGTAATGATGAAAGTAATGATGACAGCAGCTCAA 5159
QY 304 LeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeuLeu 323
Db 5160 GTTCAAGAGATCTATGAG-----GCAGCTGTCAACCTT 5192
QY 324 SerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThrMetGluGluAsp 343
Db 5193 TCTTTA-----ACTGAGGAACATTTTGAGGGCTCT----- 5222
QY 344 LysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuLysSerLysAlaLeu 363
Db 5223 -----GCTGATGTTCTGCTAGCTACACTCAGGCACACATGATGAATCAATGACTTAT 5276
QY 364 GluGluGlnGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySer 383
Db 5277 GAAGATGAGAGCCCACTAGATCATCATGGGCTTTCACTTCCAACT-----GGG 5324
QY 384 LeuProAlaPheGlyProAspThrGlnSerGluLeu-----ProThr 397
Db 5325 ATCCCTGCT-----CCTAGCACAGAAACAGAAATTAGACGTTTTACTTCCACGGCAACA 5378
QY 398 SerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProValGluPro 417
Db 5379 TCCTCGCAATTCCTCGTAAGCTCGCCACAGTTATTCAGAGATTGGAAGATAAAGCT 5438
QY 418 GlnLeuGluThrValAsp----- 423
Db 5439 GAAGCAAAAGCCCTGATGACATGTTTGAATCAAGCACCTTTGCTGATGTCAGCTATT 5498
QY 423 ----- 423
Db 5499 GCAGACCAAGTGAAATAATAACCAATTGGGCCAATTTGAAAGGACTCAGGAGGAGTAT 5558
QY 424 -----GlyAlaGluHis 427
Db 5559 GAAGACAAAAACATGCTGCTCTCTTTTCAGCCAGAAATTCCTTCAGAGCTGAGGAG 5618
QY 428 GlyLeu-----ProAspThrSerTrpSerProAlaMetAlaSerThrSer 443
Db 5619 GCATTAGTAGACCATCTCCCTATCTAAGTATTGCTACTACCCACCTTATGGATCAGACT 5678
QY 444 LeuSerGluAla-----ProProPhePhe----- 451
Db 5679 GTAAACAGAGTGCTGATGTGATGGAGGATGCAATCCCCCATATTACTGATACACAA 5738
QY 452 MetAlaSerSerIlePheSerLeuThrAspGlnGlyThrAspThrMetAlaThr----- 470
Db 5739 TTAGCAGTTTCAACATTTGCGAAGTTGTTCTTCTCAGACACCATCATCTCCCTCATCATC 5798
QY 471 -----AspGlnThrMetLeuValProGly 478
Db 5799 TACTCAGGCAAGTGAAGCCTCTGGACACACAGAGATCCCCCAGCCAGCTCTCTGCGAGGA 5858

```

```
QY 479 LeuThrIleProThrSer----- 484
Db 5859 ATAGACCTGGCTCATCTTAATGTCACAGGATTTCTTTAAGGAAATTCATGTAAT 5918
QY 485 -----AspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProAla 501
Db 5919 ATTGAAGCACTTTCACACCATCAAGTGAAGAAATACCTTCACATACCTGACCTCCCTCT 5978
QY 502 SerSerAspSerArgSerSerAlaGlyGlyLeuAsp---MetValArgHisLeuAsp 520
Db 5979 TTATCTCTCTGACACAAATTAAGAACCTTCAGAAGATGATGTAACCTGAGTTATTAGAA 6038
QY 521 GluMetAspLeuSerAspThrProAla----- 529
Db 6039 GAATGGAGCTTCTCCACAGACTTATTCCTGTGGAGGAAGTGAATCTCCAAGAT 6098
QY 530 -----ProSer--- 531
Db 6099 TTCACAAACAAACCGATGTCAGTTCTCGAGAGCAATCAAGATGTTCCACCAT 6158
QY 532 GluValProGluLeuSerGluTyrValSerValProAspHisPhe---LeuGluAspThr 550
Db 6159 AAACACCTGAGCTGGAACCTGTTATTACAACTCCGATGGAATGAATTAGAGTGCT 6218
QY 551 Thr----- 551
Db 6219 ACACAGTGGCCACACTCTACTCTCTCTCCACCTATGGGTCGAGGAGGTGGTG 6278
QY 552 -----ProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567
Db 6279 CTTGGCTAAGTCCACAGACTTTCGAGAGCGCCACGCTTCTCTCTCCAGAAATAAC 6338
QY 568 Pro-----LysGlyArgGluLeuValValPhePheSerLeuArg 580
Db 6339 CCTGAACTCAAGCAGCTTTAATCAGAGCGGAGATTCACGATAGCAGCATCAGAAC 6398
QY 581 -----ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerLeuGluTyr 598
Db 6399 CAAGTGGCAGCGAGAACTTCTGATTCATGATCAGGCAACAGTAACCTGTGGAATT 6458
QY 599 ArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThr 618
Db 6459 AAT-----ACTGAGGTGCAACACACCATTTTCCCTTCTGGAGACT 6500
QY 619 Gly-PhelysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLys 638
Db 6501 TCTAATGAACAGATTCTCTGATTG-----GCATTAATGAAGAGTCA 6542
QY 638 sMetLysPheAlaLysSerValProTyrAsnLeu-----ThrLysAlaVal 653
Db 6543 GTGGAAGGCACGGCAATCTATTACAGGACCTGATCGCTGCAAAATGAAACCGTGCCT 6602
QY 653 lHisGlyValLeuGluAspPheArgSerAlaAlaAlaGlnGlnLeuHisLeuGluLeAs 673
Db 6603 A-----ACGAGGCACCTGTTATCTCTACTGAACTTCC 6635
QY 673 pSerTyrSerLeuAsnIleGlu-----ProAlaAspGlnAla-----AspPr 687
Db 6636 TACGTATGCACC-TGTGTGCAGGATACACGCGAGACCACTGTGAACTTGATTTGATGA 6694
QY 687 oCysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGl 707
Db 6695 ATGTCACCTAATCCCTGTCGTAAATGAGGACCACTGTGTGATGGTTTTAACACA----- 6749
QY 707 uAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPr 727
Db 6750 -TTCAGGTGCTCTGCTCTCCAGTTATGTTGT----- 6782
QY 727 oGlyLeuCysGlyProGlyThrLysGluCysGluVal-----LeuGlnGlyLys 743
Db 6783 -GCACCTTGTGACAGATACCGAGACATGTGACTATGCTGCTGCGCACAAATTCAGAGGCA 6841
QY 743 s-----GlyAlaProCysArgLeuProAspHisSerGluAsnGln----- 756
```

```
Db 6842 GTGCTACAAATACTTTTGGCCCATCGACGACATGGGATGCGAGTGAACGGGAATGCCGTCT 6901
QY 757 -----AlaTyrLysThrSerValLysLysPheGlnAsnGlnGln----- 769
Db 6902 GCAGGTGCCCCATCTCACAAGCATCTCTGCTCACCAGAAACAATGTTTGTAAATCGTGT 6961
QY 770 -----AsnAsnLysValIleSerLys-----ArgAs 778
Db 6962 GGCCCATGATTATCAGTGGATAGGCTCAATCACAAGATGTTTGGACATGACTTCGGTTG 7021
QY 778 nSerGluLeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTyrGluGlyAsn 797
Db 7022 GACTGATGGCAGCACACTGCAATACGAG-----AATTGGAGACCCCAAC 7064

RESULT 8
US-09-418-780A-2
; Sequence 2, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/J998/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3104
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(2946)
US-09-418-780A-2

Alignment Scores:
Pred. No.: 0.000136 Length: 3104
Score: 144.50 Matches: 150
Percent Similarity: 34.23% Conservative: 116
Best Local Similarity: 19.31% Mismatches: 321
Query Match: 3.51% Indels: 191
DB: 4 Gaps: 32

US-10-007-270-2 (1-797) x US-09-418-780A-2 (1-3104)
QY 16 LeuGlnValGlnGlyThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAsp 35
Db 764 CTGCACCTTCAGCAGTTAAGCAAGTAGTAGTAATTTCTCCACATTCACAGAA-AAATCA 822
QY 36 Ile-----AspAsnProProArgAsn----- 42
Db 823 GTGGCAGCTGCCACCTATAAAGAAATAATATGCAAGAAATGTTTCCAGATTCACAGAA 882
QY 43 -----GluThrThrGluSerThrGluLysMetTyrLysMetSerThrMet 57
Db 883 CAATATAATGTTGGAGACTGTTAAAGTAACCTGAACAATTAAGGCACCTGTAGTGAGATT 942
QY 58 ArgArgIlePheAspLeuAlaLysHisArgThrLysArgSerAlaPhePhe---ProThr 76
Db 943 CTTAAAGAAATGCTTGCAGAGAAACATTTTCATATGCATGCGCCCTTTATATCCTGTT 1002
QY 77 GlyValLysValCysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyr 96
Db 1003 GACCTTAATGCTTTG-----GGACTCCATAACTACTATGACGTTGTCAAAATCCG 1053
QY 97 TyrArgLeuArgValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArg 116
Db 1054 ATGATCTTGGAACTATTAGGAGAAATG----- 1093
```

QY 117 IleProAspThrGlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCys 136  
Db 1084 -----GATAACCAAGAAATATAGGATGCATCTATTGGGCA----- 1122  
QY 137 LeuPheAspIleGlyLysAsnPheSerAnSerGlnGluHisLeuAspLeuGlnGln 156  
Db 1123 -----GATGTAGATTATGTTCTGATGCTCAAGTAC----- 1158  
QY 157 ArgIleLysGlnArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeu 176  
Db 1159 -----AATCCTCCAGATCAGGAAGTGTGCACAATGGCAAGAATGCTT 1200  
QY 177 GlyGluProGlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyPro 196  
Db 1201 CAGGAT-----GTTTTCGAACGCAATTTTCAAGATCCCGAATGAACCT 1245  
QY 197 PheProLeuThrProAspAspThrLeuAsnGlnLysPheLysAlaGluLeuAlaAspSer 216  
Db 1246 GTTGAGAGATGCTTTATGTTTACATCAAAACAGATATACAGAAACCACTGGTAGAG 1305  
QY 217 ThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgVal 236  
Db 1306 AACACTAATGAAGCTCTCTGAGGGAACCTTCTGATGATTTCTGAGATGAGCGAGTT 1365  
QY 237 GluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSer 256  
Db 1366 -----AAGCGTCTTGCAAGCTTCAGGACAGCTTAAA 1398  
QY 257 ProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLys 276  
Db 1399 GCTGTACATCAACAGCTCCAGCTTTGTCCCAAGTACCTTTCCCTGAAGCTAAATAAAG 1458  
QY 277 LeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGly 296  
Db 1459 AAAGAGAGTCTAAAG-----GAAAGAAAAAGAAAGGTTAAT 1500  
QY 297 SerSerSer-----ThrGluMetGlnLeuThrAlaIlePheLys 309  
Db 1501 AACAGCAATGAAATCCCAAGAAAAATGTGTGAGCAATGAGGCTAAAGAAAAAGTCCAAG 1560  
QY 310 ArgHisSerAlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLys 329  
Db 1561 AGAAAT-----CAGCCAAAGAAAGAAAGAAACAACAGTTTCATTGTT----- 1599  
QY 330 IleGluSerGluGluValIleHisGlyThrMetGluGluAspLysGlnProGluIleTyr 349  
Db 1600 CTAAATCTGAAGAT-----GAGATATGCTAAACCTATGAACAT 1641  
QY 350 LeuThrAlaThrAspLeuLysArgLeuLysSerLysAlaLeuGluGluGlnSerLeu 369  
Db 1642 -----GATGAGAAAGGAGTAAAGTCTGATATATAAACAACCTCCCTGGAGAT 1689  
QY 370 AspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyPro 389  
Db 1690 AAACCTGGCGAGTA-----GTTACATATATACATCAAGAGAGCCTCTCTGAGCAAT 1743  
QY 390 AspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSer 409  
Db 1744 TCCAAATCTGTGATGATAGATAGACTTTGAAACACTG-----AAAGCATCAACACTAAGA 1800  
QY 410 ProGluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeu 429  
Db 1801 -----GAATTAGAAAAATATGTTTCGGCA-----TGCTTA 1830  
QY 430 ProAspThrSerTrpSerProAla-----MetAlaSerThrSerLeuSer 445  
Db 1831 AGAAAGAGACCACTTAAACCTCTCTGCTAAGAAAAATATGATGTCCAAAGAGAACTTCAAC 1890  
QY 446 GluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThr 455  
Db 1891 TCACAGAAAAACAGGAATTGAAAGCGGTACTGATGTTAATATACATGTTAAATCT 1950

QY 466 AspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro---ThrSer 484  
Db 1951 AGAAAAACGTCACAAAAATCTGATAAAACGCAACATCCAAAGCTGTGAAATGTTTCC 2010  
QY 485 AspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerAsp 504  
Db 2011 CGACTGAGTGAGCAGCAGCAGCAGCAGCAGCTCATCAGAGTCTGAAAGTACGAGCAGT 2070  
QY 505 Asp-----SerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGlu 521  
Db 2071 GACTTAAGCTCTTCACAGCAGCTGATTCTGAATCAGAAATGTTCCCTAAGTTTACAGAA 2130  
QY 522 MetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrValSer 541  
Db 2131 GTAAAAACCAATGATTCTCTTCTTAAGAGCATGTAAGAAAAATGAAGAAATGAATGCATA 2190  
QY 542 ValProAsp-----HisPheLeuGluAspThrThrPro 552  
Db 2191 CTGCTTGAAGGAAGAACAGCGCTCACAGATAGGATATTGTGCAAGACACACCTCT 2250  
QY 553 Val---SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArg 571  
Db 2251 GCCAATPACTACCTTGTTCATCAGACCCACACCTTCCATGTAATGCCACCAATCACCAC 2310  
QY 572 GluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe 591  
Db 2311 CAATTAGCA-----TTT 2322  
QY 592 AsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThr-----GlnLeuLeu 609  
Db 2323 AATTATCAAGAAATTAAGACATTTACAGACTGTGAAAAACATTTACCTTTACAAATTCG 2382  
QY 610 ValPro-----TyrLeuArgSerAsnLeuThrGlyPhe----- 620  
Db 2383 CCTCCTCAGGTGATCTGAAACAGCTCTCAATGGCAATACCTGATGCATCCTCTGTT 2442  
QY 621 -----LysGlnLeuGlu 624  
Db 2443 GATAGTGACACCAACGATGTTAGAACTGTAATGCAAGCTCTCTGACAGAGGATATAAG 2502  
QY 625 IleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSer 644  
Db 2503 ATTAAGAAAT-----GCAGATTTCATGGAAAAAGTTTAGGCAACCA 2541  
QY 645 Val---ProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAla 663  
Db 2542 GTGAAACCATCAGGTGTAATGAATCCCTCAGATGAGCTTTCACCAATTTAGAAAAGCA 2601  
QY 664 Ala-----AlaGlnGlnLeu-----HisLeuGluIle 672  
Db 2602 GCATAGAAAAAGGAAGTAAAGCTCGGACACAGGAACCTCATACGGAAGCATTTGGAACAA 2661  
QY 673 AspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAla 692  
Db 2662 AATACAAAGAACTAAAGCATCTCAAGAAATCAGAGGATCTTTGGGAATGATGTTGACT 2721  
QY 693 CysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709  
Db 2722 GTAGAATCTTTTCAATAAATAAACAACAGTCTCTGGAGAGAGCAG 2772

## RESULT 9

US-09-392-714-4  
; Sequence 4, Application US/093927144

; Patent No. 6686147

; GENERAL INFORMATION:

; APPLICANT: Scanlan, Matthew J.

; APPLICANT: Gure, Ali O.

; APPLICANT: Williamson, Barbara

; APPLICANT: Chen, Yao-Tseng

; APPLICANT: Old, Lloyd J.

; TITLE OF INVENTION: Cancer Associated Antigens and Uses

; TITLE OF INVENTION: Therefor

; FILE REFERENCE: L0461/7062



QY	257	ProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLys	276
DB	1401	GCTGTACATCAACAGCTCCAGGTTTTGTCCCAAGTACCTTCGTAGCTPAATAAAAAG	1460
QY	277	LeuProGlyPheLysIleHisValLeuGlyPheArgProLysLysGlnLysAspGly	296
DB	1461	AAAGAGAAGTCTAAAAG-----GAAAGAAAAAAGAAAAAGGTTAAT	1502
QY	297	SerSerSer-----ThrGluMetGlnLeuThrAlaIlePheLys	309
DB	1503	AACAGCAATGAAATTCAGAAAAAATGTGTGACCAATGAGGCTAAAGGAAAAAGTCCAAG	1562
QY	310	ArgHisSerAlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLys	329
DB	1563	AGAAAT-----CAGCCAAAAGAAAGAAACACAGTTCATTGGT-----	1601
QY	330	IleGluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyr	349
DB	1602	CTAAATCTGAGAT-----GAAGATAATGCTAAACCTATGAACCTAT	1643
QY	350	LeuThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGluGlnSerLeu	369
DB	1644	-----GATGAGAAAGGCAGTTAAGTCTCAATATAAACAACTCCCTCGAGAT	1691
QY	370	AspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyPro	389
DB	1692	AAACTTGGCGGAGTA-----GTTACATAATACAAATCAAGAGAGCGTCTCTCGACCAAT	1745
QY	390	AspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSer	409
DB	1746	TCCAATCCTGATGAGATAGATAGATAGACTTTGAAACACTG--AAAGCATCAACACTAAGA	1802
QY	410	ProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeu	429
DB	1803	-----GAAATTAGAAAAAATATGTTTCGGCA-----TGTCTA	1832
QY	430	ProAspThrSerTyrSerProProAla-----MetAlaSerThrSerLeuSer	445
DB	1833	AGAAAGAGACCAATTAAACCTCTGCTAAGAAAATAAGTGTCCAAGAGAACAATTCAC	1892
QY	446	GluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThr	465
DB	1893	TCACAGAAAAAACAGCAATTGGAAAAGCGGTTACTGGATGTTAATAATCAGTTAAATTC	1952
QY	466	AspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro---ThrSer	484
DB	1953	AGAAAACGTCAACAAAAAATCTGATAAAACGCAACCATCCAAAGCTGTGAAAATGTTTCC	2012
QY	485	AspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAsp	504
DB	2013	CGACTGAGTGTAGAGCAGCAGCAGCAGCAGCTCATCAGAGCTCTGAAAGTAGCAGCAGT	2072
QY	505	Asp-----SerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGlu	521
DB	2073	GACTTAAGCTCTTCAGACAGCAGTGATTCTGAATCAGAAAATGTTCCCTTAAGTTACAGAA	2132
QY	522	MetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrValSer	541
DB	2133	GTAAAACCAATGATCTCCCTCTTAAAGAGCATGTAAAGAAAATGAAGAAATGAATGCATA	2192
QY	542	ValProAsp-----HisPheLeuGluAspThrThrPro	552
DB	2193	CTGCGCTGAAGGAAGAACAGGGCGTCACACAGATAGGATATTGTGTGCAAGACACACCTCT	2252
QY	553	Val---SerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArg	571
DB	2253	GCCAACTACCTGTTTCATCAGACCCACCTTCACATGTAATGCCACCAAAATCACCAC	2312
QY	572	GluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPhe	591
DB	2313	CAATTAGCA-----TTT	2324





```

/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/386,844
/ FILING DATE: 10-FEB-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CORUZZI, LAURA A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7853-041
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-8864
/ TELEFAX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6407 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: unknown
/ MOLECULE TYPE: cDNA
/ US-08-599-654-7

Alignment Scores:
Pred. No.: 0.00102 Length: 6407
Score: 141.50 Matches: 164
Percent Similarity: 31.91% Conservative: 105
Best local Similarity: 19.45% Mismatches: 356
Query Match: 3.44% Indels: 219
DB: 2 Gaps: 34

US-10-007-270-2 (1-797) x US-08-599-654-7 (1-6407)
QY 97 TyrArgLeuA-gvalCysGlnGlu-----AlaValTrpGluAlaTyArgIlePhe 113
DB 1275 TGGAGAACATCAGCTTGCACGAGCTCTGAGGTGCAAAATGGAAGTCCCATGTCTCAGAC 1334
QY 114 LeuAspArgIleProAspThrGlyGluTrpGlnAspTrpValSerIleCys----- 130
DB 1335 TGAGACTGTCTAGGTGAGTGCAGCCATGAGAGGTGGAGAGATCACTGACACTGGCT 1394
QY 131 -----GlnGlnGluThrPheCysLeuPheAspIleGlyIysAsn----- 143
DB 1395 CTTGACCAACAGACACACATCTGCAGATGTGACA--GGAAGCTGTGCTTCATATCCTGAA 1452
QY 144 -----PheSerAsnSerGlnGluHisLeuAspLeuLeu 154
DB 1453 GGTGTGAATGTTTCAAGTGTGACCCAGTCTCAGACTCTACTGTACAGTCTGGAGGAAGT 1512
QY 155 GlnGlnArgIleLysGlnArgSerPheProAspArgIysAspGluIleSerAlaGlu-- 173
DB 1513 CACACAGCATTTGGGAGATAGAGTATTTCAGAGTCTTCATCTACATCTTCTCGGAAGC 1572
QY 174 -----LysThrLeu-----GlyGluProGly 180
DB 1573 TTGAATTCATCAGCACCACTGGAGAGAGTTCAACCTTGAAGACAGCCGAGAGCCAGGC 1632
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
DB 1633 CAAGCACTAGTGTGACAGTTCGCCATGACAGAGCAGGAGTCTGGGGTCCCTCTCTC 1692
QY 201 ProAspAspThrLeuLeu-----AsnGluIleLeuAspAsnThr 213
DB 1693 GGCACCCACACCTTGGCTACTGTCTACTGTGAAACGGGGAACGCACACTGCGGTCTGTCA 1752
QY 214 LeuAsnAspThrLysMetProThrThrGlu----- 223
DB 1753 CTCACCAACACAGCATGACAGCACTCTCTGGGAAGCAGCAGCCCTGAGCGGGCCATG 1812
QY 224 ---ArgGluThrGluPheAlaValLeuGluGluGlnArgValGluLeuSerValSerLeu 242
DB 1813 CCCCAAGAAACAGAGGGTGCCTCTCTGCAC----- 1842
QY 243 ValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeu 262
DB 1812 AGCACCAACTTAGACAAATGTCTCCAACTTTCCAACTTTCACAACTTTCGAAGACCTCTCAG 2871

```

```

DB 1843 -----GTAAACGTGACGGAGACATGGGCGCTGGTCTCACGGTCACTG 1884
QY 263 AlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLys 282
DB 1885 GCGCGCTCCAGTGCACCTCGAGTCTGGGATT-----AGCTACGCTCAA 1929
QY 283 IleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSerThrGluMet 302
DB 1930 GTGCGTGGCACAGCTATTGAACAAAGAGCTTCAGGACCCACACAGACACACC----- 1983
QY 303 GlnLeuThrAlaIlePheLysArgHis-----SerAlaGluAlaLysSer 317
DB 1984 TACCTGTCTATCTACTTTCACCAAGAGAGAACCGGGGTACTGTCCATTACAGATAACAGT 2043
QY 318 ProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHis 337
DB 2044 TCATCTCAGACATGTGGAGAGCTCAACTTCTTATATAAATCTCAAACTCTTCACAT 2103
QY 338 GlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArg 357
DB 2104 TCAGAGTATTCTCTCTTTTCTCATGCTCAG-----ACTGAGAGAGTAAC 2148
QY 358 LeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThr 377
DB 2149 ATCTCATCTCTATGACGGGGAATATCTCAGCCTTCTACTGAGTCCCGAGTCTTCATACA 2208
QY 378 AspGluIleAlaGlySerLeuProAlaPheGly---ProAspThrGlnSerGluLeuPro 396
DB 2209 TCCAACTTCGCTCTACACACCCACCATTAATATGCGGACACATTCGGTGTCTTCGAC 2268
QY 397 ThrSerPheAlaValIleThrGluAspAlaThrLeuSer----- 409
DB 2269 ACTGATGTCTAGTATTGTTAGTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2328
QY 410 -----ProGluLeuProProValGluProGlnLeuGluThrValAspGlyAlaGlu 426
DB 2329 TCTTCAGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2373
QY 427 His-----GlyLeuProAspThrSerTrpSerProProAlaMetAlaSerThr 442
DB 2374 CATTTATTTCATCAATTTTACCATCAACAGGCGCTCTGTGCATCTACTATAAGTCTACC 2433
QY 443 SerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGln 462
DB 2434 TCTGATGATCCACACCA-----TGGCTCTCTCACCATCACCTTTTACCAGTATCC 2484
QY 463 GlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro 482
DB 2485 TTAACGACATCTACATCTGCC-----CCACTTTCTGTCTCACAACAACTTGCCA 2535
QY 483 ThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSer 502
DB 2536 CAGTCTCTCTTACCCCTGTCTCTGCCAGGCA-----AGGGAGACTCTCTGTGACT 2586
QY 503 SerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMet 522
DB 2587 TCATTTTCAGACATCAACATGACATCTCATGACATGCTCCATAGTAGTCAAACTGCA 2646
QY 523 AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu----- 538
DB 2647 GACCTTAAGAGCCAGACAGCACCACACCAAGAGAAAGTCATTACAGAATCAAAAGTCACCA 2706
QY 539 ---TyrValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGln 557
DB 2707 AGCTTGGTGTCTCTGCCACAGTCCACCAAGTGTAAACAGTGTAAACAACTCTCTTTGGCT 2766
QY 558 TyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValPhePhe 577
DB 2767 CCATCTCTTAACAGAGTCTCTCCACA-----GAGCAAAACCTTCCAGCCACA 2811
QY 578 SerLeuArgValAlaAsnMetAla-----PheSerAsnAspLeuPheAsnLysSer--- 594
DB 2812 AGCACCAACTTAGACAAATGTCTCCAACTTTCCAACTTTCACAACTTTCGAAGACCTCTCAG 2871

```



Qy	214	LeuAsnAspThrLysMetProThrThrGlu-----	223
Db	1753	CTCACCACACCCAGCATGAGCACCACTTCTGGGAAGCAGCGACGCCCTGCAGCGGCCATG 1812	
Qy	224	--ArgGlnThrGluPheAlaValLeuGluGluGlnArgValGluLeuSerValSerLeu 242	
Db	1913	CCCCAAGAACAAGAGGTGCTCTCTGCAC-----	1842
Qy	243	ValasnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyTyTrGlnGluLeu 262	
Db	1843	-----GTAACCGTCAGCGACACATGGCGCTGGTCTCACGGCTCACTG 1884	
Qy	263	AlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLys 282	
Db	1885	GCGCCTCCAGTGCACTCGGAGTCGCTGGGATT-----AGCTACGGTCAA 1929	
Qy	283	IleHisValLeuGlyPheArgProLysGlyGlnLysAspGlySerSerSerThrGluMet 302	
Db	1930	GTGCGTGGCCACGACTATTGAAACAAAGAGACTTCCAGCGACACACAGCACACC- 1983	
Qy	303	GlnLeuThrAlaIlePheLysArgHis-----SerAlaGluAlaLysSer 317	
Db	1984	TACCTGTCATCTACTTTACAAAGAGAACGGCGGTACTGTCCATTACAGATAACAGT 2043	
Qy	318	ProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyHis 337	
Db	2044	TCATCCTCAGACATTTGGGAGAGCTCAACTCTTATTAAAAATCTCAAACTCTTCACAT 2103	
Qy	338	GlyThrMetGluGluAspLysGlnProGluIleTyLeuThrAlaThrAspLeuLysArg 357	
Db	2104	TCAGAGTATTCTCTTTCTCATGCTCAG-----ACTGAGAGAAGTAAC 2148	
Qy	358	LeuIleSerLysAlaLeuGluGluGlnInsLeuAspValGlyThrIleGlnPheThr 377	
Db	2149	ATCTCATCTTAGCGGGAATATGCTCAGCCTTCTACTGAGTCGCCAGTTCTGCATACA 2208	
Qy	378	AspGluIleAlaGlySerLeuProAlaPheGly---ProAspThrGlnSerGluLeuPro 396	
Db	2209	TCCAACCTTCGGTCTCACACCCACCATTAAATATGCCGAACACTTCGGTTGTTCTGCAG 2268	
Qy	397	ThrSerPheAlaValIleThrGluAspAlaThrLeuSer----- 409	
Db	2269	ACTGATGCTGAGTTTGTATTGAGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2328	
Qy	410	-----ProGluLeuProProValGluProGlnLeuThrValAlaAspGlyAlaGlu 426	
Db	2329	TCTTCAGGGCTCTCTTGGCT-----CTGCCCTCTGTGTCAATCTCCAC 2373	
Qy	427	His-----GlyLeuProAspThr-SerTrpSerProAlaMetAlaSerThr 442	
Db	2374	CATTATTATTCATCAATTTTACCATCAACAGGGCCCTCTGTGCATCTACTAAAGTCTACC 2433	
Qy	443	SerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGln 462	
Db	2434	TCYGATGCATCCACACCA-----TGFTCTTCCTCAACATCACCTTACCAGTATCC 2484	
Qy	463	GlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro 482	
Db	2485	TTAACGACATCTACATCTGCC-----CCACTTCTGTCTCACAAAACACTTGCCA 2535	
Qy	483	ThrSerAspTyrsAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSer 502	
Db	2536	CAGTCATCTTCTACCCCTGTCTGCCACGGGCA-----AGGGAGACTCTCTGTGACT 2586	
Qy	503	SerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMet 522	
Db	2587	TCATTTCAGACATCAACAATGACATCATTTATGATCAATGTCCCATAGTAGTCAAACTGCA 2646	
Qy	523	AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu----- 538	
Db	2647	GACCTTAAGAGCCACAGACACCCCACCAAGAGAAGTCAATTTACAGATCAAAAGTCAACCA 2706	

Qy	539	---	TyrValSerValProAspHisPheLeuGluAAspThrThrProValSerAlaLeuGln	557
Db	2707	AGCCTGGTGTCTCTCGCCACAGAGTCCACAAAGCTGTAAACAAACAACTCTCTCTTCCT	2766	
Qy	558	TyrIleThrThrSerSerMetThrIleAlaProLySGlyArgGluLeuValValPhePhe	577	
Db	2767	CCATCCTTAACAGAGTCTCCACA	2811	
Qy	578	SerLeuArgValAlaAsnMetAla	594	
Db	2812	AGCACCAACTTAGCAAAATGTCTCCAACTTTCACAACTACCAATCTCGAAGACCTCTCAG	2871	
Qy	595	---	595	
Db	2872	CCTCTATGACCACCTCTCGCACCTGTCAAGCACAGCATCTCTGGTCACTGCGCCCTATA	2931	
Qy	602	GluGlnGlnPheThr	611	
Db	2932	GCGGTACAGACTACACTGGAAACAGCTCTCGCTGACCCATCTCGAAATACCTAGTTCCT	2991	
Qy	612	TyrLeu	629	
Db	2992	CAATCTCAACAGAGGTGGCATCAGCACAGAAAGGACCGAGTGATTTGGATGCTACC	3051	
Qy	630	AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu	649	
Db	3052	ACTGGATGATCCCTTTGACAGTGTACCCCATCATCAGCAAAAGAAATGACCAACAAAGCTT	3111	
Qy	650	ThrLysAlaValHisGlyValLeuGluAAspPheArgSerAlaAlaGlnGlnLeuHis	669	
Db	3112	---	3138	
Qy	670	LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGln	684	
Db	3139	---	3186	
Qy	684	---	684	
Db	3187	ACGGCTGAAGACTTGGCTCCCAATCTGCCACTTTCCTGCTTTCAGAGCAGCACAGTCA	3246	
Qy	685	---	695	
Db	3247	CCAACAACACTGTCCTCTTTCAGCCTCAGTCAACAGCTGTGCTGTGAACCTTGTCTTCAC	3306	
Qy	696	PheAlaGlnCysValLysAsnGluAAspThrGluGluAlaGluCysArgCysLysProGly	715	
Db	3307	AATGGCGAATGGTCCGACACACACACCGCGTGGTACCCTGACAGTGCCTCC	3366	
Qy	716	TyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCys	731	
Db	3367	TGG	3420	
Qy	732	ProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeuPro	750	
Db	3421	CCATCCACACCCATGTCACAAATACTCAGGGATCCTTTATC	3477	
Qy	751	---	766	
Db	3478	GGGTACCAGTTGGAAAAAGGGATATGCAATTTGGTTAGAACCTTCTGTGACAGAGTTTAA	3537	
Qy	767	AsnGlnGlnAsn	784	
Db	3538	TTAAAGAGACATTTCTTAATACAACTGTGGAAAAA	3594	
Qy	785	GluTyrGlu	787	
Db	3595	GAATAATGAG	3603	

RESULT 13  
US-08-944-423A-7  
; Sequence 7, Application US/08944423A  
; Patent No. 6020463  
; GENERAL INFORMATION:



```

; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,423A
; FILING DATE: 06-OCT-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/599,654
; FILING DATE: 09-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: JUN-07-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9030
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6407 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; US-08-944-423A-7

Alignment Scores:
Pred. No.: 0,00102 Length: 6407
Score: 141.50 Matches: 164
Percent Similarity: 31.91% Conservative: 105
Best Local Similarity: 19.45% Mismatches: 356
Query Match: 3.44% Indels: 219
DB: 3 Gaps: 34

US-10-007-270-2 (1-797) x US-08-944-423A-7 (1-6407)
Qy 97 TyrArgLeuArgValCysGlu-----AlaValTrpGluAlaTyrArgIlePhe 113
Db 1275 TGGAGAACATCAGCTTGGCAGCAGCTCTGAGGTGCAAAATGGAAGTCCCATGCTCAGAC 1334
Qy 114 LeuAspArgIleProAspThrGlyGluTyrGlnAspTrpValSerIleCysA----- 130
Db 1335 TGAGACTGTGTCTAGGTGAGTCGCGACCCATGAGAGGTGGAGATCACTGCACACTGGCT 1394
Qy 131 -----GlnGlnGluThrPheCysLeuPheAspIleGlyLysAsn----- 143
Db 1395 CTTGACCAACAGCAACATCTGCAGATGTGACA--GGAACTCTGCTTCATATCTCTGAA 1452
Qy 144 -----PheSerAsnSerGlnGluHisLeuAspLeuLeu 154
Db 1453 GGTGTGAATGCTTACGTGTTGACCCAGTCTTCAGACTCTACTGTACAGTCTGGAGGAAGT 1512
Qy 155 GlnGlnArgIleLysGlnArgSerPheProAspArgLysAspGluIleSerAlaGlu--- 173

```

```

Db 1513 CACACAGCATGGGAGATAGGAGTTATTTCAGAGTCTTTCATCTACATCTTCTCGGAAAGC 1572
Qy 174 -----LysThrLeu-----GlyGluProGly 180
Db 1573 TTGAATTCATCAGCACCGTGGAGAACGTTCAACCTTGGAGAGACAGCCGAGAGCCAGCG 1632
Qy 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
Db 1633 CAAGCACTAGTGCACAGTTCCGCCAATGACAGAGGACAGGACTTCTGGGTGCGCTCTCTC 1692
Qy 201 ProAspAspThrLeuLeu-----AsnGluIleLeuAspAsnThr 213
Db 1693 GGCACCCACACCTTGGCTACTGTCTACTGGAAGGGAAGCGACACTGCGGTCTGTCCACC 1752
Qy 214 LeuAsnAspThrLysMetProThrThrGlu----- 223
Db 1753 CTCACCAACACAGCATGACGACGACTTCTGGGAAGAGGCGAGCGCTGCGAGGCGCATG 1812
Qy 224 ---ArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSerValSerLeu 242
Db 1813 CCCCAAGAAACAGAGGTGCTCTCTGAC----- 1842
Qy 243 ValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeu 262
Db 1843 -----GTAAACGTGACGAGGACATGGGCTGTGTCTCACGGTCACTG 1884
Qy 263 AlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLys 282
Db 1885 GCGGCTCCAGTGCACCTCGGATCGCTGGGATT-----AGCTACCGTCAA 1929
Qy 283 IleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSerThrGluMet 302
Db 1930 GTGCGTGGCACAGCTATTGAACAAGGACTTCCAGCGACACACAGACACAC----- 1983
Qy 303 GlnLeuThrAlaIlePheLysArgHis-----SerAlaGluAlaLysSer 317
Db 1984 TACCTGTCTACTTCTTCCACCAAGGAGAACGCGGTTACTGTCTTCCATTACAGATAACAGT 2043
Qy 318 ProAlaSerAspLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHis 337
Db 2044 TCATCTCTAGACATTTGTGGAGAGCTCACTTCTTATTTAAATCTCAAACTTTCACAT 2103
Qy 338 GlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArg 357
Db 2104 TCAGAGTATTCTCTCTTCTCATGCTCAG-----ACTGAGAGAAAGTAAC 2148
Qy 358 LeuIleSerLysAlaLeuGluGluGluGlnSerLeuAspValGlyThrIleGlnPheThr 377
Db 2149 ATCTCATCTCTATGACGGGGAATATGCTCAGCCTTCTACTGTAGTCCCGAGTTCGTGATACA 2208
Qy 378 AspGluIleAlaGlySerLeuProAlaPheGly---ProAspThrGlnSerGluLeuPro 396
Db 2209 TCCAACCTTCGCTCTACACACCCACCATTAATATGCGGAACACTTCGTTGTTCTGGAC 2268
Qy 397 ThrSerPheAlaValIleThrGluAspAlaThrLeuSer----- 409
Db 2269 ACTGATGCTGAGTGTGTAGTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2328
Qy 410 -----ProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGlu 426
Db 2329 TCTTCAGGCGCTCTCTTGGCT-----CTGCGCTCTGTGTGCACAAATCCAC 2373
Qy 427 His-----GlyLeuProAspThrSerTrpSerProAlaMetAlaSerThr 442
Db 2374 CATTTATTTTCAATTTTACCAATCAACAGGCGCTCTGTGCATCTCTAAAGTCTACC 2433
Qy 443 SerLeuSerGluAlaProPhePheMetAlaSerIlePheSerLeuThrAspGln 462
Db 2434 TCTGATGATCCACACCA-----TGGTCTCTCTCACCATCCTTTTACCAGTATCC 2484
Qy 463 GlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro 482

```

Db 2485 TTAACGACATCTACATCTGCC-----CCACTTCTGTCTCACAACAAACCTTGCCA 2535  
Qy 483 ThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProAlaSer 502  
Db 2536 CAGTCACTCTTACCCCTGTCTGCCAGGCA-----AGGAGACTCTCTGTGACT 2586  
Qy 503 SerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMet 522  
Db 2587 TCATTTCAGACATCAACATGACATCATCTCATGCAATGCTCCATAGTAGTCAAACTGCA 2646  
Qy 523 AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu----- 538  
Db 2647 GACCTTAAGACGACGACACCCCAACCAAGAGAAAGTCATTACAGAAATCAAGTCACCA 2706  
Qy 539 ---TyrValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGln 557  
Db 2707 AGCCTGGTGTCTCTGCCAGAGAGTCCACCAAGCTGTAAACAACAACTCTCCCTTGGCT 2766  
Qy 558 TyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValPhePhe 577  
Db 2767 CCATCCTTAACAGAGTCTCCACA-----GAGCAACCCCTCCAGCCACA 2811  
Qy 578 SerLeuArgValAlaAsnMetAla-----PheSerAsnAspLeuPheAsnLysSer--- 594  
Db 2812 AGCACAACCTTAGCAAAATGTCTCCAACTTTCAACAACCTCATCTCGAAGACCTCTCAG 2871  
Qy 595 -----SerLeuGluTyrArgAlaLeu 601  
Db 2872 CTTCTTAAGACACTCTCTGGACCTGTCAAGCAGACATCTTGTCACCTGGCCCTATA 2931  
Qy 602 GluGlnGlnPheThr-----GlnLeuLeuValPro 611  
Db 2932 GCGGTACAGACTACAGTGGTGAACAGCTCTCGCTGACCCATCTCTGAAATACTAGTCTCT 2991  
Qy 612 TyrLeu-----ArgSerAsnLeuThrGlyPheLysGlnLeuGluLeuAsnPheArg 629  
Db 2992 CAAATCTCAACAGAGTGGTCAATCAGACAGAAAGAACCGAGTATGTGATGCTTACC 3051  
Qy 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu 649  
Db 3052 ACTGGATTGATCCCTTTGACAGGTGTACCCACATCAGCAAAAGAAATGACCACAAGCTT 3111  
Qy 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaAlaGlnLeuHis 669  
Db 3112 -----GGCGTTACAGCAGAGTACACCCAGCT----- 3138  
Qy 670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGln----- 684  
Db 3139 -----TCAGTTCCCTCGGAACATCTCTCTTCTCCCAACCAACACAGTTGTTCC 3186  
Qy 684 ----- 684  
Db 3187 AGGCTGAAGACTTGGTCCCAATCTGCCACTTTGCTGTTTCAGAGCAGCAGACAGTCA 3246  
Qy 685 -----AlaAspProCysLePheLeuAlaCysGlyGlu 695  
Db 3247 CCAACAACACTGTCTCTTCAGCCTCAGTCAACAGCTGTGTGTGAACCTTGTTCCAC 3306  
Qy 696 PheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysProGly 715  
Db 3307 AATGGCGAATGGTTCGACAGCAACACCGCGGTGTACCACTGCAGGTGCCGCTTCC 3366  
Qy 716 TyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCys-----Gly 731  
Db 3367 TGG-----CAAGGGGATGATTCAGTGTGGATGTGAATGATGCTGTGTGAAACCCCTGTC 3420  
Qy 732 ProGlyThrLysGluCysGluValLeuGlnGlyLysGlyValProCysArgLeuPro--- 750  
Db 3421 CCATCCACAGCCAGCTGTGCAACATATCTCAGGATCTCTTTATC---TGCAATGCCCGTT 3477  
Qy 751 -----AspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGln 766  
Db 3478 GGGTACCAGTTGGAAAAAGGATATGCAATTTGGTTAGAACCTTCTGTGACAGAGTTTAA 3537

Qy 767 AsnGlnGlnAsn-----AsnLysValIleSerLysArgAsnSerGlnLeuLeuThrVal 784  
Db 3538 TTAAGAGAGAACTTTTCTTAATACAACCTGTGMAAAA---CATTCAGACCTCAAGAAGTT 3594  
Qy 785 GluTyrGlu 787  
Db 3595 GAAATGAG 3603  
RESULT 14  
US-08-944-496-7  
Sequence 7, Application US/08944496  
Patent No. 6124433  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,496  
FILING DATE: 06-OCT-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6407 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
US-08-944-496-7  
Alignment Scores:  
Pred. No.: 0.00102 Length: 6407  
Score: 141.50 Matches: 164  
Percent Similarity: 31.91% Conservative: 105  
Best Local Similarity: 19.45% Mismatches: 356  
Query Match: 3.44% Indels: 219  
DB: 3 Gaps: 34  
US-10-007-270-2 (1-797) x US-08-944-496-7 (1-6407)  
Qy 97 TyrArgLeuArgValCysGlnGlu-----AlaValTyrClnAlaTyrArgIlePhe 113  
Db 1275 TGGAGAACATCAGCTTGGCCAGCAGCTCTGAGGTGCAAAATGGAAGTCCCATCTCTCAGAC 1334

QY 114 LeuAspArgIleProAspThrGlyGluTyrGlnAspTrpValSerIleCys----- 130  
Db 1335 TGAGACTGTGCTAGGTGAGTCGACCCATGAGAGGTGGAGATCACTGCACACTGGCT 1394  
QY 131 -----GlnGlnGluThrPheCysLeuPheAspIleGlyLysAsn----- 143  
Db 1395 CTTGACCAACAGACACAACTCTGCAGATGTGACA--GGAGCTCTGCTTCATATCCTGAA 1452  
QY 144 -----PheSerAsnSerGlnGluHisLeuAspLeuLeu 154  
Db 1453 GGTGTGAATGCTCAGTGTGTGACCCAGTTCTTCAGACTCTACTGTACAGTCTGGAGGAAGT 1512  
QY 155 GlnGlnArgIleLysGlnArgSerPheProAspArgLysAspGluIleSerAlaGlu--- 173  
Db 1513 CACACAGATTGGAGATAGAGATTATTCAGAGTCTTCATCTACATCTTCTCGGAAGC 1572  
QY 174 -----LysThrLeu-----GlyGluProGly 180  
Db 1573 TTGAATTTCATCAGCACCACTGGAGAACGTTTCAACCTTGAAGACAGCCGAGAGCCAGGC 1632  
QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
Db 1633 CAGCACTAGGTGACAGTTCGCCAATGTCAGAGGACAGGACTTCTGGGGTGCCTCTCTC 1692  
QY 201 ProAspAspThrLeuLeu-----AsnGluIleLeuAspAsnThr 213  
Db 1693 GGCACCCACACCTTTGGCTACTGTCTCACTGGAACGGGAACGCCACACTGCGGTCTGTCA 1752  
QY 214 LeuAsnAspThrLysMetProThrThrGlu----- 223  
Db 1753 CTCACCAACACAGCATGAGCACACTCTTGGGAAGCAGCGACCCCTGCAGCGGCCATG 1812  
QY 224 --ArgGluThrGluPheAlaValLeuGluGluGlnArgValGluLeuSerValSerLeu 242  
Db 1813 CCCCAAGAAACAGAGGTGCTCTCTGCAC----- 1842  
QY 243 ValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeu 262  
Db 1843 -----GTAACGTGACGAGCAGCATGGCGCTGTCTCACGCTCACTG 1884  
QY 263 AlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLys 282  
Db 1885 GCGCCTCCAGTCACTCGAGTGCCTGGGATT-----ACGTAGGTCAA 1929  
QY 283 IleHisValLeuGlyPheArgProLysLysGlnLysAspGlySerSerThrGluMet 302  
Db 1930 GTGCGTGCACAGCTATTGAAACAAAGGACTTCCAGCGACACACAGCACACACC- 1983  
QY 303 GlnLeuThrAlaIlePheLysArgHis-----SerAlaGluAlaLysSer 317  
Db 1984 TACCTGTCTACTCTTCCACAAAGGAGAACGGCGCTTACTGTTCATTACAGATAACAGT 2043  
QY 318 ProLaserAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHis 337  
Db 2044 TCATCCTCAGACATGTGGAGAGCTCACTCTTATATTAATCTCAAACTCTTCACAT 2103  
QY 338 GlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArg 357  
Db 2104 TCAGAGTATTCCTCTCTCTCATGCTCAG-----ACTGAGAGAAGTAAC 2148  
QY 358 LeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThr 377  
Db 2149 ATCTCATCTATGACGGGAATATGCTCAGCCTTCTACTAGTGCAGCTTCGCATACA 2208  
QY 378 AspGluIleAlaGlySerLeuProAlaPheGly---ProAspThrGlnSerGluLeuPro 396  
Db 2209 TCCAACTTCCTCTCAACACCCACCACTTAATATGCGGAACACTTCGGTGTCTTGAC 2268  
QY 397 ThrSerPheAlaValIleThrGluAspAlaThrLeuSer----- 409  
Db 2269 ACTGATGTGATTTGTTAGTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2328

QY 410 -----ProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGlu 426  
Db 2329 TCTTCAGGGCCTCTCTTGGCT-----CTGCCCTCTGTGTCAAACTCCAC 2373  
QY 427 His-----GlyLeuProAspThrSerTrpSerProAlaMetAlaSerThr 442  
Db 2374 CATTATTATTCATCAATTTTACCAACACAGGGCTCTGTGCATCTACTAAAGTCTACC 2433  
QY 443 SerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThrAspGln 462  
Db 2434 TCTGATGCATCCACACCA-----TGGTCTCTCCATCCATCCTTTACCATATCC 2484  
QY 463 GlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThrIlePro 482  
Db 2485 TTAACGACATCTACATCTGCC-----CCACTTCTGTCTCACAAACACTTGCCA 2535  
QY 483 ThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProProLaser 502  
Db 2536 CAGTCTATCTTCAACCTCTCTGCCAGGCA-----AGGAGACTCTCTGTGACT 2586  
QY 503 SerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMet 522  
Db 2587 TCATTTACAGACATCAACATGACATCATTCATGACAATGCTCCATAGTAGTCAAACTGCA 2646  
QY 523 AspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu----- 538  
Db 2647 GACCTTAAGAGCCAGACGCCACCCACCAAGAGAAAGTCATTACAGAATCAAAAGTCACCA 2706  
QY 539 ---TyrValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGln 557  
Db 2707 AGCCTGGTGTCTCTGCCACAGAGTCCACCAAGGTGTAAACAACAACTCTCTTTGGCT 2766  
QY 558 TyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePhe 577  
Db 2767 CCATCTTAAAGAGTCTCTCCACA-----GAGCAAAACCTTCCAGCCACA 2811  
QY 578 SerLeuArgValAlaAsnMetAla-----PheSerAsnAspLeuPheAsnLysSer--- 594  
Db 2812 AGCACAACCTTAGCAAAATGTCTCAACTTTTCAACACTACCATTTCTGAAGACCTCTCAG 2871  
QY 595 -----SerLeuGluTyrArgAlaLeu 601  
Db 2872 CCTCTTATGACCACTCTCTGGCACCCTGTCAAGCACAGCATCTCTGGTCACTGGCCCTATA 2931  
QY 602 GluGlnGlnPheThr-----GlnLeuLeuValPro 611  
Db 2932 GCGGTACAGACTACAGCTGGAACACAGCTCTGCTGACCCCATCTCTGAAATACTAGTTCT 2991  
QY 612 TyrLeu-----ArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg 629  
Db 2992 CAAATCTCAAGAAAGGTGGCATCAGACAGAAAGAACCGAGTGATTGTGATCTCTACC 3051  
QY 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu 649  
Db 3052 ACTGGATGATCTCTTGCACAGTGTACCACATCAGCAAAAGAAATGACCAAAAGTCT 3111  
QY 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669  
Db 3112 -----GGCGTTACAGCAGATACAGCCAGCT----- 3138  
QY 670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGln----- 684  
Db 3139 -----TCAGTTCCTCGGAACATCTCTCTCTCCCAACCCACAGTGTCTTCC 3186  
QY 684 ----- 684  
Db 3187 ACGGTGAAGACTTGGCTCCCAATCTGCCACCTTTGTCTGTTCAGAGCAGCACACAGTCA 3246  
QY 685 -----AlaAspProCysLysPheLeuAlaCysGlyGlu 695  
Db 3247 CCAACAACACTGTCTCTCTCAGCTCAGTGTGTGTGTGAAACCTTGTCTTCCAC 3306  
QY 696 PheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysProGly 715

Qy	116	ArgIleProAspThrGlyGlyTyrGlnAspTrpValSerIleCysGlnGlnGluThrPhe	135
Db	391169	AAA-----GAAACAGGGGTTTACTATGATCCTTATGAGATACTGAATATGATATCTCC	391116
Qy	136	CysLeuPheAspIleGlyLeuAsn-----PheSerAenSerGlnGluHisLeuAsp	152
Db	391115	CAACTCTTTGATGAAATGGGAATCCGTTGTTTTGATGAAAGCAAGAGAGATGAT	391056
Qy	153	LeuLeuGlnGlnArgIleGlyGlnArgSerPheProAsp	165
Db	391055	TATTTA-----AAGTATGTTGGTAACCTGACATATGGTTCTTATGATGAAAAAT	391008
Qy	166	-----ArgLyAspGluIleSerAlaGluLysThrLeu	176
Db	391007	GGTAGTGGGTTTGATCTGGTTACTCTTGAAATGACGAGTGATCTCCACTAAGATCT	390948
Qy	177	GlyGluProGlyGluThrIleValIleSerThrAspValAlaAenValSerLeuGlyPro	196
Db	390947	CAACCAACTGATGAAACATATGGTTTTCAGATGAT-----	390912
Qy	197	PheProLeuThrProAspAspThrLeuLeuAsnGluIleLeuAspAenThrLeuAenAsp	216
Db	390911	-----TTACCACCAAGAGTAAACCAACCTGAATCAGTTGAAAGATACACTATGTTTTGAT	390858
Qy	217	ThrLysMetProThrThrGluArgGluThrGluPheAlaValLeuGluGluGln-----	234
Db	390857	AACGATTTTACCACCAAGAGTAAACCAACCTGAA-----TCAGTTGAAGATAACTATGGT	390804
Qy	235	-----ArgValGluLeuSerValSerLeuValAenGlnLys-----	246
Db	390803	TTTGATAACGACCTTACCACCAAGAGTAAACCAACCTGAATCAGTTGTGACCACTTCT	390744
Qy	247	-----PheLysAlaGluLeuAlaAspSerGlnSerProTyrTrpGlnGluLeu	262
Db	390743	TCAGATGATTATTTTGCAAAACCAACCACTGATGAAAACTATGGTTTGATAACGACCTA	390684
Qy	263	AlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLys	282
Db	390683	CCA-----CCAGAAGTAAAA-----	390669
Qy	283	IleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSerThrGluMet	302
Db	390668	-----CAACCTGAATCAGTTGTTGACCAACCTTCTTCAGATGAT---	390630
Qy	303	GlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeu	322
Db	390629	-----CAUTTTGCAAAAACAACCTGAATCAACACTGATAGC	390594
Qy	323	LeuSerPheAspSerAsn-----LysIleGluSerGlu	333
Db	390593	TACAGCTTTGACAGTGATTTACTCAACCAACCTTGACCAACCTCTTTAGATGATCAT	390534
Qy	334	GluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThr	353
Db	390533	GTTTCAGTACAACCTTTTGATCACCATGAAGAGCTCAACCA-----	390495
Qy	354	AspLeuLysArgLeuIleSerLysAlaLeuGluGlnGlnSerLeuAspValGlyThr	373
Db	390494	-----GTYGCTGAAGAACAAAAATATTAATCAAGTTGA-----	390462
Qy	374	IleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSer	393
Db	390461	-----TTTGATCAAGTTCAGCTAATCTT-----GATATAATAGAG	390426
Qy	394	GluLeu-----ProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu	412
Db	390425	GAAATACACCAACCACTGCTGAAAAAAGAAATGTACTACTGATTTTGAA-----	390381
Qy	413	ProProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro-----	431
Db	390380	-----AGTAAACAGCCCAAGTAGTTGAT-----AGTTACCAATTACCAATGAT	390336
Qy	432	ThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaPro-----	448

```
Db 390335 ACAGATCAACAGACCAACAACTTTTCTCTTCATTTGAACTCAACCAACAGTTGAG 390276
QY 448 -----
Db 390275 CAGTTTGATCAAGTAATAAGCGAAGTTAAACGATCAATTCAAACCTGAAATAACTAAGGAG 390216
QY 449 ProPheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMet 468
Db 390215 CCA-----GTTTGAAGTAGTTTCAATAAACAGATAGTAGTTGAACTAGTGACTTA 390162
QY 469 AlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAla 488
Db 390161 AATTCTGAATCTAATCTTTACTTGAAACCAACAAAGATGCAACTAACAATGATTCATTA 390102
QY 489 IleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArgSer 508
Db 390101 AATTCTGAATTCATCAACTTAATAGTAATAGTGAAGAACTGCATCTGATGATGTCATTAT 390042
QY 509 SerAlaGlyGlyAspMetValArgHisLeuAspGluMetAspLeuSerAspThrPro 528
Db 390041 GAAAGTAATCTGAACCAATTCATGACTATATAATTTGGAGTGATTTATCTCAATCAAC 389982
QY 529 AlaProSerGluVal-----ProGluLeuSerGluTyrValSerValProAsp--- 544
Db 389981 AGCAATAATTCGTTAGAGTCTGAACCTGTTAAGTTTAATAGTGAACCTGCACCTGATGCA 389922
QY 545 HisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMet 564
Db 389921 CACTTTGAACTCAATCTGAACCACTGATCAAGTTCAATACGACATTTATCAAAATGAA 389862
QY 565 ThrIleAlaProLysGlyArgGluLeuValVal-----PhePheSerLeuArgValAla 582
Db 389861 GAGCTAAACCAACTCTTGACCGCCTTCTTCAGATGATTTATTTGCAAAACCAACCACT 389802
QY 583 -----AsnMetAlaPheSerAsnAspLeu-PheAsnLys----- 593
Db 389801 GATCAAACTATGTTTGTATACGACCTACCCAGACAGTAAACCAACCTGAATCAGTT 389742
QY 594 -----SerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln----- 607
Db 389741 GTTGACCAAGCCTTCTTCAGATGATCATTTTGCAAAACCAACCTGATCAACTGATGAC 389682
QY 608 -----LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLys----- 621
Db 389681 TACAGCTTTGACAGTATTTACCTCAACCAACCTTGACCAACCTTCTTTAGATGATCAT 389622
QY 622 -----GlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLys----- 638
Db 389621 GTTCAGTACAACTTTGATGATCACCATGAGAGCTCAACCACTGCTGAGAACCAAAATAAT 389562
QY 639 -----MetLysPheAlaLysSerVal-----ProTyrAsnLe 649
Db 389561 TATCAAGTTGGATTTGATCAAGTTCAAGCTAATCTTGATTAATAGAGGAATACAAACCA 389502
QY 649 uThrIleAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHi 669
Db 389501 -ACT---GCTGAAAAGAGTAACACTACTGATTTTGAAGTAAACCAAGCCCAA----- 389454
QY 669 sLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689
Db 389453 -----GTAGTTGATAGTTACCAATTTACCAATGAT---ACAGATCAACAGACCAACAC 389401
QY 689 sPheLeuAlaCysGlyGluPheAlaGlnCysValLys-----AsnGluArgThrGluGl 707
Db 389400 TTTTCTCTCTTCATTTGAAACTCAACCAAGTTGAGCAGTTTGATCAAGTAAATAGCGA 389341
QY 707 uAlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPr 727
Db 389340 AGTTAACGATCAATTCAAACCTGAAATTAACCTAAG-----GAGCC 389302
QY 727 cGlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCy 747
```

```
Db 389301 AGTTTAGAACTAGTTTCAATAAACAA-----ValIleSerLysArgAsnSer 779
QY 747 sArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAs 767
Db 389273 -----GATGTAGTTGAAACTTAGTAACCTACACTAATAATTACAGAAATTTGATAT 389224
QY 767 hGlnGlnAsnAsnLys-----ValIleSerLysArgAsnSer 779
Db 389223 TCAGTCTGATAATAAGATAACTATCATTACCAAAAAAGATTCA 389181
```

Search completed: March 2, 2004, 00:54:49  
Job time : 892 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2004, 14:40:11 ; Search time 775 Seconds  
(without alignments)  
4368.792 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117

Sequence: 1 MYLETRRAIFVFWIFLQVQ.....NSELLTVEEENHQDWEGN 757

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-O=/cgn2.1/USPTO.spool/US10007270/runat\_25022004\_164206\_27185/app.query.fasta\_1.967  
-DB=N\_Geneseq\_29Jan04 -QWTF=fastap -SUFFIX=mg -MINWATCH=0.1 -LOOFCI=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USERS=US10007270 @CGN 1 1 513 @runat\_25022004\_164206\_27185 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQ=0 -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_29Jan04.\*

1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001as.\*  
5: Geneseq2001bs.\*  
6: Geneseq2002s.\*  
7: Geneseq2003as.\*  
8: Geneseq2003bs.\*  
9: Geneseq2003cs.\*  
10: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4073	98.9	3330	7 ADA14840	ADA14840 Human int
2	4073	98.9	3330	8 ACC57946	ACC57946 Human int
3	4039.5	98.1	3263	3 AAA46205	AAA46205 cDNA enco
4	4024.5	97.8	3261	7 ADA14866	ADA14866 Human cDN
5	4024.5	97.8	3261	8 ACC57960	ACC57960 Human int
6	3619	87.9	2887	7 ADA14842	ADA14842 Human int
7	3619	87.9	2887	8 ACC57947	ACC57947 Human int
8	3526.5	85.7	2966	3 AAA46328	AAA46328 Interphot

9	3323	80.7	2244	3 AAA46329	AAA46329 Interphot
10	3323	80.7	2244	7 ADA14844	ADA14844 Human int
11	3323	80.7	2244	8 ACC57948	ACC57948 Human int
12	2548.5	61.9	3668	7 ADA14847	ADA14847 Mouse int
13	2548.5	61.9	3668	8 ACC57950	ACC57950 Mouse int
14	2192	53.2	3206	3 AAA46309	AAA46309 cDNA enco
15	1342.5	32.6	1726	7 ADA14849	ADA14849 Mouse int
16	1342.5	32.6	1726	8 ACC57951	ACC57951 Mouse int
17	929.5	22.6	1321	7 ADA14851	ADA14851 Mouse int
18	929.5	22.6	1321	8 ACC57952	ACC57952 Mouse int
19	927	22.5	4165	3 AAA46206	AAA46206 cDNA enco
20	927	22.5	4165	7 ADA14855	ADA14855 Human int
21	927	22.5	4166	8 ACC57954	ACC57954 Human int
22	885	21.5	555	3 AAA46204	AAA46204 cDNA enco
23	885	21.5	555	7 ADA14853	ADA14853 Monkey in
24	885	21.5	555	8 ACC57953	ACC57953 Monkey in
25	846.5	20.6	2364	7 ADA14857	ADA14857 Human int
26	846.5	20.6	2364	8 ACC57955	ACC57955 Human int
27	841	20.4	4204	3 AAA46310	AAA46310 cDNA enco
28	841	20.4	4204	7 ADA14862	ADA14862 Mouse int
29	841	20.4	4204	8 ACC57958	ACC57958 Mouse int
30	241	5.9	1094	3 AAA46321	AAA46321 Exon 13 o
31	192.5	4.7	1817	3 AAA46320	AAA46320 Exon 12 o
32	189.5	4.6	4139	6 ABL67071	ABL67071 Thyroid c
33	189.5	4.6	4139	6 ABL67544	ABL67544 Thyroid c
34	189.5	4.6	4139	6 ABL68884	ABL68884 Kidney ca
35	189.5	4.6	4139	6 ABK09797	ABK09797 Human ova
36	189.5	4.6	4139	6 ABN95623	ABN95623 Gene #212
37	189.5	4.6	4139	7 ACC50234	ACC50234 Breast ca
38	189.5	4.6	4139	7 ACF12907	ACF12907 Human cer
39	188.5	4.6	1572	5 AAS00585	AAS00585 Human MUC
40	188.5	4.6	1721	6 ABS76475	ABS76475 cDNA enco
41	188.5	4.6	1721	6 ABL68032	ABL68032 Ovary can
42	188.5	4.6	1721	6 ABK09743	ABK09743 Human ova
43	188.5	4.6	1721	6 ABV94067	ABV94067 Breast ca
44	188.5	4.6	1721	7 ADA50566	ADA50566 Mucin 1 (
45	188.5	4.6	1721	7 ACF12906	ACF12906 Human cer

#### ALIGNMENTS

RESULT 1

ADA14840

ID ADA14840 standard; cDNA; 3330 BP.

XX ADA14840;

XX AC

XX DT 06-NOV-2003 (first entry)

XX DE Human interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.

XX ss; gene; human; IPMC 150 isoform A; gene therapy;

XW interphotoreceptor matrix component; IPMC; ocular disorder;

XW macular degeneration; photoreceptor death; retinal detachment.

XX OS Homo sapiens.

XX FH Key

XX CDS

FT Location/Qualifiers

FT 131..2586

FT /tag= b

FT /product= "IPMC 150 isoform A"

FT /transl\_except= (pos:689..756,aa:Thr-Asp)

FT 131..150

FT /tag= a

FT /label= Signal\_sequence

FT 191..2583

FT /tag= c

FT /label= Mature\_IPMC\_150\_isoform\_A

FT 692..753

FT /tag= d

FT /note= "This region could represent intronic sequence not removed from the cDNA sequence"

XX



PN US2002160954-A1.  
 XX 31-OCT-2002.  
 PD 08-NOV-2001; 2001US-00007270.  
 PF 29-OCT-1998; 98US-00183972.  
 PR 29-OCT-1999; 99US-00430195.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA Hageman GS, Kuehn MH;  
 XX WPI; 2003-238235/23.  
 DR P-PSDB; ADA14841.  
 XX  
 PT New isolated or recombinant interphotoreceptor matrix component  
 PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 PT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.  
 XX  
 PS Claim 3; Page 29-30; 76pp; English.  
 CC The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding human  
 CC interphotoreceptor matrix component, IPMC, 150 isoform A.  
 XX  
 SQ Sequence 3330 BP; 1069 A; 737 C; 574 G; 850 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 0 Length: 3330  
 Score: 4073.00 Matches: 796  
 Percent Similarity: 97.31% Conservative: 0  
 Best Local Similarity: 97.31% Mismatches: 1  
 Query Match: 98.93% Indels: 22  
 DB: 7 Gaps: 1

US-10-007-270-2 (1-797) x ADA14840 (1-3330)

QY	1	MetTyrLeuGluThrArgAlaIlePheValPheTyrPheLeuGlnValGlnGly	20
DB	131	ATGTTTGGAACTAGAAAGACTATTTTGGTTTGGATTCTTCTCAAGTTCAGGA	190
QY	21	ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro	40
DB	191	ACCAAGATATCTCCATTAAACATATACCATCTGAAACTTGAAGACATAGACAATCCCCCA	250
QY	41	ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgile	60
DB	251	AGAAATGAACAACTGAAAGTACTGAAATAATGTACAAAATGTCAACTATGAGACAAATA	310
QY	61	PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal	80
DB	311	TTTCGATTTCGCAAGCATCGAACAAAGATCCGCAATTTTCCCAACGGGGTTAAAGTC	370
QY	81	CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg	100
DB	371	TGTCACAGGAATCCATGAAACAGATTTTAGACAGCTTTCAAGCTTATTATAGATTGAGA	430
QY	101	ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgileProAspThr	120
DB	431	GTGTGTCCAGAACAGATATGGGAGCATATCGGATCTTTCTCGATCGCATCTCTCACACA	490
QY	121	GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspile	140
DB	491	GGGGAATATCAGGACTGGGTTCAGCATCTGCCAGCAGGAGACCTTCTGCTCTTTGACATT	550

QY	141	GlyLysAsnPheSerAsnSerGlnGlnHisLeuAspLeuGlnGlnArgIleLysGln	160
DB	551	GGAAAAAACTTCAGCAATTTCCAGGAGCACCTGGATCTTCTCCAGCAGAGAAATAAAACAG	610
QY	161	ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyLysProGly	180
DB	611	AGNAGTTTCCCTGCACAGAAAAAGATGAATATCTGCAGAGAACACATTGGGAGAGCTGGT	670
QY	181	GluThrIleValIleSerThr	187
DB	671	GAACCAATTGTCTATTTCAAC-AGCAATCTACATTTCAAAGACTTGGGCGAGTATTCTAAGA	729
QY	188	-----AspValAlaAsnValSerLeuGlyProPheProLeu	199
DB	730	AAACCTCAGAGAGCAAAATTCAGATGTTCACAGCTCTCACTTGGGCTTTCCCTCTC	789
QY	200	ThrProAspAspThrLeuAsnGlnIleLeuAspAsnThrLeuAsnAspThrLysMet	219
DB	790	ACTCTGATGACACCCTCCTCAATGAAATCTCGATAATACACTCAACGACACCAAGATG	849
QY	220	ProThrThrGluArgGluThrGluPheAlaValLeuGluGluArgValGluLeuSer	239
DB	850	CCTACCAACAAAGAGAAACAGAAATTCGCTGTGTGGAGAGCAGAGGGTGGAGCTCAGC	309
QY	240	ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr	259
DB	910	GTCTCTCTGTAAACCAGAAATTCAGGCAGAGCTCGCTGACTCCCACTCCCATATTAC	269
QY	260	GlnGluLeuAlaGlyLysSerGlnIleGlnMetGlnLysIlePheLysLysLeuProGly	279
DB	970	CAGGACTAGCAGGAAGTCCCAACTTCAGATTCAGAAAGATATTTAAGAAACTTCAGGA	1029
QY	280	PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer	299
DB	1030	TTCAAAAAATCCATGTGTAGATTAGCCAAAGAAAGAAAAGATGGCTCAAGCTCC	1089
QY	300	ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla	319
DB	1090	ACAGAGATGCACTTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAAAGCCCTGCA	1149
QY	320	SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThr	339
DB	1150	AGTGACTCTCTGTCTTTTGTATCCACAAAATGAAAGTGAGGAAGTCTATCATGGAACC	1209
QY	340	MetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIle	359
DB	1210	ATGCAGGAGACAAAGCAACCAAGAAATCTATCTCACAGCTACAGACCTCAAAAGGCTGATC	1269
QY	360	SerLysAlaLeuGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu	379
DB	1270	AGCAAGCACTAGAGGAAGAACAACTTTGGATGTGGGACAAATTCAGTTCACTGATGAA	1329
QY	380	IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe	399
DB	1330	ATTGTGGATCACTGCCAGCCTTTGGTCTGTGACCACTACAGAGCTGCCCATCTTTT	1389
QY	400	AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu	419
DB	1390	GCTGTTTATACAGAGATGCTACTTTGATGCCAGAACTCTCTCTCTTGAACCCCAAGCTT	1449
QY	420	GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProProAlaMet	439
DB	1450	GAGACAGTGGACGAGCAGAGCATGTCTACCTGACACTTCTGGTCTCCACTGCTATG	1509
QY	440	AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu	459
DB	1510	GCCTCTACCTCCCTGTGAGAGCTCCACCTTTCTTTATGGCATCAAGCATCTCTCTCTG	1569
QY	460	ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu	479
DB	1570	ACTGATCAAGGCACCAACAGATACAAATGGCCACTGACCAGACAAATGCTAGTACCAGGCTC	1629

```
QY 480 ThrIleProThrSerAspTy-SerAlaIleSerGlnIleuAlaLeuGlyIleSerHisPro 499
Db 1630 ACCATCCCCACAGTGATTAATTCGCAATCAACCACTGGCTCGGGAATTCACATCCA 1689
QY 500 ProAlaSerSerAspSerArgSerAlaGlyGluAspMetValArgHisLeu 519
Db 1690 CTGCAATCTTCAGATGACAGCGATCAAGTCAGGTGGCGAGATATGGTCAGACACTA 1749
QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539
Db 1750 GATGAATGGATCTGTCTGACACTCTGCCCATCTGAGGTACAGAGCTCAGCGAATAT 1809
QY 540 ValSerValProAspHisPheLeuGluAspThrProValSerAlaLeuGlnTyrIle 559
Db 1810 GTTCTGTCCAGATCAATCTTGAGGATACCACTCTGTCTGAGCTTACAGTATATC 1869
QY 560 ThrThrSerSerMetThrIleAlaProGlyGlyArgGluLeuValValPhePheSerLeu 579
Db 1870 ACCACTAGTCTATGACCAATGCCCCCAAGGCCGAGAGCTGGTAGTGTCTTTCAGTCTG 1929
QY 580 ArgValAlaAanMetAlaPheSerAsnAspIleuPheAsnLysSerSerLeuGluTyrArg 599
Db 1930 CGTGTGCTAAATGCGCTTCTCAACAGACCTGTTCACAGAGCTCTCTGGAGTACCGA 1989
QY 600 AlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrIleuArgSerAsnLeuThrGly 619
Db 1990 GCTCTGGAGCAACAATTCACACAGCTGCTGTTCATATCTACGATCCATCTTACAGGA 2049
QY 620 PheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMet 639
Db 2050 TTTAAGCAACTGGAATTAATCTTAACCTCAGAAACGGGAGTGTGATGTGCAATAGCAAAATG 2109
QY 640 LysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAsp 659
Db 2110 AAGTTTGCTAGTCTGTGCCGTATTAACCTCAAGAGCTGTGCACGGGTCTTGGAGAT 2169
QY 660 PheArgSerAlaAlaGlnGlnLeuHisLeuGluLeuAspSerTyrSerLeuAsnIle 679
Db 2170 TTTGCTTCTGTGCGCCCAACAATCTCATCTGGAATAGACAGCTACTCTCTCAACATT 2229
QY 680 GluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCys 699
Db 2230 GAACAGCTGTATCAAGCAGATCCCTGCAAGTTCTGTGGCTGCGCGAATTTGCCAATGT 2289
QY 700 ValLysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGln 719
Db 2290 GTAAAGACGAACGAGCTGAGGAAGCGAGTGTGCTGCAAAACAGGATATGACAGCCAG 2349
QY 720 GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluVal 739
Db 2350 GGGAGCCTGGACGGTCTGGAAACCAAGGCTCTGTGGCCCTGGCAAAAGGAATGCGAGGTC 2409
QY 740 LeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLys 759
Db 2410 CTCAGGGAAGGGAGCTCCATGAGGTGTGCAGATCACTCTGAATCAAGCATACAAA 2469
QY 760 ThrSerValLysPheGlnAsnGlnAsnLysValIleSerLysArgAsnSer 779
Db 2470 ACTAGTGTAAAGTTCAAAATCAACAAATAACAGGTAATCAGTAAAGAAATCT 2529
QY 780 GluLeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTyrGluGlyAsn 797
Db 2530 GAATTACTGACCGTAGAATATGAAGAATTTAAACCATCAAGATTGGGAAGGAAT 2583
```

RESULT 2  
ID ACC57946

AC ACC57946 standard; cDNA; 3330 BP.

XX ACC57946;

XX 11-AUG-2003 (first entry)

DE Human interphotoreceptor matrix IPM 150, isoform A, cDNA.

XX Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;  
KW receptor; ophthalmological; gene therapy; gene; ss.  
XX Homo sapiens.  
XX OS  
XX Key Location/Qualifiers  
XX CDS 131..2586  
XX FT /\*tag= a  
XX FT /product= "IPM 150"  
XX FT /transl\_except= (pos:668..756,aa:Thr-Asp)  
XX FT sig\_peptide 131..190  
XX FT /\*tag= b  
XX PN WO2003039346-A2.

XX 15-MAY-2003.

XX 08-NOV-2002; 2002WO-US036090.

XX 08-NOV-2001; 2001US-0007270.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Hageman GS, Kuehn MH;

XX WPI; 2003-441440/41.

XX P-PSDB; ABR42342.

XX New interphotoreceptor matrix proteins and polynucleotides, useful for  
PT treating or preventing photoreceptor death or retinal detachment, or for  
PT treating ocular disorders.

XX Claim 1; Page 77; 105pp; English.

XX The present sequence is that of cDNA encoding isoform A of novel human  
CC interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
CC interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
CC is located on chromosome 6q13-q15, a region that also contains loci for  
CC progressive bifocal choroidretinal atrophy, autosomal dominant Stargardt's  
CC -like macular dystrophy, North Carolina macular dystrophy and Salla  
CC disease. Members of the IPMC gene family have been identified in humans,  
CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2  
CC Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The  
CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
CC antibodies that specifically bind the polypeptides, and vectors  
CC comprising the polynucleotides. A claimed method of treating or  
CC preventing photoreceptor death or retinal detachment involves  
CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
CC claimed is a method for identifying a compound capable of modulating IPMC  
CC gene expression

XX SQ Sequence 3330 BP; 1069 A; 737 C; 674 G; 850 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 0 Length: 3330  
Score: 4073.00 Matches: 796  
Percent Similarity: 97.31% Conservative: 0  
Best Local Similarity: 97.31% Mismatches: 1  
Query Match: 98.93% Indels: 22  
DB: Gaps: 1

US-10-007-270-2 (1-797) x ACC57946 (1-3330)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTyrIlePheLeuGlnValGlnGly 20  
Db 131 ATGTATTTCGAAACTAGAGAGCTATTTTGTGTTTTCGATTTTCTCCAGTTCAAGGA 190

QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAsnProPro 40  
Db 191 ACCAAGATATCTCCATTAAACATATACCATTTGAACTAAAGATAGACATATCCCCA 250

QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgile 60

Db 251 AGAAAAAGAACTGAAAGTACTGAAAAAATGTACAAAAATGTCAACTATGAGACGAATA 310  
Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
Db 311 TTCGATTGGCAAGACACGAACAAAAAGATCCGATTTTCCCAACGGGGGTTAAAGTC 370  
Qy 81 CysProGlnGlnSerMetLysGlnLleLeuAspSerLeuGlnAlaTyTyArgLeuArg 100  
Db 371 TGTCCACAGGAATCCATGAAACAGATTTTAGACAGCTCTCAAGCTTATTATAGATTGAGA 430  
Qy 101 ValCysGlnGlnAlaValTrpGlnAlaTyArgLlePheLeuAspArgLleProAspThr 120  
Db 431 GGTGTGCAGAAAGCAGATGGAAGACATATCGGATCTTTCGGATCGCATCCCTGCACACA 490  
Qy 121 GlyIuTyGlnAspTrpValSerLleCysGlnGlnGlnThrPheCysLeuPheAspLle 140  
Db 491 CGGGAATATCAGCATGGGTGACATCTGCCAGCAGGAGACCTTCTGCTCTCTTGACATT 550  
Qy 141 GlyLysAsnPheSerAsnSerGlnGlnHisLeuAspLeuGlnGlnArgLleLysGln 160  
Db 551 GGAATAAACTTCAGCAATTCAGGAGCACCTGGATCTTCTCCAGCAGAGATTAACAG 610  
Qy 161 ArgSerPheProAspArgLysAspGluLleSerAlaGluLysThrLeuGlyGluProGly 180  
Db 611 AGAAGTTTCCCTGACAGAAAGATGAATATCTGCAGAGNAGACATTGCGGAGAGCCTGGT 670  
Qy 181 GluThrLleValLleSerThr----- 187  
Db 671 GAAACATTGTTCATTTCAC- AGCAATCTACATTTCAAAGACTTGGGCGAGTATTC TAAGA 729  
Qy 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
Db 730 AAACCTCAGAGACCAATTCAGATGTTGCCAAGCTCCTCATTTGGGCGCTTCCCTCTC 789  
Qy 200 ThrProAspAspThrLeuLeuAsnGlnLleLeuAspAsnThrLeuAsnAspThrLysMet 219  
Db 790 ACTCTGTATGACACCTCTCCTCAATGAAATTCGATAATACATCAACGACACCAAGATG 849  
Qy 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSer 239  
Db 850 CTTACAAAGAAAGAGAAACAGAAATTCGCTGTGTGGAGGACGAGAGGTGGAGCTCAGC 909  
Qy 240 ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyTy 259  
Db 910 GTCTCTCTGTTAAACAGAAATCAAGGACAGAGCTCGCTGACTCCAGTCCCCATATTAC 969  
Qy 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysLlePheLysLysLeuProGly 279  
Db 970 CAGGAGCTAGCAGGAAGTCCCAACTTCAGATGCAAAAGATATTTAAGAAATCTCCAGGA 1029  
Qy 280 PheLysLysLleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer 299  
Db 1030 TTCAAAAAATCCATGTGTTAGATTGACCAAAAGAAAGAAAGATGGCTCAAGTCC 1089  
Qy 300 ThrGluMetGlnLeuThrAlaLlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
Db 1090 ACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAAGCCCTGCA 1149  
Qy 320 SerAspLeuLeuSerPheAspSerAsnLysLleGluSerGluGluValTyHisGlyThr 339  
Db 1150 AGTGACTCTCTGCTTTGATTCACAAAAATTGAAGTGAGGAAGTCTATCATGGAACC 1209  
Qy 340 MetGluGluAspLysGlnProGluLleTyLeuThrAlaThrAspLeuLysArgLeuLle 359  
Db 1210 ATGGAGGAGGACAAAGCAACAGAAATCTATCTCACAGCTACAGACTCAAAAGGCTGATC 1269  
Qy 360 SerLysAlaLeuGluGlnGlnSerLeuAspValGlyThrLleGlnPheThrAspGlu 379  
Db 1270 AGCAAGCCTAGAGGAAGAACAAATCTTTGGATGTGGGACCAATTCAGTTCTACTGATGNA 1329  
Qy 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399

Db 1330 ATTGCTGGATCACTGCCAGCCTTTGGTCTCTGACACCCCAATCAGAGCTGCCACATCTTTT 1389  
Qy 400 AlaValLleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
Db 1390 GCTGTTTATAACAGAGATGCTACTTTAGTCCAGAACTTCTCTCTGTTGAACCCAGCTT 1449  
Qy 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProProAlaMet 439  
Db 1450 GAGACAGTGGACGGACGAGCATGCTTACTCTGACACTTCTTGGTCTCCACCTGCTATG 1509  
Qy 440 AlaSerThrSerLeuSerGluAlaProPhePheMetAlaSerSerLlePheSerLeu 459  
Db 1510 GCCTCTACCTCCCTGTCCAGAAAGCTCCACCTTCTTATGGCATCAAGCATCTCTCTCTG 1569  
Qy 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
Db 1570 ACTGATCAAGGACCAACAGATACATGGCCACTGACACAGCAATGCTAGTACAGGGCTC 1629  
Qy 480 ThrLleProThrSerAspTySerAlaLleSerGlnLeuAlaLeuGlyLleSerHisPro 499  
Db 1630 ACCATCCCCCAGCTGATTATTTCGAATCAGCAACTGGCTCTGGGAATTTTCACATCCA 1689  
Qy 500 ProAlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeu 519  
Db 1690 CCTGCACTCTTCAGATCAGACCGCATCAAGTGCAGGTGGCAAGATATGTCAGACACCTA 1749  
Qy 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTy 539  
Db 1750 GATGAAATGGATCTGTGACACTCTCTGCCCATCTGAGGTACACAGCTCAGCGAATAT 1809  
Qy 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyLle 559  
Db 1810 GTTCTCTGCCAGATCATTTCTTGGAGGATACACCTCTCTCTCAGCTTTACAGTATATC 1869  
Qy 560 ThrThrSerSerMetThrLleAlaProLysGlyArgGluLeuValValPhePheSerLeu 579  
Db 1870 ACCACTAGTTCTATGACCAATGCCCCCAAGGGCCGAGAGCTGGTAGTGTCTTCACTCTG 1929  
Qy 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyArg 599  
Db 1930 CGTGTGTTAAACATGGCTTCTCCAACGACCTGTCTCAACAGAGCTCTCTGGAGTACCGA 1989  
Qy 600 AlaLeuGlnGlnGlnPheThrGlnLeuLeuValProTyLeuArgSerAsnLeuThrGly 619  
Db 1990 GCTCTGGAGCAACAATTCACACAGCTGTGGTTTCCATATCTAGCATCCCAATCTTACAGGA 2049  
Qy 620 PheLysGlnLeuGluLleLeuAsnPheArgAsnGlySerValLleValAsnSerLysMet 639  
Db 2050 TTTAAGCAACTTGAATACTTAACTTTCAGAAACGGGAGTGTGATTGTGAATAGCAAAATG 2109  
Qy 640 LysPheAlaLysSerValProTyAsnLeuThrLysAlaValHisGlyValLeuGluAsp 659  
Db 2110 AAGTTTGTAAAGTCTGTGCCGTATACTCACCAGGCTGTGCACGGGTCTTGGAGGAT 2169  
Qy 660 PheArgSerAlaAlaGlnGlnLeuHisLeuGluLleAspSerTyTrSerLeuAsnLle 679  
Db 2170 TTTCTGTCTCTGCAGCCCAACCACTCCATCTCGAAATAGACAGCTACTCTCTCAACAT 2229  
Qy 680 GluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCys 699  
Db 2230 GAACCACTGATCAAGCAGATCCCTGCAAGTTCCTGCGCTGCGCGCAATTTGCCCAATGT 2289  
Qy 700 ValLysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyAspSerGln 719  
Db 2290 GTAAAGAACCAAGACTGAGGAAGGGAGTGTGCTGCAACACAGGATATGACGCCAG 2349  
Qy 720 GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluVal 739  
Db 2350 GGGAGCCTGACGCTCTGGAAACCAAGCCTCTGTGTGCCCTGTGGCACAAGGAATCGGAGTC 2409  
Qy 740 LeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyLys 759  
Db 2410 CTCAGGGAAGGGAGCTCCATGAGTTGCCAGATCACTCTGAAATCAAGCATACAAA 2469



Db 1028 GAGATGCAACTTACGGCCATCTTTAAGAGACACAGTCGGAAGCAAAAGCCCTGCAAGT 1087  
Qy 321 AspleuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThrMet 340  
Db 1088 GACCTCCTGCTCTTTGATTCACACAAATTTGAAGTGGAGAGTCTATCATGGAACCATG 1147  
Qy 341 GluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIleSer 360  
Db 1148 GAGGAGGACAGCAACCAACCAATCTATCTACAGCTACAGACCTCAAAAGGCTGATCAGC 1207  
Qy 361 LysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380  
Db 1208 AAAGCACTAGAGGAAGAACATCTTTGGATGTGGGCAAAATTCAGTCACTGATGAAT 1267  
Qy 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
Db 1268 GCTGGATCACTGCCAGCCTTTGGTCTGACACCCCAATCAGAGCTGCCACATCTTTTGCT 1327  
Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProValGluProGlnLeuGlu 420  
Db 1328 GTTATAACAGAGGATGCTTGTAGTCCAGAACTTCTCTGTTGAACCCACGCTTGAG 1387  
Qy 421 ThrValAspGlyAlaGluHisGlyLeuProAspThrSerTyrPheSerLeuThr 440  
Db 1388 ACAGTGGACGGACAGACGATGCTTACCTGACACTTCTCTGCTGCCACCTGCTATGCC 1447  
Qy 441 SerThrSerLeuSerGluAlaProPhePheMetAlaSerSerIlePheSerLeuThr 460  
Db 1448 TCTACTCTCCTGTGAGAGCTCCACTTCTTTATGGCATCAGCACTCTCTCTGACT 1507  
Qy 461 AspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThr 480  
Db 1508 GATCAAGGCACACAGATACAAATGGCCACTGACAGACAAATGCTAGTACCAAGGCTCACC 1567  
Qy 481 IleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro 500  
Db 1568 ATCCCAACAGAGATATCTCAATCAGCAACCTGCTGCGGAATTTCACTCCACCT 1627  
Qy 501 AlaSerSerAspAspSerArgSerAlaGlyGlyGluAspMetValArgHisLeuAsp 520  
Db 1628 GCATCTTCAGATGACAGCCGATCAAGTCAGGTGCGAAGATATGTCAGACACCTAGAT 1687  
Qy 521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrVal 540  
Db 1688 GAAATGGATCTCTGACACTCTCTCCCATCTGAGGTACCAAGCTCAGCGCAATATGTT 1747  
Qy 541 SerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThr 560  
Db 1748 TCTGTCACAGATCATCTTGGAGGATACCACTCTCTGCTCAGCTTTACAGTATATCACC 1807  
Qy 561 ThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeuArg 580  
Db 1808 ACTAGTCTTATGACCATGCCCCCAAGGCCGAGAGCTGAGTGTCTTTCAGTCTGGT 1867  
Qy 581 ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAla 600  
Db 1868 GTTGCTTAACTGGCTCTTCCACACGCTTTTCACAAAGAGCTCTCTGAGTACCGAGCT 1927  
Qy 601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
Db 1928 CTGGAGCAACAATTACACAGCTGTGTGTTCCATATCTACGATCCAAATCTTACAGGATTT 1987  
Qy 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
Db 1988 AAGCAACTTGAATATCTTAACCTCAGAAACCGGAGCTGTGATTTGTAATAGCAAAATGAG 2047  
Qy 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660  
Db 2048 TTGTCTAAGTCTGTGCGGTATTAACCTCAGCAAGGCTGTGCACGGGCTCTTGGAGGATTT 2107  
Qy 661 ArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680

Db 2108 CGTCTGTGTCAGCCCAACACTCCATCTGGAAATAGACAGCTACTCTCTCAACATTGAA 2167  
Qy 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
Db 2168 CCAGCTTGATCAAGCAGATCCCTGCAAGTTCCTGGCTCGCGCAATTTGCCCAATGTGTA 2227  
Qy 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGly 720  
Db 2228 AAGACGACGACGACCTGAGGAACGGAGTGTGCTGCAAAACCAAGGATATGACAGCCAGGG 2287  
Qy 721 SerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740  
Db 2288 AGCCTGAGCGCTGAGAACCAAGCTCTGTGG-CTGGCACAAGGAATGCGAGTCTCTC 2346  
Qy 741 GlnGlyLysGlyValProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThr 760  
Db 2347 CAGGGAAGGAGCTCCATGCG-GTTCAGATCACTCTGAAAATCAGCATACAAAAT 2404  
Qy 761 SerValLysPheGlnAsnGlnGlnAsnLysValIleSerLysArgAsnSerGlu 780  
Db 2405 AGTGTAAAAAGTTCCAAATCACAAAATAACAAGTAATCAGTAAAGAAATTTCTGAA 2464  
Qy 781 Leu-LeuThrValGluTyrGluGluPheAsnHisGlnAspTyrGluGlyAsn 797  
Db 2465 TTATCTGACCGTAGAATATGAAGAATTTAACCATCAGATTGGAGGAAT 2516

RESULT 4  
ADA14866  
ID ADA14866 standard; cDNA; 3261 BP.  
XX ADA14866;  
XX 06-NOV-2003 (first entry)  
DE Human cDNA encoding variant IPMC 150 isoform A.  
XX ss; gene; human; IPMC 150 isoform A; gene therapy;  
KW interphotoreceptor matrix component; IPMC; ocular disorder;  
KW macular degeneration; photoreceptor death; retinal detachment.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT CDS 128..2443  
FT /'tag= a  
FT /product= "Variant IPMC 150 isoform A"  
XX US2002160954-A1.  
XX 31-OCT-2002.  
XX 08-NOV-2001; 2001US-00007270.  
XX 29-OCT-1998; 98US-00183972.  
XX 29-OCT-1999; 99US-00430195.  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX Hageman GS, Kuehn MH;  
XX WPI; 2003-238235/23.  
XX P-PSDB; ADA14867.  
XX New isolated or recombinant interphotoreceptor matrix component  
XX polynucleotide and polypeptide, useful for diagnosing, preventing,  
XX treating or prognosticating ocular disorders, e.g. macular degeneration  
XX or retinal detachment.  
XX Claim 3; Page 63-66; 76pp; English.  
XX The invention relates to an isolated or recombinant interphotoreceptor  
XX matrix component (IPMC) polynucleotide. Also disclosed is a vector  
XX comprising a promoter of an interphotoreceptor matrix component (IPMC)

CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding  
 CC variant human interphotoreceptor matrix component, IPMC, 150 isoform A.  
 XX

50 Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;

## Alignment Scores:

Pred. No.: 4,32e-316 Length: 3261  
 Score: 4024.50 Matches: 793  
 Percent Similarity: 99.62% Conservations: 1  
 Best Local Similarity: 99.50% Mismatches: 3  
 Query Match: 97.75% Indels: 3  
 DB: 7 Gaps: 0

US-10-007-270-2 (1-797) x ADA14866 (1-3261)

Qy 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
 Db 128 ATGTAATTGGAACTAGAGAGCTATTATTTTGTGTTTGGATTTTCTCCAAAGTTCAGGA 187  
 Qy 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
 Db 188 ACTAAGATATCTCCATTACATATACCATTCGAAACTTAAGCATAGACATCCCCCA 247  
 Qy 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
 Db 248 AGAATGAACAACTGAAAGTACTGAAAAAATGTACAAAATGTCAACTATGAGACGAATA 307  
 Qy 61 PheAspLeuAlaLysHisArgTyrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 Db 308 TTCGATTTGGCAAGCATCGACAAAAGATCCGATTTTCCACGGGGTTAAAGTC 367  
 Qy 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 368 TGTCACAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTATAGATTGAGA 427  
 Qy 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 Db 428 GTGTGTGAGGAGCAGTATGGGAGCATATCGGATCTTTCGGATCCGATCCCTCGACACA 487  
 Qy 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 Db 488 GGGGAATATCAGGACTGGGTCAGCATCTGCCAGCAGGAGACCTTCTGCTCTTTGACATT 547  
 Qy 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgIleLysGln 160  
 Db 548 GGAATAAACTTCAGCAATTCAGAGACACCTGGATCTTCTCCAGCAGAGAAATAAACAG 607  
 Qy 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 Db 608 AGAAGTTTCCCTGCAGAAAAGATGAATATCTGCAGAGAGACATTTGGAGAGCTGGT 667  
 Qy 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 Db 668 GAAACCATTTGTCAITTCACAGATGTTGCCAACGCTCTCACTTGGGCTTTCCCTCTCACT 727  
 Qy 201 ProAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
 Db 728 CCTGATGACACCCCTCTCAATGAATTTCTCGATTAATACATCTCAACGACACCAAGATGCCT 787  
 Qy 221 ThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSerVal 240  
 Db 788 ACAACAGAAAGAGAAACAGAAATTCGTGTGTGTGGAGGAGCAGAGGGTGGAGCTCAGGCTC 847  
 Qy 241 SerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGln 260  
 Db 848 TCTCTGGTAAACCAAGATTCAGAGCAGAGCTGCTGACTCCCACTCCCATATTACCAG 907  
 Qy 261 GluLeuAlaGlyLysSerGlnGlnMetGlnLysIlePheLysLysLeuProGlyPhe 280

Db 908 GAGCTAGCAGGAAAGTCCCACTTCAGATGCAGAAAGATATTAAAGAACTTCCAGGATTTC 967  
 Qy 281 LysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSerThr 300  
 Db 968 AAAAAATCCATGTGTAGGATTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCACA 1027  
 Qy 301 GluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProLaser 320  
 Db 1028 GAGATGCACACTTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAAGCCCTCAAGT 1087  
 Qy 321 AspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThrMet 340  
 Db 1088 GACCTCTCTGTTTGTGATTCACCAAAATTTGAAGTGAAGAGTCTATCATCGGAACCATG 1147  
 Qy 341 GluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIleSer 360  
 Db 1148 GAGGAGGACAAAGCAACCAAGATCTATCTCAGCTACAGACCTCCAAAGCGTGTATCAGC 1207  
 Qy 361 LysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380  
 Db 1208 AAAGCACTAGAGGAAGAAACATCTTTGGATGTGGGACAAATTCAGTTCATGTAGAAATT 1267  
 Qy 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
 Db 1268 GCTGGATCACTGCCAGCCTTTGGTCTGCACACCAATCAGAGCTGCCACATCTTTTGTCT 1327  
 Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProValGluProGlnLeuGlu 420  
 Db 1328 GTTATAACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTGTGTAACCCAGCTTGAG 1387  
 Qy 421 ThrValAspGlyValAlaGluHisGlyLeuProAspThrSerTrpSerProAlaMetAla 440  
 Db 1388 ACAGTGGAGCGGAGCAGACATGGTCTACCTGCACACTTCTGTCTCTCCACCTGTATGCC 1447  
 Qy 441 SerThrSerLeuSerGluAlaProPhePheMetAlaSerSerIlePheSerLeuThr 460  
 Db 1448 TCTACTCTCTGTCCAGAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTGTACT 1507  
 Qy 461 AspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThr 480  
 Db 1508 GATCAAGGACCAACAGATACATGGCCACTGACCCAGACAAATGTAGTACAGGGCTCACC 1567  
 Qy 481 IleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro 500  
 Db 1568 ATCCCCCAGCAGTATATTCTGCAATCAGCAACTGGCTCTGGAAATTTCACTCACTCACT 1627  
 Qy 501 AlaSerSerAspAspSerArgSerSerAlaGlyGlyLeuAspMetValArgHisLeuAsp 520  
 Db 1628 GCATCTTCAGATGACAGCCGATCAAGTCAGGTGGCGAAGATATGGTCAGACACCTAGAT 1687  
 Qy 521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrVal 540  
 Db 1688 GAAATGGATCTGTCTGACACTCTGCCCCCATCTGAGGTACCAGAGCTCAGCGAATATGTT 1747  
 Qy 541 SerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThr 560  
 Db 1748 TCTGTCCCAGATCACTTCTTGAGGATACCACTCTCTGCTCAGCTTTTACAGTATATCACC 1807  
 Qy 561 ThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeuArg 580  
 Db 1808 ACTAGTCTTATGACCATTTGCCCCCAAGGCGGAGAGCTGGTAGTGTCTTCTCAGTCTCGT 1867  
 Qy 581 ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAla 600  
 Db 1868 GTTGTCTAATGCTCTCTCCAAACGACCTGTTTCAACAGAGCTCTCTCGAGTACCGAGCT 1927  
 Qy 601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
 Db 1928 CTGGAGCAACCAATTCACAGCTGCTGTTTCCATATCTACGATCCATCTTACAGGATTT 1987  
 Qy 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640



Db 1988 AGCAACTTGAATACTTAACCTTCAGAAACGGAGTGTGATTGTGAATGCAAAATGAAG 2047  
 Qy 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660  
 Db 2048 TTTGCTAAAGTCTGTCCCGTATAACCTCAACCAAGGTGTGCACGGGGTCTTTGGAGATTTT 2107  
 Qy 661 ArgSerAlaAlaGlnGlnLeuHisLeuGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 680  
 Db 2108 CTTTCTGTGTGACGCCCAACACTCCATCTGGAATATAGACACTTCTCTCAACATTGAA 2167  
 Qy 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
 Db 2168 CCAGCTGATCAAGCAGATCCCTGCAAGTTCCTGGCCTGCGCGCAATTTGCCAATGTGTA 2227  
 Qy 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGly 720  
 Db 2228 AAGAAGCAAGGACTGAGAGACGGAGTGTCTGTCGAACACGAGATATGACAGCCAGGG 2287  
 Qy 721 SerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740  
 Db 2288 AGCCTGGAGCGGTCTGGAACCAAGGCTCTGTGG-CCTGGCACAAGGAATGGAGTCTCTC 2346  
 Qy 741 GlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThr 760  
 Db 2347 CAGCGAAGAGGAGCTCCATGGG--GTTCCAGATCACTCTGAAATCAAGCATACAAAAC 2404  
 Qy 761 SerValLysLysPheGlnAsnGlnGlnAsnLysValLysSerLysArgAsnSerGlu 780  
 Db 2405 AGTGTTAA-AGTTCAAAATCACAAAATACCAAGGTAAATCAGTAAAGAAATTCGTGAA 2463  
 Qy 781 LeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTrpGluGlyAsn 797  
 Db 2464 TTACTGACCGTAGAATATGAAGATTTAAACCATCAAGATTGGGAAGGAAT 2514  
 RESULT 5  
 ID ACC57960 standard; cDNA; 3261 BP.  
 XX AC ACC57960;  
 XX 11-AUG-2003 (first entry)  
 DE Human interphotoreceptor matrix IPM 150, isoform A variant, cDNA.  
 XX Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;  
 KW receptor; ophthalmological; gene therapy; gene; ss.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 CDS 128..2443  
 FT /\*tag= a  
 FT /product= "IPM 150"  
 XX WO2003039346-A2.  
 XX 15-MAY-2003.  
 XX 08-NOV-2002; 2002WO-US036090.  
 XX 08-NOV-2001; 2001US-00077270.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 XX Hageman GS, Kuehn MH;  
 XX WPI; 2003-441440/41.  
 DR P-PSDB; ABR42354.  
 XX New interphotoreceptor matrix proteins and polynucleotides, useful for  
 PT treating or preventing photoreceptor death or retinal detachment, or for  
 PT treating ocular disorders.  
 XX

PS Claim 1; Page 91-94; 105pp; English.  
 XX The present sequence is that of cDNA encoding a variant of isoform A of  
 CC novel human interphotoreceptor matrix 150 (IPM 150), a member of the  
 CC newly identified interphotoreceptor matrix component (IPMC) gene family.  
 CC The cDNA was isolated from a human retinal cDNA library. The IPM 150 gene  
 CC is located on chromosome 6q13-q15, a region that also contains loci for  
 CC progressive bifocal chorioretinal atrophy, autosomal dominant Stargardt's  
 CC like macular dystrophy, North Carolina macular dystrophy and Salla  
 CC disease. Members of the IPMC gene family have been identified in humans,  
 CC monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2 IPMG2). The  
 CC subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The  
 CC invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,  
 CC antibodies that specifically bind the polypeptides, and vectors  
 CC comprising the polynucleotides. A claimed method of treating or  
 CC preventing photoreceptor death or retinal detachment involves  
 CC administering an IPMC polynucleotide, polypeptide or antibody. Also  
 CC claimed is a method for identifying a compound capable of modulating IPMC  
 CC gene expression  
 XX  
 SQ Sequence 3261 BP; 1039 A; 721 C; 663 G; 837 T; 0 U; 1 Other;  
 Alignment Scores:  
 Pred. No.: 4,328-316 Length: 3261  
 Score: 4024.50 Matches: 793  
 Percent Similarity: 99.62% Conservative: 1  
 Best Local Similarity: 99.50% Mismatches: 3  
 Query Match: 97.75% Indels: 3  
 DB: Gaps: 0  
 US-10-007-270-2 (1-797) x ACC57960 (1-3261)  
 Qy 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
 Db 128 ATGTATTTCGAAACTAGAAAGACTATTTTGTGTTTTCGATTTTCTCCAACTTCAAGA 187  
 Qy 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
 Db 188 ACTAAAGATATCTCCATTAACTATACCATTTCTGAACTAAAGACATAGACAAATCCCCA 247  
 Qy 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgIle 60  
 Db 248 AGAATGAAACCAACTGAAAGTACTGAAAAATGTACAAAATGTCAAAATATGACATATGAGACGAATA 307  
 Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 Db 308 TTCGATTTCGCAAGCATCGAAACAAAGATCCGATTTTCCCAACGGGGGTAAAGTC 367  
 Qy 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 368 TGTCACACAGGAATCCATGAAACAGATTTTAGACAGTCTTCAAGCTTATTATAGATTGAGA 427  
 Qy 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 Db 428 GTGTGTGAGAAAGCATATGGGAAGCATATCGGATCTTTCTGGATCGCATCCCTGACACA 487  
 Qy 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGlnThrPheCysLeuPheAspIle 140  
 Db 488 GGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAGGAGACCTTCTGCCCTCTTGACATT 547  
 Qy 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGln 160  
 Db 548 GGAATAAACTTCAGCAATTTCCAGGAGCACCTTGGATCTTCTCCAGCAGAGAATAAAACAG 607  
 Qy 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGluProGly 180  
 Db 608 AGAAGTTTCCCTGACAGAAAGATGAATATTTCTGCAGAGAAACATTTGGAGAGCTGGT 667  
 Qy 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 Db 668 GAATCCATTGTCTATTTCAACAGATGTTGCCAAGCTCTCACTTGGGCTTTCCTCTCACT 727  
 Qy 201 ProAspAspThrLeuLeuAsnGlnIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220

```
Db 728 CCTGATGACACCCCTCCCAATGAAATTCGATAATACACTCAACGACACCAAGATGCCT 787
Qy ThrThrGluArgGluThrGluPheAlaValLeuGluGluArgValGluLeuSerVal 240
Db 788 ACAACAGAAAGAGAAACAGAAATTCGCTGCTGTGGAGGAGCAGAGGCTGAGCTCAGGCTC 847
Qy 241 SerLeuValAenGlnLysPheGlyAlaGluLeuAlaAspSerGlnSerProTyrTyrGln 260
Db 848 TCTCTGGTAAACCAAGAAATTCAGAGCAGAGCTCGCTGACTCCCAAGTCCCATATTACCA 907
Qy 261 GluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPhe 280
Db 908 GAGCTAGCAGAAAGTCCCACTTCAGATGCAAAAGATATTAAAGAACTTCAGAGTTC 967
Qy 281 LysIleLysLeuGlyPheArgProLysLysGluLysAspGlySerSerThr 300
Db 968 AAAAAATCCATGTCTTAGGATTTAGACCAAGAAAGAAAGATGCTCAAGCTCCACA 1027
Qy 301 GluMetGlnLeuThrAlaIlePheIysArgHisSerAlaGluAlaLysSerProAlaSer 320
Db 1028 GAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAGCAAAAGCCCTGCAAGT 1087
Qy 321 AspLeuLeuSerPheAspSerAsnLysIleGluSerGluValTyrHisGlyThrMet 340
Db 1088 GACCTCCTGCTTTTGATTTCCACAAATTCGAAAGTGAAGTCTATCATGGAACCATG 1147
Qy 341 GluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIleSer 360
Db 1148 GAGGAGGCAAGCAACCAAGAAATCTATCTCACGTACAGACCTCAAAAGGCTGATCAGC 1207
Qy 361 LysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380
Db 1208 AAGCACTAGAGGAGAACACATCTTTGATGTGGGACACATTCAGTTCACTGATGAAT 1267
Qy 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400
Db 1268 GCTGGATCACCTGCCAGCCTTTGGTCTGACACCAATCAGAGCTGCCCATCTTTTGCT 1327
Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProValGluProGlnLeuGlu 420
Db 1328 GTTATACAGAGGATGCTACTTTGATCCAGAACTTCTCTCTGTGAACCCAGCTTGAG 1387
Qy 421 ThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrpSerProAlaMetAla 440
Db 1388 ACAGTGGACGAGCAGACGATGCTACCTGACACTTCTTGCTCCACCTGCTATGCCC 1447
Qy 441 SerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThr 460
Db 1448 TCTACCTCCCTGTCAGAAAGCTCCACCTTTCTTTATGGCATCAAGCATCTTCTCTGACT 1507
Qy 461 AspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThr 480
Db 1508 GATCAGGACCAACAGATACATATGACCACTGACGACATGCTAGTACAGGGCTCACC 1567
Qy 481 IleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro 500
Db 1568 ATCCCAACAGTGATATTCTGCAATCAGCACTGCTCTGGGAATTCACATCCACCT 1627
Qy 501 AlaSerSerAspAspSerArgSerSerAlaGlyGlyLeuAspMetValArgHisLeuAsp 520
Db 1628 GCATCTTCAGATGACAGCCGATCAAGTGCAGTGGCGAAGATATGTCAGACACCTAGAT 1687
Qy 521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrVal 540
Db 1688 GAAATGGATCTGCTGACACTCTGACACTCTGCCCCATCTGAGGTACAGAGCTCAGCGAATATGTT 1747
Qy 541 SerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThr 560
Db 1748 TCTGTCCAGATCATCTTCTGGAGGATACCACTCTCTGCTCAGCTTTACAGTATATCACC 1807
Qy 561 ThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeuArg 580
```

```
Db 1808 ACTAGTCTTATGACCATTTGCCCTCCCAAGGCGAGAGCTGTAGTGTCTTTCAGTCTGCGT 1867
Qy 581 ValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAla 600
Db 1868 GTTGCTAAACATGCGCTTCTCCAAACGACCTGTCAACAAGAGCTCTCTGGAGTACCGAGCT 1927
Qy 601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620
Db 1928 CTGGAGCAACAATCACAGCTGCTGTGTTCCATATCTACGATCCATCTTACAGATTT 1987
Qy 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640
Db 1988 AAGCAACTTGAATTAATTAACCTTCAGAAACGGAGCTGTGATTGTGAATAGCAAAATGAAG 2047
Qy 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660
Db 2048 TTTGTGTAAGTCTGTGCGGTATAACCTCCCAAGGCTGTGCACGGGTCTTGGAGATTTT 2107
Qy 661 ArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680
Db 2108 CTTTCTGTGCGAGCCCACTCCATCTGGAAATAGACAGCTACTCTCTCAACATTGAA 2167
Qy 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700
Db 2168 CCAGCTGATCAAGCAGATCCCTGCAAGTTCTTGGCTGCGCGAATTTGCCCAATGTGA 2227
Qy 701 LysAsnGluArgThrGluGluAlaGlyCysArgCysLysProGlyTyrAspSerGlnGly 720
Db 2228 AAGAAGCAACGAGCTAGGAGCGAGGTGCTGCTCAAAACAGGATATGACAGCCAGGG 2287
Qy 721 SerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740
Db 2288 AGCTGGACGCTTGGAAACCAAGCTCTGTGG-CTTGGCACAAGGAATCGAGGCTCCTC 2346
Qy 741 GlnGlyLysGlyAlaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThr 760
Db 2347 CAGGGAAGGAGGAGCTCCATGCG--GTTCCAGATCACTCTGAAAATCAAGCATACAAACT 2404
Qy 761 SerValLysLysPheGlnAsnGlnGlnAsnAsnLysValIleSerLysArgAsnSerGlu 780
Db 2405 AGTGTTAA-AGTTCCAAAATCAACAATAACAAGGTAATCAGTAAAGAAATCTGAA 2463
Qy 781 LeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTrpGluGlyAsn 797
Db 2464 TTACTGACCGTAGAATATGAGAAATTTAACCATCAAGATTGGGAAGGAAAT 2514
RESULT 6
ADA14842 standard; cDNA; 2887 BP.
ID ADA14842
AC AC
XX ADA14842;
XX 06-NOV-2003 (first entry)
DT Human interphotoreceptor matrix component, IPMC, 150 isoform B cDNA.
DE ss; gene, human; IPMC 150 isoform B; gene therapy;
XX interphotoreceptor matrix component; IPMC; ocular disorder;
KW macular degeneration; photoreceptor death; retinal detachment.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 5..2143
CDS /tag= a
FT /partial
FT /product= "IPMC 150 isoform B"
FT /note= "No start codon given. Encodes residues 8-719 of
XX {seqid:4}"
XX
XX US2002160954-A1.
XX 31-OCT-2002.
XX PD
```

XX 08-NOV-2001; 2001US-00007270.  
 XX PF  
 XX 29-OCT-1998; 98US-00183972.  
 PR 29-OCT-1999; 99US-00430195.  
 XX PA  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 XX PI  
 XX Hageman GS, Kuehn MH;  
 XX WPI; 2003-238235/23.  
 DR P-PSDB; ADA14843.  
 XX  
 PT New isolated or recombinant interphotoreceptor matrix component  
 PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 PT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.  
 XX  
 PS Claim 3; Page 33-34; 76pp; English.  
 CC The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding human  
 CC interphotoreceptor matrix component, IPMC, 150 isoform B.  
 XX  
 SQ Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: Length: 2887  
 Score: 3619.00 Matches: 711  
 Percent Similarity: 90.00% Conservative: 0  
 Best Local Similarity: 90.00% Mismatches: 1  
 Query Match: 87.90% Indels: 78  
 DB: 7 Gaps: 1  
 US-10-007-270-2 (1-797) x ADA14842 (1-2887)  
 QY 8 AlaIlePheValPheThrIlePheLeuGlnValGlnGlyThrLysAspIleSerIleAsn 27  
 DB 5 GCTATTTTGTGTTTGGATTTTCTCCAAGTCAAGGAACCAA----- 49  
 QY 28 IleTyrHisSerGluThrLysAspIleAsnProProArgAsnGluThrThrGluSer 47  
 DB 49----- 49  
 QY 48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysArg 67  
 DB 49----- 49  
 QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87  
 DB 49----- 49  
 QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuA-gValCysGlnGluAlaValTrp 107  
 DB 50-----GTGTGTCCAGGAAGCAGTATGG 70  
 QY 108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTrpVal 127  
 DB 71 GAAGCATATCGGATCTTTCTGGATCGCATCCCTGACACAGGGGAATATCAGGACTGGGTC 130  
 QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147  
 DB 131 AGCATCTGCAGCAGAGACCTTCTGCTCTTTGACATTTGGAAAAAATTCAGCAATTC 190  
 QY 148 GlnGluHisLeuAspLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167

DB 191 CAGGAGCACCTGGATCTTCTCCAGCAGAGAAATAAAACAGAGAAAGTTTCCCTCAGACAAAA 250  
 QY 168 AspGluIleSerAlaGluLysThrLeuGlyGluProGlyGluThrIleValIleSerThr 187  
 DB 251 GATGAAATATCTGCAGAGAAAGACATTTGGGAGAGCTGGTGAACCACTTGTCTATTTCAACA 310  
 QY 188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
 DB 311 GATGTTGCCAAGCTCTCACTTGGGCTTTCCCTCTCTCACTCTGTATGACACCTCTCCTCAAT 370  
 QY 208 GluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGlu 227  
 DB 371 GAAATCTCGATAATACACTCAACGACACCAAGATGCTTACACAGAAAGAGAGAAACAGAA 430  
 QY 228 PheAlaValIleGluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPhe 247  
 DB 431 TTCCCTGTGTTGGAGGAGCAGAGGGTGGAGCTCAGGCTCTCTCTGGTAAACACAGAGTTT 490  
 QY 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGln 267  
 DB 491 AAGGCAGAGCTGCTGACTCCAGTCCCATATATTACAGGAGCTAGCAGAAAGTCCCAA 550  
 QY 268 LeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGly 287  
 DB 551 CTTTCAGATGCAAAAGATATTTAAGAAACTTCCAGGATTCAAAAAATCCATGTGTTAGGA 610  
 QY 288 PheArgProLysLysGlyLysAspGlySerSerSerThrGluMetGlnLeuThrAlaIle 307  
 DB 611 TTTAGACCAAGAAAGAAAGATGGCTCAAGTCCACAGAGATGCAACTTACGGGCATC 670  
 QY 308 PheLysArgHisSerAlaGluLysSerProAlaSerAspLeuLeuSerPheAspSer 327  
 DB 671 TTTAAGAGACACAGTCGAGAAAGCAAAAGCCCTGCAAGTGACTCTCTGCTTTTGATTC 730  
 QY 328 AsnLysIleGluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGlu 347  
 DB 731 AACAAATTTGAAGTGAAGAGTCTATCATGGAACCATGAGAGAGGACAAAGCAACAGAA 790  
 QY 348 IleTyrLeuThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGln 367  
 DB 791 ATCTATCTCAGCTACAGACTCAAGCTCAAAAGCTGATCAGCAAAAGCCTAGAGGAAGAACAA 850  
 QY 368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
 DB 851 TCTTTGGATGTTGGGACAAATTCATGTTCACTGATGAATTTGCTGGATCATCTGCAGCTTT 910  
 QY 388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407  
 DB 911 GGTCTCTGACACCAATCAGAGCTGCCCATCTTTTGTCTGTATATAACAGAGGATGCTACT 970  
 QY 408 LeuSerProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGluHis 427  
 DB 971 TTGAGTCCAGAACTTCTCTCTGTTGAACCCCTGAGCTTGACAGAGTGGACGAGAGCAT 1030  
 QY 428 GlyLeuProAspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAla 447  
 DB 1031 GGTCTACCTGACACTTCTGTTGCTCTCCACTGCTGCTGTGCTCTACCTCTCTGTCAGAGCT 1090  
 QY 448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467  
 DB 1091 CCACCTTCTCTTATGTCATCAAGCATCTCTCTCTGACTGATCAAGGCCACACAGATACA 1150  
 QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487  
 DB 1151 ATGGCCACTGACACGACCAATGTAGTACCAAGGCTCACCATCCCCACCACTGATTATTCT 1210  
 QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArg 507  
 DB 1211 GCAATCAGCCCACTGGCTCTGGGAATTTCACTCCACTGCTGCTCTTCAGATGACAGCCGA 1270  
 QY 508 SerSerAlaGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527  
 DB 1271 TCAAGTGCAGGTGGCAAGATATGGTCAGACACCTAGATGAATGGATCTGTGACTACT 1330

```

QY 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547
Db 1331 COTGCCCATCTGAGTACACAGGGCTCAGCGAATACAGTTTCTGTCCAGATCAATTTCTTG 1390
QY 548 GluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567
Db 1391 GAGGATACACATCTCTGTCTACGTTTACGATATACCATAGTTCTATGACCATTTGCC 1450
QY 568 ProLysGlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
Db 1451 CCCAAGGGCCGAGAGCTGGTAGTGTCTTCACTAGCTGCGTGTGCTAAACATGGCCCTTCTCC 1510
QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGlnGlnPheThrGln 607
Db 1511 AACGACCTGTTCACACAGAGCTCTCGAGAGACCGAGCTCTGGAGCAACAATTCACACAG 1570
QY 608 LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627
Db 1571 CTGCTGGTTCCATATCTACGATCCCAATCTTACAGGATTTAAGCAACTTGAATACTTAAC 1630
QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647
Db 1631 TTCAGAAACGGGAGTGTGATTTGTAATAGCAAAATGAAGTTTGCTAAGTCTGTGCCGTAT 1690
QY 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667
Db 1691 AACCTCACCAAGGCTGTGCAGGGGTCTTGGAGATTTTCGTTCTGTGCGGCCCAACAA 1750
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687
Db 1751 CTCCTATCTGGAAATAGACAGCTACTCTCTCAACATTGAACTGATCAAGCAGATCCC 1810
QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707
Db 1811 TGCAGATTCTCGGCTGCGGCGAATTTGCCCAATGTGTAAGAAGCAACGGACTGAGGAA 1870
QY 708 AlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727
Db 1871 GCGAGTGTCTGCTCAACACAGGATATGACAGCCAGGGAGCTGGACGCTCTGGAACCA 1930
QY 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747
Db 1931 GGCCTCTGTGCCCTGGCACAAAGGAATCGCAGGTCTCTCCAGGAAAGGGAGCTCCATGC 1990
QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767
Db 1991 AGGTGCGCAGATCACTCTGAAAATCAGCATACAAAACACTAGTGTAAAAAGTTCCAAAT 2050
QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787
Db 2051 CAACAAAAATAACAAGGTAAATCAGTAAAGAAATTTCTGAATTTACTGACCGTAGAATATGAA 2110
QY 788 GluPheAsnHisGlnAspTyrGluCysAsn 797
Db 2111 GAATTTAAACCATCAAGATTGGGAAGGAAT 2140
RESULT 7
ACCS57947
ID ACC57947 standard; cDNA; 2887 BP.
XX ACC57947;
AC ACC57947;
XX
XX 11-AUG-2003 (first entry)
DE Human interphotoreceptor matrix IPM 150, isoform B, cDNA.
XX
XX Human; interphotoreceptor matrix; IPM 150; chromosome 6q13-q15; IPMC;
KW receptor; ophthalmological; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers

```

```

CDS
FT 2. .2143
FT /*tag= a
FT /product= "IPM 150"
FT /partial
FT /note= "No start codon"
XX
XX WO2003039346-A2.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002WO-US036090.
XX
XX 08-NOV-2001; 2001US-00077270.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2003-441440/41.
XX
XX New interphotoreceptor matrix proteins and polynucleotides, useful for
XX treating or preventing photoreceptor death or retinal detachment, or for
XX treating ocular disorders.
XX
XX Claim 1; Page 78-79; 105pp; English.
XX
XX The present sequence is that of cDNA encoding isoform B of novel human
XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified
XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene
XX is located on chromosome 6q13-q15, a region that also contains loci for
XX progressive bifocal chorioretinal atrophy, autosomal dominant Stargardt's
XX -like macular dystrophy, North Carolina macular dystrophy and Salla
XX disease. Members of the IPMC gene family have been identified in humans,
XX monkey, cow, goat, rabbit, dog, cat, pig, mouse and rat IPM. 2
XX Subfamilies are designated IPM 150 (or IPMG1) and IPM 200 (or IPMG2). The
XX invention provides IPM 150 and IPM 200 polynucleotides and polypeptides,
XX antibodies that specifically bind the polypeptides, and vectors or
XX comprising the polynucleotides. A claimed method of treating or
XX preventing photoreceptor death or retinal detachment involves
XX administering an IPMC polynucleotide, polypeptide or antibody. Also
XX claimed is a method for identifying a compound capable of modulating IPMC
XX gene expression
XX
XX Sequence 2887 BP; 899 A; 659 C; 606 G; 723 T; 0 U; 0 Other;

```

Alignment Scores:

Pred. No.:	2,788-283	Length:	2887
Score:	3619.00	Matches:	711
Percent Similarity:	90.00%	Conservative:	0
Best Local Similarity:	90.00%	Mismatches:	1
Query Match:	87.90%	Indels:	78
DB:	8	Gaps:	1

US-10-007-270-2 (1-797) x ACC57947 (1-2887)

```

QY 8 AlaIlePheValPheTrpIlePheLeuGlnValGlnGlyThrLysAspIleSerIleAsn 27
Db 5 GCTATTTTGTGTTTGTGATTTTCTCCAAGTTCAGGAACCCAAA----- 49
QY 28 IleTyrHisSerGluThrLysAspIleAspAsnProProArgAsnGluThrThrGluSer 47
Db 49 ----- 49
QY 48 ThrGluLysMetTyrLysMetSerThrMetArgIlePheAspLeuAlaLysHisArg 67
Db 49 ----- 49
QY 68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87
Db 49 ----- 49
QY 88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTrp 107

```

50 -----GTGTCTCAGGAAGCAGTATCG 70  
108 GluAlaTyrArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTrpVal 127  
71 GAAGCATATCGGATCTTTCTGGATCGATCCCTGACACAGGGGAATATCAGGACTGGGTC 130  
128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147  
131 AGCATCTGCCAGCAGGAGACCTTCTGCTCTTTGACATTTGGAAAAAACTTCAGCAATTC 190  
148 GlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
191 CAGGAGCACCTCGATCTCTCTCCAGCAGAGATAAAACAGAGAAGTTTCCCTGCACAGAAA 250  
168 AspGluIleSerAlaGluLysThrLeuGlyGluProGlyGluThrIleValIleSerThr 187  
251 GATGAATATCTGCAGAGAAGACATTTGGAGAGCTGTGTGAACCATTTGCATTTCAACA 310  
188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrLeuLeuAsn 207  
311 GATGTTCACACGCTCACTTTGGGCTTTCCCTCTCACTCTCTGATGACACCTCTCTCAAT 370  
208 GluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGluLysGluThrGlu 227  
371 GAAATCTCGATAATACACTCAACGACACCAAGATGCTTACACAGAAAGAGAAACAGAA 430  
228 PheAlaValLeuGluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPhe 247  
431 TTCGCTGTGTGGAGGACAGAGGTGGAGCTCAGCGCTCTCTGTGTAAACACAGAGTTTC 490  
248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGln 267  
491 AAGGCAGAGCTCGCTGACTCCAGTCCCATATTAACAGGAGCTAGCAGGAAAGTCCCAA 550  
268 LeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGly 287  
551 CTTCAGATGCAAAAGATATTTAAGAACTTCAGAGTTCAAAAATTCATGTTAGGA 610  
288 PheArgProLysLysGluLysAspGlySerSerThrGluMetGlnLeuThrAlaIle 307  
611 TTTAGACCAAGAAAGAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGCCCATC 670  
308 PheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSer 327  
671 TTTAAGAGACACAGTGCAGAGCAAAAGCCCTGCAAGTACCTCTCTGTTGATTC 730  
328 AsnLysIleGluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGlu 347  
731 AACAAATTTGAAGTGAAGAGTCTATCATGGAACCATGGAGGAGGACCAAGCAACAGAA 790  
348 IleTyrLeuThrAlaThrAspLeuLysArgIleLeuSerLysAlaLeuGluGluGln 367  
791 ATCTATCTCACAGCTACAGACCTCAAAAGGCTGATCAGCAAGCACATAGAGGAAGACAA 850  
368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387  
851 TCTTTGGATGTGGGACAAATTCAGTTCACTGATGAATTTGGTGCATCTCTCCAGCCTTT 910  
388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407  
911 GGTCTCTGACACCAATCAGAGTGCACCATCTTTTGTCTTTATATAACAGAGGATGCTACT 970  
408 LeuSerProGluLeuProProValGluProGlnLeuGluThrValAspGlyValaGluHis 427  
971 TTGAGTCCAGAACTTCTCTCTTTGAACCCAGCTTGAGACAGTGGAGCGAGCAGAGCAT 1030  
428 GlyLeuProAspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAla 447  
1031 GGTCTACCTGACATCTTGGCTCTCCACTGCTAAGGCTCTTACCTCTCTGTCAGAGCT 1090  
448 ProProPhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrAspThr 467  
1091 CCACCTTTCTTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGCGCACAGATACA 1150

QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487  
Db 1151 ATGGCCATGTGACAGACAATGCTAGTACCAGGCTCACCATCCCACAGTGATATTCT 1210  
QY 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArg 507  
Db 1211 GCAATCAGCCAACTGGCTCTGGGAATTTACATCCACCTGCATCTTCAGATGACAGCCGA 1270  
QY 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527  
Db 1271 TCAAGTCAGGTGGGGAAGATATGTCAGACACCTAGATGAATGAATGATCTCTCTGACACT 1330  
QY 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547  
Db 1331 CTGTCCCATCTGAGGTACCGGCTCAGCGAATACGTTTCTGTCCAGATCAATTTCTTG 1390  
QY 548 GluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567  
Db 1391 GAGGATACCATCTCTCTGAGTTTACAGTATATCACCATAGTTCTATGACCAATGCC 1450  
QY 568 ProLysGlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587  
Db 1451 CCCAAGGCCGAGAGCTGGTAGTGTCTTCAGTCTGCGTGTGCTAACATGSCCTTCTCC 1510  
QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln 607  
Db 1511 AACGACCTGTTTCAACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACAG 1570  
QY 608 LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627  
Db 1571 CTGTGTTTCCATATCTAGATCCAAATCTTACAGATTTAAGCAACTTGAATATCTTAAC 1630  
QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647  
Db 1631 TTCAGAAACGGGAGTGTGATTGTGAATAGCAAAATGAAGTTTGTCTGTCGCGTAT 1690  
QY 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667  
Db 1691 AACCTCACAAGGCTGTGCACGGGCTTTGGAGGATTTTGTCTCTGTCGAGCCCAACA 1750  
QY 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687  
Db 1751 CTCCATCTGAAATAGACAGCTACTCTCTCAACAATTGAACCAAGCTGATCAAGCAGATCCC 1810  
QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707  
Db 1811 TGCAAGTTCTCTGCGCTGCGCGAATTTGCCAATGTGTAAAGAACGACGAGCTGAGGA 1870  
QY 708 AlaGluCysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727  
Db 1871 GCGGAGTGTCTGTGCAACAGATATGACAGCCAGGGGAGCTGACCGGTCTGGAACCA 1930  
QY 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlnGlyLysGlyAlaProCys 747  
Db 1931 GGCCTCTGTGGCCCTGGCACAAGGAATCGAGGTCTCTCAGGGAAGGGAGCTCCATGC 1990  
QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767  
Db 1991 AGTTGCCAGATCACTCTGAAATTAAGCATCAAAACTAGTGTATAAAGTTCCAAAT 2050  
QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787  
Db 2051 CAACAAAATAACAAGGTAATCAGTAAAGAAATTTGAAATTACTGACCCGTAGAAATGAA 2110  
QY 788 GluPheAsnHisGlnAspTrpGluGlyAsn 797  
Db 2111 GAATTTAACCATCAAGATTGGGAAGGAAAT 2140

RESULT 8

AAA46328

ID AAA46328 standard; DNA; 2966 BP.

XX

AC

AAA46328;

XX

04-SEP-2000 (first entry)

XX

Interphotoreceptor matrix proteoglycan (IPM150) splice variant.

DE

XX

Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200; chromosome 6q13-q15; ocular disease; retinal detachment; choriorretinal degeneration; retinal degeneration; cone degeneration; age related macular degeneration; photoreceptor degeneration; retinal pigment epithelium degeneration; mucopolysaccharidosis; rod- cone dystrophy; cone-rod dystrophy; ss.

XX

Homo sapiens.

OS

WO2000026367-A2.

XX

11-MAY-2000.

XX

29-OCT-1999; 99WO-US025440.

PF

29-OCT-1998; 98US-00183972.

PR

(IOWA ) UNIV IOWA RES FOUND.

XX

Hageman GS, Kuehn MH;

PI

WPI; 2000-365516/31.

DR

Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for preventing, diagnosing and treating ocular disorders such as retinal detachment and choriorretinal degeneration.

PT

Claim 3; Fig 18; 183pp; English.

XX

The present sequence represents a splice variant of an interphotoreceptor matrix (IPM) proteoglycan, designated IPM150. The sequence is missing exon 2. The protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome 6q13-q15, between markers CHLC.GATALLF10 and D6S284. The IPM proteins may be used to supplement a patients own production of the protein or to rectify alterations in their nucleic acids that result in expression of an inactive protein. The IPM nucleic acids may be used in this way to treat ocular diseases such as retinal detachment, choriorretinal degeneration, retinal degeneration, age related macular degeneration, photoreceptor degeneration, rPE (retinal pigment epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also be used to assay for other modulators of IPM proteoglycan expression and activity that may be used to treat ocular diseases. The nucleic acids and proteins may also be used as diagnostic reagents to detect the presence of IPM nucleic acids and their products in samples from patients according to standard methodologies

CC

Sequence 2966 BP; 918 A; 587 C; 624 G; 737 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.:	9.11e-276	Length:	2966
Score:	3526.50	Matches:	707
Percent Similarity:	89.62%	Conservative:	1
Best Local Similarity:	89.49%	Mismatches:	81
Query Match:	85.66%	Indels:	1
DB:	3	Gaps:	1

US-10-007-270-2 (1-797) x AAA46328 (1-2966)

QY

8 AlaIlePheValPheTrIlePheLeuGlnValGlnGlyThrLysAspIleSerIleAsn 27

DB

5 GCTATTTTGGTTTGGATTTTCTCCAGTTCAGAACCAAA----- 49

QY

28 IleTyrHisSerGluThrLysAspIleAspAsnProProArgAsnGluThrThrGluSer 47

DB

49 ----- 49

48 ThrGluLysMetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArg 67

QY

49 ----- 49

DB

68 ThrLysArgSerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLys 87

QY

49 ----- 49

DB

88 GlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTrp 107

QY

50 -----GTGTGTTCAGGAAGCAGTATGG 70

DB

108 GluAlaTyrArgIlePheIleuAspArgIleProAspThrGlyGluTyrGlnAspTrpVal 127

QY

71 GAAGCATATCGGATCTTTCTGGATCGCATCTCCACAGGGGAATATCAGAGTGGGTTC 130

DB

128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147

QY

131 AGCATCTGCCAGCAGAGACCTTCTGCCTCTTTGCACATTGGAAAAAATCTTCAGCAATTCC 190

DB

148 GlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167

QY

191 CAGGAGCACCTGGATCTTCTCCAGCAGAGAATAAAACAGAGAGTTTCCCTCAGCAAAAA 250

DB

168 AspGluIleSerAlaGluLysThrLeuGlyGluProGlyGluThrIleValIleSerThr 187

QY

251 GATGAATATCTGCACAGAGACATTTGGAGAGCTGGTGAACCATTTGTCAATTCACA 310

DB

188 AspValAlaAsnValSerLeuGlyProPheProLeuThrProAspAspThrIleuLeuAsn 207

QY

311 GATGTTGCCAAGCTCTCACTTTGGGCTTTCCCTCTCTCACTCTGATGACACCTCTCCTCAAT 370

DB

208 GluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGlu 227

QY

371 GAAATTCGGAATATACACTCAACGACACCAAGATGCTTACACAGAAAGAGAAACAGAA 430

DB

228 PheAlaValLeuGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPhe 247

QY

431 TTCGCTGTGTTGGAGGAGCAGAGGGTGGAGCTCAGCGTCTCTCTGGTAAACCCAGAAAGTTC 490

DB

248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGln 267

QY

491 AAGGACAGAGCTGCTGACTCCAGTCCCAATATTACCAGGAGCTAGCAGGAAAGTCCCAA 550

DB

268 LeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGly 287

QY

551 CTTTCAGATGCAAAAGATATTTAAGAACTTCCAGGATTCAAAAAATCCATGTGTAGGA 610

DB

288 PheArgProLysLysGluLysAspGlySerSerThrGluMetGlnLeuThrAlaIle 307

QY

611 TTTAGACCAAAAGAAAAAGATGGCTCAAGCTCCACAGAGATGCAACTTACGGCCATC 670

DB

308 PheLysArgHisSerAlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSer 327

QY

671 TTTAAGACACACAGTGCAGAGCAAAAAGCCCTCGCAGTGCACCTCTCTCTTTGATTCC 730

DB

328 AsnLysIleGluSerGluValTyrHisGlyThrMetGluGluAspLysGlnProGlu 347

QY

731 AACAAAAATTGAAAGTGAGGAAGTCTATCATGGAACCATGAGGAGGCAAGCAACAGAA 790

DB

348 IleTyrLeuThrAlaThrAspLeuLysArgIleSerLysAlaLeuGluGluGln 367

QY

791 ATCTATCTCAGCTACAGACCTCAAAAGGCTGATCAGCAAGCAAGCAAGCAAGCAAGCA 850

DB

368 SerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPhe 387

QY

851 TCTTTGGATGTGGGACAAATTCAGTTCACTGATGAATTTGCTGGATCACTGCCGCTTT 910

DB

388 GlyProAspThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThr 407

QY

911 GGTCTCTGACCCCAATCAAGAGCTGCCCATCTTTTGTCTGTATTAACAGAGATGCTACT 970

DB



```
QY 408 LeuSerProGluLeuProValGluProGlnLeuGluThrValAspGlyAlaGluHis 427
Db 971 TTGAGTCCAGAACTTCCTCTGTTGAACCCAGCTTGAGACAGTGGACGGAGAGACAT 1030
QY 428 GlyLeuProAspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAla 447
Db 1031 GGTCTACCTGACACTTCCTGCTCCACCTGCTATGGCTCTACCTCCCTGTCAGAGCT 1090
QY 448 ProProPheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467
Db 1091 CCACCTTTCTTTATGGCATCAAGCATCTCTCTGACTGATCAAGGCACACAGATACA 1150
QY 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTrpSer 487
Db 1151 ATGGGCATGACACAGCAATGCTAGTACAGGGCTCACCATCCACAGATGATTTCT 1210
QY 488 AlaIleSerGlnLeuAlaGlyIleSerHisProProAlaSerSerAspSerArg 507
Db 1211 GCAATCAGCAACTGGCTCTGGGAATTTACATCCACCTGCATCTTCAGATGACAGCCGA 1270
QY 508 SerSerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527
Db 1271 TCAAGTGCAGGTGGCGAGATATGCTCAGACACCTAGATGAATGGATCTCTGTGACACT 1330
QY 528 ProAlaProSerGluValProGluLeuSerGluTrpValSerValProAspHisPheLeu 547
Db 1331 CTGTGCCCCATCTGAGGTACCGAGGCTCAGCGAATACGTTTCTGTCCAGATCAATTTCT 1390
QY 548 GluAspThrProValSerAlaLeuGlnTrpIleThrThrSerSerMetThrIleAla 567
Db 1391 GAGGATACCACTCCCTGTCTCAGCTTTACAGTATATCACCACTAGTTCTTATGACCATGGC 1450
QY 568 ProLysGlyValGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
Db 1451 CCNAGGGCCGAGAGCTGTAGTGTCTTCAGTCTGCGTGTGCTAACTAGCGCTTCTCC 1510
QY 588 AsnAspLeuPheAsnLysSerSerLeuGluTrpArgAlaLeuGluGlnGlnPheThrGln 607
Db 1511 AACGACCTGTTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACACAG 1570
QY 608 LeuLeuValProTrpLeuArgSerLeuLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627
Db 1571 CTGCTGGTTCCATATCTACGATCCAACTTACAGATTTAGCAACTTGGAAATACCTAAC 1630
QY 628 PheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTrp 647
Db 1631 TTCAGAAACGGAGTGTGATTGTGAATAGCAAAATGAAGTTTGCTAAGTCTGTGCGGTAT 1690
QY 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667
Db 1691 AACCTCACAAGGCTGTGCACGGGGTCTTGGAGGATTTTCGTTCTGCTGCAGGCCCAACA 1750
QY 668 LeuHisLeuGluIleAspSerTrpSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687
Db 1751 CTCCATCTGGAATAGACAGCTACTCTCTCAACATTAACACAGCTGATCAAGCAGATCCC 1810
QY 688 CysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGlu 707
Db 1811 TGCAGTCTCTGCGCTCGCGCAATTTGCCAATGTGTGAAGAACGAAACGGAAGTGAAGAA 1870
QY 708 AlaGluCysArgCysLysProGlyTrpAspSerGlnGlySerLeuAspGlyLeuGluPro 727
Db 1871 GCGAGTGTGCTGCAACACAGATATGACGCCAGGGAGCTGAGCGGTCTGGAACA 1930
QY 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747
Db 1931 GGCCTCTGTGG-CCTGGCAAAAGGAATGCGAGGTCTCTCAGGAAAGGGAGCTCCATGCG 1989
QY 748 ArgLeuProAspHisSerGluAsnGlnAlaTrpLysThrSerValLysLysPheGlnAsn 767
Db 1990 G--GTTCCAGATCACTCTGAAATCAAGCATACAAACCTAGTGTAA--AAGTTCCAAAT 2046
QY 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTrpGlu 787
```

```
Db 2047 CAACAAATAACAGGTAATCAGTAAAGAAATTCGTAATTACTACCGTAGAATATGAA 2106
QY 788 GluPheAsnHisGlnAspTrpGluGlyAsn 797
Db 2107 GAATTTAACCATCAAGATTGGGAGGAAT 2136

RESULT 9
AAH46329
ID AAA46329 standard; DNA; 2244 BP.
XX AC AAA46329;
XX 04-SEP-2000 (first entry)
DE Interphotoreceptor matrix proteoglycan (IPM150) splice variant.
XX Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;
XX chromosome 6q13-q15; ocular disease; retinal detachment;
XX choriorretinal degeneration; retinal degeneration; cone degeneration;
XX age related macular degeneration; photoreceptor degeneration;
XX retinal pigment epithelium degeneration; mucopolysaccharidosis;
XX rod- cone dystrophy; cone-rod dystrophy; ss.
XX Homo sapiens.
XX OS
XX PN WO2000026367-A2.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-US025440.
XX 29-OCT-1998; 98US-00183972.
XX (IOWA ) UNIV IOWA RES FOUND.
XX Hageman GS, Kuehn MH;
XX WPI; 2000-365616/31.
XX
XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for
XX preventing, diagnosing and treating ocular disorders such as retinal
XX detachment and choriorretinal degeneration.
XX
XX Claim 3; Fig 19; 183pp; English.
XX
XX The present sequence represents a splice variant of an interphotoreceptor
XX matrix (IPM) proteoglycan, designated IPM150. The sequence comprises an
XX additional intron after exon 5. The protein is an IPM component (IPMC).
XX Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene
XX is located on chromosome 6q13-q15, between markers CHLC, GAT11F10 and
XX D6S284. The IPM proteins may be used to supplement a patients own
XX production of the protein or to rectify alterations in their nucleic
XX acids that result in expression of an inactive protein. The IPM nucleic
XX acids may be used in this way to treat ocular diseases such as retinal
XX detachment, choriorretinal degeneration, retinal degeneration, age related
XX macular degeneration, photoreceptor degeneration, RPE (retinal pigment
XX epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-
XX cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may
XX also be used to assay for other modulators of IPM proteoglycan expression
XX and activity that may be used to treat ocular diseases. The nucleic acids
XX and proteins may also be used as diagnostic reagents to detect the
XX presence of IPM nucleic acids and their products in samples from patients
XX according to standard methodologies
XX
XX Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;
```

```
Alignment Scores:
Pred. No.: 1,95e-259 Length: 2244
Score: 3323.00 Matches: 667
Percent Similarity: 95.56% Conservative: 0
Best Local Similarity: 95.56% Mismatches: 10
Query Match: 80.71% Indels: 23
```

DB: 3 Gaps: 1  
US-10-007-270-2 (1-797) x AAA46329 (1-2244)  
QY 1 MetTyrLeuGluThrArgAlaAlaPheValPheThrPheLeuGlnValGlnGly 20  
DB 151 ATGATATTTGGAACTAGAGAGCTATTTTGGTATTTTGGATTTTCTCCAAGTTCAGGA 210  
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro 40  
DB 211 ACCAAAGATATCTCCATTAACATATACCATTTCTGAACATAAGACATAGACAATNCCCA 270  
QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgIle 60  
DB 271 AGAAATGAACAACTGAAGTACTGAAAAATGTACAAATGTCAACTATAGAGCAATA 330  
QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
DB 331 TTCGATTTGGCAAGNATCGAACAAAAGATCCGCAATTTTCCCAACGGGGTTAAAGTC 390  
QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
DB 391 TGTCCACAGGAATCCATGAACAGATTTTAGACAGTCTTCAAGCTTATTATAGATTGAGA 450  
QY 101 ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
DB 451 GTGTGTACAGGAAGCAGCATGGAGCATATCGGATCTTCTGGATCGCATCCCTGACACA 510  
QY 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
DB 511 GGGGAATATCAGGATCGGTGAGCATCTGCCAGCAGGAGAGCTTCTGCCTCTTTGACATT 570  
QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnArgIleLysGln 160  
DB 571 GGAAAAAACTTCAGCAATTCAGGAGCACTTGGATCTTCTCCAGCAGAGNATPAAACAG 630  
QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
DB 631 AGAAGTTTCCCTGACAGAAAAAGATGAAATATCTGCAGAGAGACATTTGGGAGAGCTGGT 690  
QY 181 GluThrIleValIleSerThr----- 187  
DB 691 GAAACCATGTCAATTTCAAC-AGCAATCTCATTTCAAGACTTGGGAGTATTTCTAAGA 749  
QY 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
DB 750 AAACCCCTCAGAAGACCAATTCAGATGTTGCCAAGCTTCACTTGGGCTTTCCCTCTC 809  
QY 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
DB 810 ACTCCTGTATGACACCTCTCAATGGAAATCTCGATATATACACTCAACGACACCAAGATG 869  
QY 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSer 239  
DB 870 CCTACAACAGAAAGAAACAGATTCCTGTGTGGAGGAGCAGAGGGTGGAGCTCAGC 929  
QY 240 ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
DB 930 GTCTCTCTGGTAAACAGCAAGTTCAAAGCAGAGCTCGCTGACTCCCACTCCCATATTAC 989  
QY 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysValLeuProGly 279  
DB 990 CAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAAACTTCCAGGA 1049  
QY 280 PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer 299  
DB 1050 TTCAAAAAATCCATGTGTAGGATTTAGACCAAGAAAGAAAAAGATGGCTCAAGCTCC 1109  
QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
DB 1110 ACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAGGCAAAAGCCCTGCA 1169  
QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThr 339

RESULT 10  
ADA14844

DB 1170 AGTGACCTCTCTCTTTGATTCCAAACAAAATGAAAGTGAAGAGTCTTATCATGAAACC 1229  
QY 340 MetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIle 359  
DB 1230 ATGGAGGAGGACAAAGCAACCAAGAAATCTATCTCACAGCTACAGACTCAAAAGGCTGATC 1289  
QY 360 SerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
DB 1290 AGCAAGCACTAGAGAAAGAAACAATCTTTGGATGTGGGACAAATTCAGTTCACTCATGAA 1349  
QY 390 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
DB 1350 ATTGCTGGATCTACTGCCAGCTTTGGTCTTGACACCCCAATCAGAGCTGCCACATCTTT 1409  
QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
DB 1410 GCTGTTTATACAGAGGATGCTACTTTGAGTCCAGAACTTCTCTCTGTGAAACCCAGCTT 1469  
QY 420 GluThrValAspGlyValGluHisGlyLeuProAspThrSerTyrSerProProAlaMet 439  
DB 1470 GAGACAGTGCAGGAGCAGAGCATGGTCTACCTGACACTTCTTGCTCTCCACTGCTATG 1529  
QY 440 AlaSerThrSerLeuSerGluAlaProPhePheMetAlaSerSerIlePheSerLeu 459  
DB 1530 GGCCT-ACCTCCCTGTGCAAGCTCCACCTTCTTTATGGCATCAAGCATCTCTCTCTG 1588  
QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
DB 1589 ACTGATCAAGGACCAACAGATACATGGCCACTGACACGACAAATGCTAGTACAGGGCTC 1648  
QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
DB 1649 ACCATCCCCCAGTGATTTCTGCAATCAGCCAACTGGCTCTGGAAATTTCAATCCA 1708  
QY 500 ProAlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeu 519  
DB 1709 CCTGCTCTTTCAGATGACAGCCGATCAAAGTGCAGTGGCGAAGGATGGACAGACCTTA 1768  
QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539  
DB 1769 GATGAANTGGATCTGTCTGACACTCTCTGCCCATCTGAGGTACAGAGCTCAGCGAATAT 1828  
QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
DB 1829 GTTTCCTGCCAGATCATTTCTTGGAGGATACCACTCTCTGTCTCAGCTTTACAGTATATC 1888  
QY 560 ThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuValValPhePheSerLeu 579  
DB 1889 ACCACTAGTTCTATGACCATTCGCCCAAGGGCCGAGAGCTGTAGTGTCTTCTCAGTCTG 1948  
QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArg 599  
DB 1949 CGTGTGTGCTAACATGSCCTTCTCCAAAGACCTGTTTCAACAGAGCTATTTGGAGTACCGA 2008  
QY 600 AlaLeuGluGlnPheThrGlnLeuValProTyrLeuArgSerAsnLeuThrGly 619  
DB 2009 GCTCTGAGCAACAATTCACAGCTGTGTGTTCCATATCTACGATCCCAATCTTACAGGA 2068  
QY 620 PheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMet 639  
DB 2069 TTTAGCACTTGGAAATCTTAACCTCAGAAACGGGAGTGTGATGTGTAATAGCAAAATG 2128  
QY 640 LysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAsp 659  
DB 2129 AAGTTTGTCAAGTCAAGTGCCTTAACTCACAAGGGCTGTGCACGGGGTCTTTGGAGGAT 2188  
QY 660 PheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeu 677  
DB 2189 TTTCGTTCTGCTGCAGCCCAACAATCCATCTGGAAATAGACAGCTACTCTCTC 2242

ID ADAL4844 standard; cDNA; 2244 BP.  
 AC ADAL4844;  
 XX  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Human interphotoreceptor matrix component, IPMC, 150 isoform C cDNA.  
 XX  
 KW ss; gene; human; IPMC 150 isoform C; gene therapy;  
 KW interphotoreceptor matrix component; IPMC; ocular disorder;  
 KW macular degeneration; photoreceptor death; retinal detachment.  
 XX  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 151..747  
 FT FT /\*tag= b  
 FT FT /product= "IPMC 150 isoform C"  
 FT FT 151..200  
 FT FT /\*tag= a  
 FT FT /note= "Signal sequence"  
 FT FT 201..744  
 FT FT /\*tag= c  
 FT FT /note= "Mature IPMC 150 isoform C"  
 FT FT unsure 265..267  
 FT FT /\*tag= d  
 FT FT /note= "Encodes Pro"  
 FT FT unsure 346..348  
 FT FT /\*tag= e  
 FT FT /note= "Encodes His"  
 XX  
 PN US2002160954-A1.  
 XX  
 PD 31-OCT-2002.  
 XX  
 XX 08-NOV-2001; 2001US-00007270.  
 PF  
 XX 29-OCT-1998; 98US-00183972.  
 PR  
 XX 29-OCT-1999; 99US-00430195.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 XX Hageman GS, Kuehn MH;  
 PI  
 XX WPI; 2003-238235/23.  
 DR  
 XX P-PSDB; ADAL4845.  
 XX  
 PT New isolated or recombinant interphotoreceptor matrix component  
 FT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 FT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.  
 XX  
 PS Claim 3; Page 36-37; 76pp; English.  
 XX  
 CC The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding human  
 CC interphotoreceptor matrix component, IPMC, 150 isoform C.  
 XX  
 SQ Sequence 2244 BP; 692 A; 530 C; 461 G; 559 T; 0 U; 2 Other;

Alignment Scores:  
 Pred. No.: 1,95e-259 Length: 2244  
 Score: 3323.00 Matches: 667  
 Percent Similarity: 95.56% Conservative: 0  
 Best Local Similarity: 95.56% Mismatches: 10  
 Query Match: 80.71% Indels: 23

DB: 7 Gaps: 1  
 US-10-007-270-2 (1-797) x ADAL4844 (1-2244)  
 Qy 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTyrIlePheLeuGlnValGlnGly 20  
 Db 151 ATGTATTGGAACTAGAGAGCTATTTTGTGTTTGGATTTTCTCCAAGTTCAAGGA 210  
 Qy 21 ThrLysAspIleSerIleLeuTyrHisSerGluThrLysAspIleAspAsnProPro 40  
 Db 211 ACCAAAGATATCTCCATTACCATATACCATCTCGAACTAAAGACATACCAATNCCC 270  
 Qy 41 ArcAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
 Db 271 AGAANTGAACAACACTGAAGTACTGAAAAAATGTCAAAATGTCAACTATGAGACGA 330  
 Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValVal 80  
 Db 331 TTCGATTGGCAAGNATCGAACAAAAAGATCGCATTTTCCCAACGGGGTTAAAGTC 390  
 Qy 81 CysProGlnCysSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 391 TGTCACAGGAATCCATGAACAGATTTTAGACAGTCTTCAAGCTTATTATAGATTGAGA 450  
 Qy 101 ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 Db 451 GTGTGTCCAGGAACGACATGGGAAGCATATCGCATCTTCTCGATCGCATCCCTGACACA 510  
 Qy 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 Db 511 GGGGAATATCAGGACTGGGTGAGCATCTCCAGCAGGAGACCTTCTGCGCTCTTTGACATT 570  
 Qy 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgIleLysGln 160  
 Db 571 GGAATAAACTTCAGCAATTCACAGAGACCTGGATCTTCTCCAGCAGAGAATAAAACAG 630  
 Qy 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 Db 631 AGAAGTTTCCTGCACAGAAAAGATGAATATCTGCAGAGAAGACATTGGGAGAGCCTGT 690  
 Qy 181 GluThrIleValIleSerThr----- 187  
 Db 691 GAAACCATTTGCTATTTCAC -AGCAATCTACATTTCAAAGACTTGGGCAGTATTCTAAGA 749  
 Qy 188 -----AspValAlaAsnValSerLeuGlyProPheProLeu 199  
 Db 750 AAACCCCTCAGAGAGCAAAATCAAGATGTTCACAGTCTCACTTGGGCTTTTCCCTCTC 809  
 Qy 200 ThrProAspAspThrLeuLeuGlnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
 Db 810 ACTCCTGATGACACCTCTCTCAATGGAAATCTCGAATAATACCTCAACGACCAAGATG 869  
 Qy 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSer 239  
 Db 870 CCTACACAGAAAGAGAAACAGAAATTCGCTGTGTGGAGGAGCAGAGGCTGGAGCTCAG 929  
 Qy 240 ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
 Db 930 GTCTCTCTGTGTAACCAAGATTCAAGGAGAGCTCGCTGACTCCAGTCCCATATTAC 989  
 Qy 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGly 279  
 Db 990 CAGAGCTACAGAAAGTCCCACTTCAGATGCAAAAGATATTTAAGAACTTCACAGA 1049  
 Qy 280 PheLysLysIleHisValLeuGlyPheArgProLysLysGlyLysAspGlySerSerSer 299  
 Db 1050 TTCAAAAAATCCATGTGTAGGATTTAGACCAAAAGAAAAAGATGGCTCAAGCTCC 1109  
 Qy 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
 Db 1110 ACAGAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAACCAAAAGCCCTGCA 1169  
 Qy 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThr 339



US-10-007-270-2 (1-797) x ACC57948 (1-2244)

QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
DB 151 ATGTATTTGGAACTAGAGAGCTATTTTGTGTTTGGATTTTCTCCAAAGTTCAAGGA 210  
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
DB 211 ACCAAGATATCTCCATTAAACATATACCATTTCTGAACATAAGACATAGACAATNCCCA 270  
QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
DB 271 AGAATGAACAACTGAAGTACTGAAAAATGTACAAAATGTCAACTATGAGACGATA 330  
QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPheProThrGlyValLysVal 80  
DB 331 TTCGATTTGGCAAGNATCGAACAAAGATCGCGATTTTCCCAACGGGGTTTAAAGTC 390  
QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
DB 391 TGTCACAGGAATCCATGAACAGATTTTACAGCTCTTCAAGCTTATTATAGATTGGA 450  
QY 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
DB 451 GTGTCTCAGGAAGCAGCATGGAGCATATCGGATCTTTCTGGATCGCATCCCTGACACA 510  
QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
DB 511 GGGGAATATCAGGACTGGGTGAGCATCTGCCAGCAGGAGACTTCTGCCTCTTTGACATT 570  
QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGln 160  
DB 571 GGAAAAAACTTCAGCAATTTCCAGGAGCACCTGGATCTTCTCCAGCAGAGAATAAAACAG 630  
QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
DB 631 AGAAGTTTCCCTGCAGAGAAAAGATGAATATCTGCAGAGAGACATTTGGGAGCCCTGGT 690  
QY 181 GluThrIleValIleSerThr----- 187  
DB 691 GAAACCAATGTCTTCAAC-AGCAATCTACATTTCAAGACTTGGGCAGTATTCTAAGA 749  
QY 188 -----AspValAlaIleValSerLeuGlyProPheProLeu 199  
DB 750 AAACCCCTCAGAGAGCAAAATTCAGATGTTGCCACGCTCTCACTTGGGCCTTTCCCTCTC 809  
QY 200 ThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMet 219  
DB 810 ACTCTGATGACACCTCTCTCAATGGAAATCTCGATAATACACTCAACGACACCCAGATG 869  
QY 220 ProThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSer 239  
DB 870 CCTACAACAGAAAGAGAAACAGAAATTCGTGTTGGAGAGCAGAGGGGTGAGCTCAGC 929  
QY 240 ValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyr 259  
DB 930 GTCTCTCTGGTAAACCAAGATTCAGGAGAGCTCGCTGACTCCAGTCCCAATATTAC 989  
QY 260 GlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGly 279  
DB 990 CAGGAGCTAGCAGGAAAGTCCCACTTCAGATGCAAAAGATATTAAAGAACTTCCAGGA 1049  
QY 280 PheLysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSer 299  
DB 1050 TTTCAAAAAATCCATGTGTGTAGATTTAGACCAAAAGAAAGAAAGATGGCTCAAGCTCC 1109  
QY 300 ThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAla 319  
DB 1110 ACAGAGATCCAACTTACGGCCATCTTTAGAGACACAGTCAGAGAGCAAAAGCCCTGCA 1169  
QY 320 SerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluValTyrHisGlyThr 339

RESULT 12  
ADA14847  
ID ADA14847 standard; cDNA; 3668 BP.

DB 1170 AGTGACCTCTCTCTTTGATTCCCAAAAATTGGAAGTGGAAGTCTATCATCGAACC 1229  
QY 340 MetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAspLeuLysArgLeuIle 359  
DB 1230 ATGGAGGAGACAAAGCAACCAAAATCTATCTCACAGCTACAGACCTCAAAAGGCTGATC 1289  
QY 360 SerLysAlaLeuGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGlu 379  
DB 1290 AGCAAGACACTAGAGAGAGACAACTTTGGATGTGGGACAAATTCAGTTCACATGAA 1349  
QY 380 IleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPhe 399  
DB 1350 ATTGCTGGATCACTCGACGCTTTGGTCTCTGACACCAATCAGAGCTGCCACATCTTT 1409  
QY 400 AlaValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeu 419  
DB 1410 GCTGTTATACAGAGATGCTACTTTGAGTCCAGAACTTCTCTCTGTGAACCCAGCTT 1469  
QY 420 GluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTyrSerProProAlaMet 439  
DB 1470 GAGACAGTGGACGGAGCAGAGCATGGTCTACCTGACACATCTTCTGCTCCACCTGTATG 1529  
QY 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeu 459  
DB 1530 GGCCT-ACCTCCCTGTGAGAGCTCCACCTTTCTTATGGCATCAGCATCTTCTCTCTG 1588  
QY 460 ThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeu 479  
DB 1589 ACTGATCAGGACCAACAGATACATGGCCACTGACACGACAACTGCTAGTACAGGCTC 1648  
QY 480 ThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisPro 499  
DB 1649 ACCATCCCAACCAAGTATTATTCTGCAATCAGCCAACTGGCTCTGGAAATTTCAATCCA 1708  
QY 500 ProAlaSerSerAspAspSerArgSerAlaGlyGlyGluAspMetValArgHisLeu 519  
DB 1709 CTGTCATCTTCAGATGACAGCCGATCAAGTGCAGGTGGCGAAGGTATGGACAGACCTA 1768  
QY 520 AspGluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyr 539  
DB 1769 GATGAATGGATCTGTCTGACACTCTGCCCCATCTGAGGTACCAGAGCTCGTGTAGTGTCTTCACTCTG 1828  
QY 540 ValSerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIle 559  
DB 1829 GTTCTGTCCCAGATCATTTCTTGAGGATACCATCTCTGCTCAGCTTACAGTATATC 1888  
QY 560 ThrThrSerSerMetThrIleAlaProLysGlyA-gGluLeuValValPhePheSerLeu 579  
DB 1889 ACCACTAGTCTATGACCATTTGCCCCCAAGGCGGAGAGCTGGTAGTGTCTTCACTCTG 1948  
QY 580 ArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArg 599  
DB 1949 CGTGTGTAAACATGGCCCTTCTCCAAACGACCTGTTCACCAAGAGCTATTGGAGTACCGA 2008  
QY 600 AlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGly 619  
DB 2009 GCTCTGGACCAACATTCACAGCTGTGGTTCCTATATCTACGATCCCAATCTTACAGCA 2068  
QY 620 PheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMet 639  
DB 2069 TTTTAAGCAACTTGAATACTTAACCTTCAAGAAACGGAGTGTGATTGTGAATAGCAAAATG 2128  
QY 640 LysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAsp 659  
DB 2129 AGTTTGTAAAGTCAGTCCGCTATTAACCTCACCAAGGCTGTGCACGGGTCTTGGAGGAT 2188  
QY 660 PheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeu 677  
DB 2189 TTTTCGTCTCTGTCAGCCCAACACACTCCATCTGGAATAGACAGACTACTCTCTC 2242

```

XX ADA14847;
XX
XX 06-NOV-2003 (first entry)
XX
XX Mouse interphotoreceptor matrix component, IPMC, 150 isoform A cDNA.
XX
XX ss: gene; mouse; IPMC 150 isoform A; gene therapy;
XX KW interphotoreceptor matrix component; IPMC; ocular disorder;
XX KW macular degeneration; photoreceptor death; retinal detachment.
XX
XX OS Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 196..2592
XX /tag=a
XX /product="IPMC 150 isoform A"
XX
XX US2002160954-A1.
XX
XX 31-OCT-2002.
XX
XX 08-NOV-2001; 2001US-00007270.
XX
XX 29-OCT-1999; 98US-00193972.
XX 29-OCT-1999; 99US-00430195.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX PA Hageman GS, Kuehn WH;
XX
XX PI WPI; 2003-238235/23.
XX
XX DR P-PSDB; ADA14848.
XX
XX New isolated or recombinant interphotoreceptor matrix component
XX PT polynucleotide and polypeptide, useful for diagnosing, preventing,
XX PT treating or prognosticating ocular disorders, e.g. macular degeneration
XX PT or retinal detachment.
XX
XX PS Claim 3; Page 39-41; 76pp; English.
XX
XX CC The invention relates to an isolated or recombinant interphotoreceptor
XX CC matrix component (IPMC) polynucleotide. Also disclosed is a vector
XX CC comprising a promoter of an interphotoreceptor matrix component (IPMC)
XX CC gene operatively linked to the IPMC polynucleotide. The IPMC
XX CC polynucleotides, polypeptides and antibodies are useful for diagnosing,
XX CC preventing, treating or prognosticating ocular disorders, e.g. macular
XX CC degeneration, photoreceptor death or retinal detachment. They are also
XX CC useful for identifying a compound capable of modulating IPMC gene
XX CC expression in a cell. The present sequence represents cDNA encoding mouse
XX CC interphotoreceptor matrix component, IPMC, 150 isoform A.
XX
XX SQ Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;

Alignment Scores:
Pred. No.: 2,376-196 Length: 3668
Score: 2548.50 Matches: 528
Percent Similarity: 75.12% Conservative: 79
Best Local Similarity: 65.35% Mismatches: 180
Query Match: 61.90% Indels: 21
DB: 7 Gaps: 9

US-10-007-270-2 (1-797) x ADA14847 (1-3668)
QY 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
DQ ::::
DB 196 ATGAATTTTCAATTAACATGCTATCTTGTGTTGGGATTTTCTCCAGATTCAAGGA 255
QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
DQ ::::
DB 256 ATCAAGATACCTCTATTAAATATTCAGTCTGAATTAATAACATAGAACCAACCCCA 315
QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgile 60

316 AGAATCGAAACAACTTGAAGTACTTCAACAGTGCACAAAGTGTCAACCATGAACGAATA 375
61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80
376 TTCGATTTCGAAGCTTCGAACCAAGATCAGCAGCTTTTCCCA---GCTGCTAACATC 432
81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
433 TGCCACAGGAATCCTTGAGACAGATTTTGAAGTCTTCAAGATATTATATAGCTGAGA 492
101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
493 GTATGTCAAGAAAGTGTGTGGAAGCATATCGTATCTTCTGACCGCAATTCCTGACACA 552
121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGlnThrPheCysLeuPheAspIle 140
553 GAGGAATATCAAGACTGGGTGAGCTCTGCCAGAAAGAAACCTTCTGCCCTCTTTGACATT 612
141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGln 160
613 GGGAAAAAAGCTTCCAGCAACTCCAGGAGCACCTAGATCTTCTTCCAGCAGAGATAAAGAG 672
161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGluProGly 180
673 AGAAGCTTCCCTGGGAGGAAAGATGAGACAGAGCTCCATGGAGACATGGAAGCACCTACT 732
181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
733 GAAGCCCTGTGTGTCACCAAGATGTTTCCAGGATGTCCCTGGGGCCCTTCCACATTCTCT 792
201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220
793 TCTGATGACACAGACCTCAAGGAGATTTCTAGTGTCCACCTCAAGCAGACATCAAAAGCCC 852
221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGlnGln 234
853 ACAACAGAAAGTAAACACAGAACCTATTACGTTGTCTGAATTTCTCA-----TCAGAGGAG 906
235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254
907 AGGTGGAATTCAGCATCTCTCTGCCAACACACAGGTTCAAGCAGAGCTCAACCACTCT 966
255 GlnSerProTyrTyrGlnGlnLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274
967 GGGTCACCACTATACAGGAACTGGTGGACAGTCCCACTGCGTTCGAAAAGATATTT 1026
275 LysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysGluLys 294
1027 AGAAACTTCCAGGATTCGAGAAATCCGTGATTAGGATTTAGACCAAGAAAGAGAGA 1086
295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314
1087 GATGGTTCAAGCTCCACAGAAATACAGCTTATGGCCATCTTTAAGAGGAGCACCATGAGAA 1146
315 AlaLysSerProAlaSerAspLeuSerPheAspSerAsnLysIleGluSerGluGlu 334
1147 GCAAAAAGCCCTGATAGTCACTCTCTTGTATTCACAAATTTGAAAAGTGAAGA 1206
335 ValTyrHisGlyThrMetGluLysGlnProGluIleTyrLeuThrAlaThrAsp 354
1207 ATCCATCATGGAGTCATA--GAAGACAAACCAACAGAAACCTACCTCACAGCTACAGAC 1263
355 LeuLysArgLeuIleSerLysAlaLeuGluGlnGlnSerLeuAspValGlyThrIle 374
1264 CTCAAAAAATCATCATCACTACTAGTAGGAGCCTGTCTCTGTGAGAGGGAATTT 1323
375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394
1324 CAAATCGGTGATGAAGTTACTGGACACTC-----TTCAGACCTGTCAGTCAACAGAT 1377
395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414

```



Db 1378 CTGCCCAAGCCCTTCTGATGTCACAGAGATGCCACTTGTAGTCCAGAACTTCCTTC 1437  
Qy 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro----- 430  
Db 1438 GTTAGCCCTAGGCTTGAGGAGTGGACAGAGAAGATCTGAGCTGCTGGAATGCTCTCC 1497  
Qy 431 ---AspThrSerThrProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449  
Db 1498 AAGACAGTCTTGCTGCTCCTGATCATGCTCAATTTCCGATCAGAAATCTACT 1557  
Qy 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469  
Db 1558 TCGTTT---ACACCTAGCATCTCTCTAGATGCTCAAAGCCCTCCCTTGATGACC 1614  
Qy 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspThrSerAlaIle 489  
Db 1615 ACTGGCCCAACAGACATCATCCCAAGCCCATCTCTCCACATCATGATTTCTACCATC 1674  
Qy 490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspAspSerArgSer 509  
Db 1675 CGCCAATTGCTCTGGAATCGTCACATTTGGCTGCTGATCTCCAGTGACAGAGCTGATC 1734  
Qy 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529  
Db 1735 ACAAGCAGCCATGACACAATCCGAGACCTAGATGGCATGCTGTCTGACACGCCGCC 1794  
Qy 530 ProSerGluValProGlnLeuSerGluTyValSerValProAspHisPheLeuGluAsp 549  
Db 1795 TTGTCAGAAATATCAGACTGATGATGATGATCTGCGCTCGGTCAGTTCTTGAGATG 1854  
Qy 550 ThrThrProValSerAlaLeuGlnTyIleThrThrSerSerMetThrIleAlaProLys 569  
Db 1855 ACCACACCCATCCCAACAGTTCATGCTCATCCACCCAGCTCCGAGACCATTCGCCAAG 1914  
Qy 570 GlyArgGluLeuValPhePheSerLeuValGValAlaAsnMetAlaPheSerAsnAsp 589  
Db 1915 GGCAGAGAGCTAGTGATCTTCAGCCTCGGTTGCTTAACATGCGTTCCTCTATGAC 1974  
Qy 590 LeuPheAsnLysSerSerLeuGluTyArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609  
Db 1975 CTGTTCAACAAGATCTCTCGAGTATCAAGCCCTGGAACACGATTCACAGACCTGCTG 2034  
Qy 610 ValProTyLeuArgSerAsnLeuThrGlyPheLeuGlnLeuGluLeuLeuAsnPheArg 629  
Db 2035 GTTCCCTATCTACGATCGAATCTTCGGGATTTAAGCAATCGAAATATCTCAGTTCAGA 2094  
Qy 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyArgLeu 649  
Db 2095 AACGGAAGTGTGATCGTGAACACCAAGTCCGTTTGAAGGCGGTACCTTACAACCTC 2154  
Qy 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669  
Db 2155 ACCGAGCCCTGCGCGGGTCTTGGAGGATCTTCGGTCCACCGAGCTCAAGGGCTCAAT 2214  
Qy 670 LeuGluIleAspSerTySerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689  
Db 2215 CTGGAATCGAAGACTACTCTCCGATGATGAACAGCTGATCAGCGGATCTCTGCAAA 2274  
Qy 690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709  
Db 2275 CTCTAGACTGTGCAAAATTCGCCAGTGTGTAAGAATGAGTGGACAGAGGAAGCAGAG 2334  
Qy 710 CysArgCysLysProGlyTyArgSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729  
Db 2335 TGTGCTGTCAGACAGGACATGAGACCGGAGCCCTGATACACCTGTAACCTC 2394  
Qy 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749  
Db 2395 TGTCCCTCTGA---AAGACTTGTGTGGCGCGCGAGAACACCACTCATGACGCCA 2451  
Qy 750 ProAspHisSerGluAsnGlnAlaTyLysThrSerValLysLysPheGlnAsnGlnGln 769  
Db 2452 CCAGATCACTCTACAAACCAAGCTCAGGAACCTGGTGTAAAAAGCTA-----CGTCAG 2505

Qy 770 AsnAsnLysValIleSerLysArgAsnSerGluLeuThrValGluTyArgGluPhe 789  
Db 2506 CAAATTAAGTAGTCAAGAAAGAAATTTCAAACATATCAGCTATAGATTGAAGAATTT 2565  
Qy 790 AsnHisGlnAspTrpGluGlyAsn 797  
Db 2566 GAAGACCAGGACTGGGAGGGAAT 2589  
RESULT 13  
ACC57950  
ID ACC57950 standard; cDNA; 3668 BP.  
XX ACC57950;  
AC ACC57950;  
DT 11-AUG-2003 (first entry)  
XX  
DE Mouse interphotoreceptor matrix IPM 150, isoform A, cDNA.  
XX  
KW Mouse; interphotoreceptor matrix; IPM 150; chromosome 9; IPMC; receptor;  
XX ophthalmological; gene therapy; gene; ss.  
OS Mus sp.  
FH Key Location/Qualifiers  
CDS 196..2592  
FT /\*tag= a  
FT /product= "IPM 150"  
XX  
XX WO2003039346-A2.  
XX  
XX 15-MAY-2003.  
XX  
XX 08-NOV-2002; 2002WC-US036090.  
XX  
XX 08-NOV-2001; 2001US-00077270.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX  
XX Hageman GS, Kuehn MH;  
XX  
XX WPI; 2003-441440/41.  
XX P-PSDB; ABR42345.  
XX  
XX New interphotoreceptor matrix proteins and polynucleotides, useful for  
XX treating or preventing photoreceptor death or retinal detachment, or for  
XX treating ocular disorders.  
XX  
XX Claim 1; Page 81-82; 105pp; English.  
XX  
XX The present sequence is that of cDNA encoding isoform A of novel mouse  
XX interphotoreceptor matrix 150 (IPM 150), a member of the newly identified  
XX interphotoreceptor matrix component (IPMC) gene family. The IPM 150 gene  
XX is located on chromosome 9. Members of the IPMC gene family have been  
XX identified in humans, monkey, cow, goat, rabbit, dog, cat, pig, mouse and  
XX rat IPM. 2 Subfamilies are designated IPM 150 (or IPM1) and IPM 200 (or  
XX IPM2). The invention provides IPM 150 and IPM 200 polynucleotides and  
XX polypeptides, antibodies that specifically bind the polypeptides, and  
XX vectors comprising the polynucleotides. A claimed method of treating or  
XX preventing photoreceptor death or retinal detachment involves  
XX administering an IPMC polynucleotide, polypeptide or antibody. Also  
XX claimed is a method for identifying a compound capable of modulating IPMC  
XX gene expression  
XX  
XX Sequence 3668 BP; 1093 A; 876 C; 762 G; 934 T; 0 U; 3 Other;  
SQ  
Alignment Scores:  
Pred. No.: 2,37e-196 Length: 3668  
Score: 2548.50 Matches: 528  
Percent Similarity: 75.12% Conservative: 79  
Best Local Similarity: 65.35% Mismatches: 180  
Query Match: 61.90% Indels: 21  
Gaps: 9  
DB:

US-10-007-270-2 (1-797) x ACC57950 (1-3668)

Qy	1	MetTyrLeuGluThrArgAlaIlePheValPheThrIlePheLeuGlnValGlnGly	20
Db	196	ATGAATTTTCAAATTAACATCTATCTTGTGTTTGGGATTTTCTCCAAGTTCAAGGA	255
Qy	21	ThrLysAspIleSerIleAsnIleTyrHisSerGlnThrLysAspIleAspAsnProPro	40
Db	256	ATCAAGAATACCTCTATTAAATAATATACGTTCTGAAATTAATAACATAGACAAACCCCA	315
Qy	41	ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle	60
Db	316	AGAAATCGAAACAATTGAAAGTACTTCAACAGTCGACAAAGTGTCACCATGAAACGAAATA	375
Qy	61	PheAspLeuAlaIlyHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal	80
Db	376	TTTGATTTTCCCAAGCTTCGAACCAAAAGATCAGCATCTTTCCCA---GCTGCTAACATC	432
Qy	81	CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg	100
Db	433	TGTCACACAGATCTTGGACACAGATTTTACAGAGCTTTCACAGATATATATAGACTGAGA	492
Qy	101	ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr	120
Db	493	GTATGTCAAGAAAGTGGTGGGAAGCATATCGTATCTTTCTGGACCGAAATCTCTGCACACA	552
Qy	121	GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGlnThrPheCysLeuPheAspIle	140
Db	553	GAGGAATATCAAGACTGGGTGAGCTCTGCCAGAAAGAAACCTTCTGCCCTTTTGACATT	612
Qy	141	GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGln	160
Db	613	GGGAAAAATCTCAGCAACTCCCGAGGACCACTAGATCTTCTTCAGCAGAGAAATAAAGACAG	672
Qy	161	ArgSerPheProAspArgLysAspGluLeuSerAlaGluLysThrLeuGlyProGly	180
Db	673	AGAAGCTTCCCTGGGAGGAAAGATAGACAGACCCCTCCATGGAGACACTGGGAAGCACCTACT	732
Qy	181	GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr	200
Db	733	GAAGCCCTGTGGTACCCACAGATGTTTCCAGGATGTCCTTGGGGCCCTTCCCACTTCCT	792
Qy	201	ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro	220
Db	793	TCTGATGACACAGACCTCAAGGAGATCTCAGTGTCACTCCCTCAAGGACATTTCAAAAGCCG	852
Qy	221	ThrThrGluArgGluThr-----GluPheAlaValLeuGluGlnGln	234
Db	853	ACAAAGAAAGTAAACAGAACCTATTCACTGCTGTGAATTTCTCA-----TCAGAGGAG	906
Qy	235	ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer	254
Db	907	AAGGTGGAATTCAGCATCTCTCTGCCAAACACACAGGTTCAAGGCAGAGCTCACCAACTCT	966
Qy	255	GlnSerProTyrTyrGlnGlnLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe	274
Db	967	GGCTCACCATATACAGGAACCTGGTGGGACAGTCCCAACTGCAGTTGCAAAAGATATT	1026
Qy	275	LysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysGluLys	294
Db	1027	AAGAACTTCCAGGATTCGGAATAATCGGTATTAGGATTTAGACCAAGAAAGAAAGAA	1086
Qy	295	AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu	314
Db	1087	GATGGTTCAAGTTCACAGAAATACAGTCTTATGGCCATCTTTAAGAGGGACCATGCGAA	1146
Qy	315	AlaLysSerProAlaSerAspLeuSerPheAspSerAsnLysIleGluSerGluGlu	334
Db	1147	GCAAAAGCCCTGATAGTCACTACTGCTCTTGTATTCACAAATAATTTGAAGTGAAGA	1206
Qy	335	ValTyrHisGlyThrMetGluGluAspLysGlnProGluLysIleTyrLeuThrAlaThrAsp	354
Db		-----	
Qy	355	LeuLysArgLeuIleSerLysAlaLeuGluGlnGlnSerLeuLeuAspValGlyThrIle	374
Db	1264	CTCAAAAATCTCATCACTACTAGATGGAGACCTGTCTTGGTAGAAGGGAAAAT	1323
Qy	375	GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu	394
Db	1324	CCATTCGGTGATGAAGTTACTGGGACACTC-----TTCAGACCTGTCTCACTGAACCCAGAT	1377
Qy	395	LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro	414
Db	1378	CTGCCAAGCCCTGCTGATGTCCAGAGGATGCCATTTTGTAGTCCAGAACTTCTCTTC	1437
Qy	415	ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro-----	430
Db	1438	GTTGAGCCTTAGGCTTGAGGCAGTGACAGAGAAGGATCTGAGTGCCTGGAAATGTCCTCC	1497
Qy	431	---AspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProPro	449
Db	1498	AAAGACAGTTCITGGTCTCCACTGTATCAGCCTCAATTTCCCGATCAGAAAAATCTACCT	1557
Qy	450	PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla	469
Db	1558	TCGTTT---ACACCTAGCATCTTCTCTAGATGCTCAAGCCCTCCCTCCCTTGTATGACC	1614
Qy	470	ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIle	489
Db	1615	ACTGGGCCAACAGCACTCATCCCAGGCCACTCTCCCACTATCGATTATTTACCATC	1674
Qy	490	SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArgSerSer	509
Db	1675	CGCAATTTGCTGTGAATCGTCACATTTGGCTGTCATCTCCAGTGAACAGAGAGCTGATC	1734
Qy	510	AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla	529
Db	1735	ACAAGCAGCCATGACAAATCCGAGACCTTAGTGCCATGGATGTCTGACACGCCACGCC	1794
Qy	530	ProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAsp	549
Db	1795	TTGTCAGAAATATACAGACTGAGTGGATAGCATTTCTGCTCGGTCAGTTCTTGGAGATG	1854
Qy	550	ThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLys	569
Db	1855	ACCACACCCATCCAAACAGTACGGTTCATCCACCACAGCTCCGAGACATTTGCCACCAAG	1914
Qy	570	GlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAsp	589
Db	1915	GGCAGAGGCTAGTGGTATTCTTCAGCCTGGTGTGTGTACATGCGCGTTCTCTCTATGAC	1974
Qy	590	LeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu	609
Db	1975	CTGTTCAACAAGAGTTCTCTGGAGTATCAAGGCCCTGGAAACACGATTTCCACAGACTGCTG	2034
Qy	610	ValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuG	

QY 710 CysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729  
 DB 2335 TGTGGTGCAGACAGGACATGAGCCACGAGGACCTGGACTACAGACCTGGAACCTC 2394  
 QY 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749  
 DB 2395 TGTCCCTCGA---AAGACTTGTGGCGCGCGGAGAACAGCACTCCTGCGAGGCCA 2451  
 QY 750 ProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsnGlnGln 769  
 DB 2452 CCAGATCACTCTACAAACCAAGCTCAGGAACCTGGTGTAAAAAGCTA-----CGTCAG 2505  
 QY 770 AsnAsnLysValLysSerLysArgAsnSerGluLeuLeuThrValGluTyrGluGluPhe 789  
 DB 2506 CAAAAATAAGGTAGTCAAGAAAGAAATCTTAACACTATCAGCTATAGGATTGAAGAATT 2565  
 QY 790 AsnHisGlnAspTyrGluGlyAsn 797  
 DB 2566 GAAGACCAGGACTGGGAGGGAAT 2589  
 RESULT 14  
 AAA46309  
 ID AAA46309 standard; cDNA; 3206 BP.  
 AC AAA46309;  
 XX  
 DT 04-SEP-2000 (first entry)  
 XX  
 XX cDNA encoding an interphotoreceptor matrix proteoglycan (IPM150).  
 DE Interphotoreceptor matrix; IPM; proteoglycan; IPM150; IPMC; IPM200;  
 XX chromosome 6q13-q15; ocular disease; retinal detachment;  
 KW chorioretinal degeneration; retinal degeneration; cone degeneration;  
 KW age related macular degeneration; photoreceptor degeneration;  
 KW retinal pigment epithelium degeneration; mucopolysaccharidosis;  
 KW rod- cone dystrophy; cone-rod dystrophy; ss.  
 XX Mus sp.  
 XX  
 PH Location/Qualifiers  
 FT 1. .2130  
 FT /\*tag= a  
 FT /transl\_except= (pos: 16. .18, aa: Val)  
 FT /transl\_except= (pos: 55. .57, aa: Ala)  
 FT /transl\_except= (pos: 58. .60, aa: Tyr)  
 FT /transl\_except= (pos: 73. aa: Asp)  
 FT /transl\_except= (pos: 234. .236, aa: Xaa)  
 FT /transl\_except= (pos: 271. .273, aa: Xaa)  
 FT /transl\_except= (pos: 403. .405, aa: Xaa)  
 FT /transl\_except= (pos: 2107. .2109, aa: Xaa)  
 FT /product= "interphotoreceptor matrix proteoglycan IPM150"  
 FT /note= "Xaa is an unspecified amino acid"  
 XX  
 FN WO200026367-A2.  
 XX  
 PD 11-MAY-2000.  
 XX  
 XX 29-OCT-1999; 99WO-US025440.  
 XX  
 XX 29-OCT-1998; 98US-00183972.  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 XX Hageman GS, Kuehn MH;  
 XX WPI; 2000-365616/31.  
 XX P-PSDB; RAY93338.  
 XX  
 XX Nucleic acids encoding interphotoreceptor matrix proteoglycans useful for  
 XX preventing, diagnosing and treating ocular disorders such as retinal  
 XX detachment and chorioretinal degeneration.  
 XX

PS Claim 2; Fig 6A; 183pp; English.

XX The present sequence encodes an interphotoreceptor matrix (IPM) proteoglycan, designated IPM150. The protein is an IPM component (IPMC). Two subfamilies of IPMCs, IPM150 and IPM200, exist. The human IPM150 gene is located on chromosome 6q13-q15, between markers CHLC.GATA1P10 and D6S284. The IPM proteins may be used to supplement a patient's own production of the protein or to rectify alterations in their nucleic acids that result in expression of an inactive protein. The IPM nucleic acids may be used in this way to treat ocular diseases such as retinal detachment, chorioretinal degeneration, retinal degeneration, age related macular degeneration, photoreceptor degeneration, RPE (retinal pigment epithelium) degeneration, cone degeneration, mucopolysaccharidosis, rod-cone dystrophy and cone-rod dystrophy. The nucleic acids and proteins may also be used to assay for other modulators of IPM proteoglycan expression and activity that may be used to treat ocular diseases. The nucleic acids and proteins may also be used as diagnostic reagents to detect the presence of IPM nucleic acids and their products in samples from patients according to standard methodologies

SX Sequence 3206 BP; 937 A; 778 C; 686 G; 793 T; 0 U; 12 Other;

#### Alignment Scores:

Pred. No.: 1.57e-167 Length: 3206  
 Score: 2192.00 Matches: 457  
 Percent Similarity: 74.08% Conservative: 69  
 Best Local Similarity: 64.37% Mismatches: 164  
 Query Match: 53.24% Indels: 20  
 DB: Gaps: 8

US-10-007-270-2 (1-797) x AAA46309 (1-3206)

QY 99 LeuArgValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIlePro 118  
 DB 25 ATCAAGTATGTCAGAGTCGTGGAGAGATGATGATATCTTCTGGNAGATTCCT 84  
 QY 119 AspThrGlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPhe 138  
 DB 85 GACACAGAGGAATATCAAGGCTGGGTGAGCTCTGCCAGAGAAGAACCTCTGCCTCTTT 144  
 QY 139 AspIleGlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgIle 158  
 DB 145 GACATTGGGAAAAAATCTGAGCACTCCAGAGACCATAGATCTTCTCAGCAGAGATA 204  
 QY 159 LysGlnArgSerPheProAspArgLysAspLysSerAlaGluLysThrLeuGlyGlu 178  
 DB 205 AAACAGAGAGCTTCCCTCGGAGGAAAGATGWAGACGCTCCATGGAGACACTGGAAGCA 264  
 QY 179 ProGlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProphePro 198  
 DB 265 CCTACTGRAGCCCTGTGGTACCCACAGATGTTTCCAGGATGTCCTGGGGCCMTCCCA 324  
 QY 199 LeuThrProAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLys 218  
 DB 325 CTTCCTTCTGATGACACAGACCTCAAGAGATCTTCAGTGTCCCTCAAGGACATTCAA 384  
 QY 219 MetProThrThrGluArgGluThr-----GluPheAlaValLeuGlu 232  
 DB 385 AAGCCCAACACAGAAAGTAAACACCACTATTCAVGTGTCTGAATTTCTCA-----TCA 438  
 QY 233 GluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAla 252  
 DB 439 GAGGAGAGGTGGATTTCAGCATCTCTGCCAAACACAGAGTTCAGGTCAGAGTCACC 498  
 QY 253 AspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLys 272  
 DB 499 AACTCTGGGTCAACATACCTACAGAACTGGTGGGACAGTCCCAACTGCGAGTTGCAAAAG 558  
 QY 273 IlePheLysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLys 292  
 DB 559 ATATTTAAGAAACTTCCAGGATTCGGAGAAATCCGTGATTAGGATTTAGACCAAGAAA 618  
 QY 293 GluLysAspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSer 312

```

Db 619 GAGAGATGTTCAAGCTCCACAGAAATACAGCTTATGGCCATCTTTAAGAGGGACCAT 678
Qy 313 AlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSer 332
Db 679 GCAGACCAAAAGCCCTGATAGTACATCTACTGCTCTTGAATCCACAAATTTGAATC 738
Qy 333 GluGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAla 352
Db 739 GAAAGATCCATCATGAGGTCATA---GAAGACAAACCAACAGAAACCTACCTCACAGCT 795
Qy 353 ThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGly 372
Db 796 ACAGACCTCAAAAACCTCATACACTACTAGATGGAGACCTGCTTGGTAGAGG 855
Qy 373 ThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGln 392
Db 856 AAAATTCATTCGGTGTAGTGAATTACTGGGACACTC-----TTCAGACCTGTCACTGAA 909
Qy 393 SerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeu 412
Db 910 CCAGATCTGCCAAGCCCTTGGTGTGATGTACAGAGATGCCACTTTGAGTCCAGAACTT 969
Qy 413 ProProValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro----- 430
Db 970 CTTTCGTTGAGCTAGCTAGCTTGGAGGAGTGGACAGAGAGGATCTGAGCTGCTGGAATG 1029
Qy 431 -----AspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAla 447
Db 1030 TCTCTCAAGACAGATGTTGGTCTCCACCTGTATCAGCCTCAATTTCCCGATCAGAAAT 1089
Qy 448 ProProPheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThr 467
Db 1090 CTACCTTCGTTT---ACACCTAGCATCTTCTCTAGATGCTCAAGCCCCCTCCCTTG 1146
Qy 468 MetAlaThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSer 487
Db 1147 ATGACCACTGGCCCAACAGACACTCATCCCGACAGCCCACTCTCCCACTATCATTATCT 1206
Qy 488 AlaIleSerGlnLeuAlaLeuGlyIleSerHisProAlaSerSerAspSerArg 507
Db 1207 ACCATCGCCAAATGCTCTGGAAATCGTCACATTTGGCTTGCATCTCCAGTGACAGAG 1266
Qy 508 SerSerAlaGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThr 527
Db 1267 CTGATCACAAGCAGCCATGACAAATCCGAGACCTAGATGGCATGGATGTGTGCACAG 1326
Qy 528 ProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeu 547
Db 1327 CCAGCCTTGTCAAGAAATATCAGAACTAGAGTGGATACGATTCTGCTCGGGTCAGTCTTG 1386
Qy 548 GluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAla 567
Db 1387 GAGATGACCAACACCCATCCCAACAGATACGGTTTCATCACCACCGCTCCGAGACCATGCC 1446
Qy 568 ProLysGlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSer 587
Db 1447 ACCAAGGCGCAGAGAGTAGTGGTATTCTTCAGCCTCGTGTTCCTAAACATGCGCTCTCC 1506
Qy 588 AsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGln 607
Db 1507 TATGACCTGTTCAACAGAGTCTCTGGAGTATCAAGCCCTCGAACACGATTCACAGAC 1566
Qy 608 LeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsn 627
Db 1567 CTGCTGGTTCCCTTATCTACGATCGAATCTTACGGGATTTAAGCAACTGGAAATACCTCAGC 1626
Qy 628 PheArgAsnLysSerValIleValAsnSerLysMetLysPheAlaLysSerValProTyr 647
Db 1627 TTCAGAAACGGAAGTGTGATCGTGAACAGCAAGTCCGGTTTGCAAGCGGTACCTTAC 1686
Qy 648 AsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGln 667

```

```

Db 1687 AACCTCACCCAGGCGCTGCGGGGTCTTGGAGGATCTTGGTCCACCGCAGCTCAAGGG 1746
Qy 668 LeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspPro 687
Db 1747 CTCAATCTGGAATCGAAAGACTACTCCTCTGCACATTGAACCGACTGATCAGCGGATCCC 1806
Qy 688 CysLysPheLeuAlaCysGlyGlyPheAlaGlnCysValLysAsnGluArgThrGluGlu 707
Db 1807 TGCAAACTCCCTAGACTGTGGCAATTTGCCAGTGTGTAAAGAATGATGGACAGAGAA 1866
Qy 708 AlaGluCysArgCysLysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluPro 727
Db 1867 GCAGAGTGTCTCTGCAGACAGGACATGAGAGCCACCGGACCTGGACTACCAGACCTG 1926
Qy 728 GlyLeuCysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCys 747
Db 1927 AACCTCTGTCCCTCGGA---AAGACTTGTGTGCGCGCGAGAACCAAGCAACTCCATGC 1983
Qy 748 ArgLeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysLysPheGlnAsn 767
Db 1984 AGGCCACAGATCACTTCTACAAACCAAGCTCAGGAACCTGGTGTAAANAGCTA----- 2037
Qy 768 GlnGlnAsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluTyrGlu 787
Db 2038 CGTCAGCAAAATAAGGTAGTCAGAAAGAAATTTCTAACTATCAGCTATAGGATTTTGA 2097
Qy 788 GluPheAsnHisGlnAspTyrGluGlyAsn 797
Db 2098 GAATTTGAARACCAGGACTGGGAGGAAAT 2127

RESULT 15
ADA14849
ID ADA14849 standard; cDNA; 1726 BP.
XX ADA14849;
XX
XX 06-NOV-2003. (first entry)
XX Mouse interphotoreceptor matrix component, IPMC, 150 isoform D cDNA.
XX ss; gene; mouse; IPMC 150 isoform D; gene therapy;
XX interphotoreceptor matrix component; IPMC; ocular disorder;
XX macular degeneration; photoreceptor death; retinal detachment.
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 140..1540
XX /tag= b
XX /product= "IPMC 150 isoform D"
XX sig_peptide 140..199
XX /tag= a
XX /label= Signal_sequence
XX mat_peptide 200..1537
XX /tag= c
XX /label= Mature_IPMC_150_isoform_D
XX US2002160954-A1.
XX
XX 31-OCT-2002.
XX
XX 08-NOV-2001; 2001US-00007270.
XX
XX 29-OCT-1998; 98US-00183972.
XX 29-OCT-1999; 99US-00430195.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Hageman GS, Kuehn MH;
XX
XX WPI; 2003-238235/23.
XX P-PSDB; ADA14850.
XX

```

PT New isolated or recombinant interphotoreceptor matrix component  
 PT polynucleotide and polypeptide, useful for diagnosing, preventing,  
 PT treating or prognosticating ocular disorders, e.g. macular degeneration  
 PT or retinal detachment.

XX  
 PS Claim 3; Page 43-44; 76pp; English.

CC The invention relates to an isolated or recombinant interphotoreceptor  
 CC matrix component (IPMC) polynucleotide. Also disclosed is a vector  
 CC comprising a promoter of an interphotoreceptor matrix component (IPMC)  
 CC gene operatively linked to the IPMC polynucleotide. The IPMC  
 CC polynucleotides, polypeptides and antibodies are useful for diagnosing,  
 CC preventing, treating or prognosticating ocular disorders, e.g. macular  
 CC degeneration, photoreceptor death or retinal detachment. They are also  
 CC useful for identifying a compound capable of modulating IPMC gene  
 CC expression in a cell. The present sequence represents cDNA encoding mouse  
 CC interphotoreceptor matrix component, IPMC, 150 isoform D.

XX SQ Sequence 1726 BP; 541 A; 383 C; 388 G; 414 T; 0 U; 0 Other;

# Alignment Scores:

Prd. No.: 4, 94e-99 Length: 1726  
 Score: 1342.50 Matches: 310  
 Percent Similarity: 44.96% Conservative: 51  
 Best Local Similarity: 38.61% Mismatches: 99  
 Query Match: 32.61% Indels: 343  
 DB: 7 Gaps: 9

US-10-007-270-2 (1-797) x ADA14849 (1-1726)

Qy 1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
 Db 140 ATGAATTTTCAAAATAAATGATGCTATCTTTGTTTGGGATTTTCTCCAAAGTTCAAAGA 199  
 Qy 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnPro 40  
 Db 199 ----- 199  
 Qy 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgIle 60  
 Db 199 ----- 199  
 Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 Db 199 ----- 199  
 Qy 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 200 -----ATCAA 205  
 Qy 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 Db 206 GTATGTCAAGAGTCGTGTGGGAAGCATATCGTATCTTTCTGGACCGAATTCCTGACACA 265  
 Qy 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 Db 266 GAGGATATCAAGACGTGGGTGACCCCTCTGCCAGAAAGAAACCTTCTGCCTCTTTGACATT 325  
 Qy 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnIleArgIleLysGln 160  
 Db 326 GGGAAAAAATTCAGCAACTCCAGGAGCACCCTAGATCTTCTTCAGCAGAGAATAAAACAG 385  
 Qy 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 Db 386 AGAAGCTTCCTGGGGAAGATGAGACAGCCCTCATGGAGACACTGGAGACACTTACT 445  
 Qy 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 Db 446 GAAGCCCTGTGTACCCACAGATGTTCCAGGATGTCCTGGGGCCATTCCTCCACTTCT 505  
 Qy 201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
 Db 506 TCTGATGACACAGACCTCAAGGAGATTTCTCAGTGTCAACCTCAAGGACATTCAAAAGCCC 565

Qy 221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGluGln 234  
 Db 566 ACAACGAAGAGTATACAGAAACCTATTTCAGTGTCTGAATTTCTCA-----TCAGAGGAG 619  
 Qy 235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254  
 Db 620 AAGGTGGAGTTACGATCTCTCTGCCAAACACACAGGTTCAGGCAGAGCTCACCACACTCT 679  
 Qy 255 GlnSerProTyrTrpGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274  
 Db 690 GGGTCACCACTACACAGGAACCTGGTGGGACACTCCCACTGCAGTTGCAAAAGATATTT 739  
 Qy 275 LysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysGluLys 294  
 Db 740 AAGAACTTCCAGGATTCGAGAAATCCGCTGTTATAGGATTTAGACCAAGAAAGAA 799  
 Qy 295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314  
 Db 800 GATGGTTCAAGCTCCACAGAAATACAGCTTATGGCCATCTTTAAGAGGGACCATGCAGAA 859  
 Qy 315 AlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGlu 334  
 Db 860 GCAAAAAGCCCTGATAGTCACTACTCTCTCTGTGATTCACAAATAATTGAAGTGAAGA 919  
 Qy 335 ValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAsp 354  
 Db 920 ATCCATCATGGAGTCATA--GAAGACAAACACCAACCAACCTTACCTCAGACTCAGAC 976  
 Qy 355 LeuLysArgLeuLysSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIle 374  
 Db 977 CTCAAAAAATCATCATCACTACTAGTAGAGGACCTGTCTTGTAGAGGGAATAATT 1036  
 Qy 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394  
 Db 1037 CCATTCGGTGTGAAGTTACTGGGACACTC-----TTCAGACCTGTCTCACTGAACAGAT 1090  
 Qy 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414  
 Db 1091 CTGCCCCAAGCCCTTGTCTGATGTCACAGAGGATGCCACTTTGAGTCCAGAACTTCCTTTC 1150  
 Qy 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuProAspThrSerTrp 434  
 Db 1151 GTTGAGCTTAGCTTGAGGCGAGTGGAC----- 1177  
 Qy 435 SerProAlaMetAlaSerThrSerLeuSerGluAlaProProphePheMetAlaSer 454  
 Db 1177 ----- 1177  
 Qy 455 SerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMet 474  
 Db 1177 ----- 1177  
 Qy 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494  
 Db 1177 ----- 1177  
 Qy 495 GlyIleSerHisProProAlaSerSerAspSerArgSerSerAlaGlyGlyGluAsp 514  
 Db 1177 ----- 1177  
 Qy 515 MetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaProSerGluValPro 534  
 Db 1177 ----- 1177  
 Qy 535 GluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThrThrProValSer 554  
 Db 1177 ----- 1177  
 Qy 555 AlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGlyArgGluLeuVal 574  
 Db 1177 ----- 1177

```
QY 575 ValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsnLysSer 594
Db 1177 ----- 1177
QY 595 SerLeuGluTyrArgAlaLeuGluGlnPheThrGlnLeuLeuValProTyrLeuArg 614
Db 1177 ----- 1177
QY 615 SerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIle 634
Db 1178 -----AGAGAGGATCTGAGCTG 1195
QY 635 ValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHis 654
Db 1195 ----- 1195
QY 655 GlyValLeuGluAspPheArgSerAlaAlaAlaGlnGlnLeuHisLeuGluIleAspSer 674
Db 1195 ----- 1195
QY 675 TyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGly 694
Db 1196 -----CCTGTGATCAGCGGATCCCTGCAACTTCTAGACTGTGSC 1237
QY 695 GluPheAlaGlnCysValLysAsnGluA-zgThrGluGluAlaGluCysArgCysLysPro 714
Db 1238 AATTTGCCCAGTGTGTAAAGATGAGTGGACAGAGAAAGCAGAGTGTGCTGCACAGACAG 1297
QY 715 GlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThr 734
Db 1298 GGACATGAGAGCCACGGGACCCCTGGACTACCGAGCCCTGAACCTCTGTCCCCCTGGA--- 1354
QY 735 LysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeuProAspHisSerGlu 754
Db 1355 AAGACTTGTGTGCGCGCCGAGAGAACAGCACTCCATGAGGCCAACAGATCACTCTACA 1414
QY 755 AsnGlnAlaTyrLysThrSerValLysLysPheGlnAsnGlnGlnAsnLysValIle 774
Db 1415 AACCAAGCTCAGGAACTGGTGTAAAAAGCTA-----CGTCAGCAAAATAAGGTAGTC 1468
QY 775 SerLysArgAsnSerGluLeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTrp 794
Db 1469 AAGAAAAGAAATTTCTAAACTATCAGCTATAGGATTTGAAGAAATTTGAGACCAGGACTGG 1528
QY 795 GluGlyAsn 797
Db 1529 GAGGAAAT 1537
```

Search completed: March 1, 2004, 21:06:43  
Job time : 922 secs



GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2004, 18:13:35 ; Search time 7927 Seconds  
(without alignments)  
4357.815 Million cell updates/sec

Title: US-10-007-270-2

Perfect score: 4117

Sequence: 1 MLETRRAIFVFWFLQVQG.....NSELLTVYEYEFNHQDHGHN 797

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlh

-MODEL=frame+ p2n.model -DEV=xlh

-Q/cg2\_1/USPTO.spool/US10007270/runat\_25022004\_164207\_27193/app\_query.fasta\_1.967

-DB=GenEmbl -OFMT=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000

-USER=US10007270 @CGN 1.1 5239 @runat\_25022004\_164207\_27193 -NCPU=6 -ICPU=3

-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.pl.\*

25: em.ro.\*

26: em.ste.\*

27: em.un.\*

28: em.un.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4117	100.0	3268	9	AF047492 Homo sapi
2	2759	67.0	3552	4	AB047844 Bos tauri
3	2548.5	61.9	3668	10	AF266478 Mus muscu
4	2546.5	61.9	2924	10	BC022970 Mus muscu
5	2543.5	61.8	2850	10	AB047843 Rattus no
6	2453	59.6	3675	10	AF229929 Mus muscu
7	1842.5	44.8	4953	5	AB070714 Gallus ga
8	933	22.7	3989	9	AF157624 Homo sapi
9	927	22.5	4165	9	AF173155 Homo sapi
10	911.5	22.1	4010	10	AY174061 Mus muscu
11	899	21.8	816	9	HSINPG33
12	899	21.8	90786	9	AL392166 Human DNA
13	899	21.8	132145	2	AL359817 Homo sapi
14	899	21.8	160719	2	AL157379 Homo sapi
15	886	21.5	4368	10	RUU76717 Rattus norv
16	885	21.5	555	9	AF047491 Macaca fa
17	875	21.3	6951	10	BC048863 Mus muscu
18	510.5	12.4	248573	2	AC096467 Rattus no
19	483.5	11.7	171412	2	AC120388 Mus muscu
20	408.5	9.9	537	9	HSINPG02
21	408.5	9.9	132145	2	AL359817 Homo sapi
22	408.5	9.9	186301	9	AL356962 Human DNA
23	406.5	9.9	444	9	HSINPG10
24	384	9.3	477	9	HSINPG15
25	382.5	9.3	206937	5	EX001018 Zebrafish
26	380	9.2	448	9	HSINPG14
27	317	7.7	178064	2	AC023311 Homo sapi
28	317	7.7	178157	2	AC023311 Homo sapi
29	315.5	7.7	183965	9	AC130436 Homo sapi
30	315.5	7.7	187899	9	AC068764 Homo sapi
31	315	7.7	203971	2	AC093008 Homo sapi
32	315	7.7	270051	2	EX649245 Danio rer
33	310	7.5	222615	2	HSINPG03
34	308	7.5	222615	2	AC098280 Rattus no
35	264.5	6.4	60914	2	AC135246 Danio rer
36	246	6.0	294851	2	EX649242 Danio rer
37	245	6.0	135646	2	AC119976 Mus muscu
38	245	6.0	171061	2	AC109266 Mus muscu
39	245	6.0	227553	2	AC116453 Mus muscu
40	243.5	5.9	159816	2	AC136044 Rattus no
41	241	5.9	1094	9	F271363812
42	241	5.9	160042	2	AC027757 Homo sapi
43	234.5	5.7	377	9	HSINPG07
44	195.5	4.7	219082	2	AC098274 Rattus no
45	194	4.7	311	9	HSINPG06

ALIGNMENTS

RESULT 1

```

AF047492      3268 bp      mRNA      linear      PRI 26-OCT-1999
LOCUS      Homo sapiens interphotoreceptor matrix proteoglycan 150 (IMPG1)
DEFINITION      mRNA, complete cds.
ACCESSION      AF047492
VERSION      AF047492.2      GI:6118565
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 3268)
AUTHORS      Kuehn, M.H. and Hageman, G.S.
TITLE      Expression and characterization of the IPM 150 gene (IMPG1)
Product, a novel human photoreceptor cell-associated
chondroitin-sulfate proteoglycan
JOURNAL      Matrix Biol. 18 (5), 509-518 (1999)
MEDLINE      20068045
PubMed      10601738
REFERENCE      2 (bases 1 to 3268)
AUTHORS      Kuehn, M.H. and Hageman, G.S.
TITLE      Direct Submission
JOURNAL      Submitted (10-FEB-1998) Ophthalmology and Visual Sciences,
University of Iowa, 200 Hawkins Drive, 11190E PPF, Iowa City, IA
52240, USA
REFERENCE      3 (bases 1 to 3268)
AUTHORS      Kuehn, M.H. and Hageman, G.S.
TITLE      Direct Submission
JOURNAL      Submitted (26-OCT-1999) Ophthalmology and Visual Sciences,
University of Iowa, 200 Hawkins Drive, 11190E PPF, Iowa City, IA
52240, USA
REMARK      Sequence update by submitter
COMMENT      On Oct 26, 1999 this sequence version replaced gi:2906231.
FEATURES
source      1..3268
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /chromosome="6"
             /map="between markers D6S280 and D6S1659"
             /tissue_type="retina"
             1..3268
gene      1..3268
             /gene="IMPG1"
             131..2524
CDS      131..2524
             /gene="IMPG1"
             /note="IPM 150"
             /codon_start=1
             /product="interphotoreceptor matrix proteoglycan 150"
             /protein_id="AAC03789.2"
             /db_xref="GI:6118565"
             /translation="MYLETRAFVFWFIQVQTKDISINIVHSHTKIDNPPRNET
             TESTEKMYKSTWRIPTDLAKHRTKSAFFPTGVKVCPOESMKQILDSLQAYVLRVC
             QEAWEAYRIFLDRIPTDGYQWVGICQOETFCFLDIGNFSNQHLDLQRIKO
             RSPDRKDEISAEKTLGEGCTIVISDVANVSLGPPPLTPDPTLLNLDNTLNDTK
             MPTTERTEFANLEQORVELSVLNQKFAELADSQSPYQELAGSKSLQWQKLFKK
             LPQKHLVGFPRKKGSSSTEMQTLAIFRKHSAKSPASDLSDLSFDSNKSIEE
             VYGTGMEEDQPIYILATDLKLLSKALEEQSLDVGITQFTDEIAGSLPAPGPTQ
             SELTPSAVITDQGTDMATDQWLVPGTLIPTDYSASISQALGISHPPASDDRSR
             FMASISFLDQGTDMATDQWLVPGTLIPTDYSASISQALGISHPPASDDRSR
             SAGGEDMVRHLDMDLSDTPAPSEVPSVDPDFLEDTPVSALQVITTSMTI
             APKRELVFVFSIRVANVAFSNDLENKSLFVLEALQOFTQLLVPLVRLSNLTGFKOLE
             ILNPRGVSIVNKMFKASVPYNLKVAVHGVLEDFRSAAQQLHLSDSYSLNIEPA
             DQADPCKFLAGFAQCVRNTEREAEKRCRPGTDSQGLDGLPELPGFGPTKEKLEVL
             QGKGAFCRLPDHSENAKYTSVKFQNFQNNKRVISKRNSELLTVEEYEFNHDQWEGN"
ORIGIN
Alignment Scores:
Pred. No.:      1..44e-277      Length:      3268
Score:      4117.00      Matches:      797
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      9      Gaps:      0

```

```

US-10-007-270-2 (1-797) x AF047492 (1-3268)
QY      1 MetTyrLeuGluThrArgArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20
DB      131 ATGTATTGGAAACATAGAGAGCTATTATTTGTTTGGATTTTCTCCAGTTCAAGGA 190
QY      21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40
DB      191 ACCAAGATATCTCCATTAACATATACATCTTGAACATTAAGACATAGACATCCCCCA 250
QY      41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgile 60
DB      251 AGAAATGAACCACTGAAAGTACTGAAAAATGTACAAAATGTCAAACTATGAGACGAATA 310
QY      61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80
DB      311 TTCGATTGGCAAGCATCGAACAAAAAGATCCGCATTTTCCCAACGGGGGTTAAAGTC 370
QY      81 CysProGlnGluSerMetLysGlnIleLysAspSerLeuGlnAlaTyrTyrArgLeuArg 100
DB      371 TGTCACAGGATCCATGAAACAGATTTAGACAGCTTCTCAAGCTTATTATAGATTGAGA 430
QY      101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
DB      431 GTGTGTCAGGAAGCATGATGGAAAGCATATCGGATCTTTCTGGATCGCATCCCTGACACA 490
QY      121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140
DB      491 GGGAAATATCAGGACTGGTGCAGCATCTGCCAGCAGGAGACCTTCTGCCTCTTTGACATT 550
QY      141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIleLysGln 160
DB      551 GGAAAAAATCTTCAGCAATTTCCAGGAGCACCCTGGATCTTCTCCAGCAGAGAATAAAACAG 610
QY      161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180
DB      611 AGAAGTTTCCCTGACAGAAAAGATGAATATCTCAGAGAAGACATTTGGGAGAGCCCTGGT 670
QY      181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
DB      671 GAAACCATTTGTCATTTCAACAGATGTTGCCAACCTCTCCTTGGGCTTTTCCCTCTCACT 730
QY      201 ProAspPheThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220
DB      731 CCTGATGACACCTCTCAATGAAATCTCGATAATACCTCAACACGACACCAAGATCGCT 790
QY      221 ThrThrGluArgGluThrGluPheAlaValLeuGluGlnArgValGluLeuSerVal 240
DB      791 ACAACGAAAGAGAAACAGAAATTCGCTGTGTGGAGAGCAGAGGGTGGAGCTCAGGCTC 850
QY      241 SerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSerGlnSerProTyrTyrGln 260
DB      851 TCTCTGGTAAACACAGAGTTCAAGGCAGAGCTCGCTGACTCCCACTCCCACTCCCATATTAC 910
QY      261 GluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePheLysLysLeuProGlyPhe 280
DB      911 GAGCTAGCAGAAAAGTCCCACTTCAGATGCAAAAGATATTATAAGAACTTCCAGATTTC 970
QY      281 LysLysIleHisValLeuGlyPheArgProLysLysGluLysAspGlySerSerSerThr 300
DB      971 AAAAAATCCATGTGTAGGATTTAGACCAAAAGAAAGAAAGATGCTCAAGCTCCACACA 1030
QY      301 GluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGluAlaLysSerProAlaSer 320
DB      1031 GAGATGCAACTTACGGCCATCTTTAAGAGACACAGTGCAGAAAGCAAAAGCCCTCGAAGT 1090
QY      321 AspLeuLeuSerPheAspSerAsnLysIleGluSerGluGluValTyrHisGlyThrMet 340
DB      1091 GACCTCCTGTCTTTTGTATCCCAAAAATTTGAAAGTGGAGAGTCTATCATGGAACCATG 1150
QY      341 GluGluAspLysGlnProGluIleTyrIleuThrAlaThrAspLeuLysArgLeuIleSer 360

```

Db 1151 GAGGAGCAACACCAAGCAATCTATCTCAGAGCTACAGACCTCAAAAGGCTGATCAGC 1210  
 Qy 361 LysAlaLeuGluGluGlnSerLeuAspValGlyThrIleGlnPheThrAspGluIle 380  
 Db 1211 AAAGCACTAGAGGAAGAAACAATCTTTGGATGTGGGACAAATTCAGTTCACTGATGAAT 1270  
 Qy 381 AlaGlySerLeuProAlaPheGlyProAspThrGlnSerGluLeuProThrSerPheAla 400  
 Db 1271 GTTGATCACTCCAGGCTTTGGTCTGACACCAATCAGAGCTGCCACATCTTTGCT 1330  
 Qy 401 ValIleThrGluAspAlaThrLeuSerProGluLeuProProValGluProGlnLeuGlu 420  
 Db 1331 GTTATAACAGAGAGATGCTACTTTGAGTGCAGAACTTCTCTGTGTAACCCAGCTTGAG 1390  
 Qy 421 ThrValAspGlyAlaGluHsiGlyLeuProAspThrSerTyrProAlaMetAla 440  
 Db 1391 ACAGTGGAGCGAGAGAGATGGTCTACTGACATCTTGTGCTCCACCTGCTATGGCC 1450  
 Qy 441 SerThrSerLeuSerGluAlaProProPhePheMetAlaSerSerIlePheSerLeuThr 460  
 Db 1451 TCTACTCTCCTGTCAGAGCTCCACCTTCTTTATGGCATCAAGCATCTTCTCTGACT 1510  
 Qy 461 AspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMetLeuValProGlyLeuThr 480  
 Db 1511 GATCAAGGACCCACAGATACAAATGGCCACTGACCAACAATGCTAGTACCAGGCTCACC 1570  
 Qy 481 IleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGlyIleSerHisProPro 500  
 Db 1571 ATCCCCACCAAGATATTTGTCATCATGCCACTGGCTCTGGGAATTTCACTCCACCT 1630  
 Qy 501 AlaSerSerAspAspSerArgSerSerAlaGlyGlyGluAspMetValArgHisLeuAsp 520  
 Db 1631 GCATCTTCAGATGACAGCGCATCAAGTCAGTGGCGAAGATATGCTCAGACACTAGAT 1690  
 Qy 521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGluTyrVal 540  
 Db 1691 GAAATGGATCTGTCGACATCTCTCCCACTGAGGTACAGAGCTCAGCGAATATGTT 1750  
 Qy 541 SerValProAspHisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThr 560  
 Db 1751 TCTGTCCACAGATCAATTTCTTGAGGATACCACTCTCTGCTCAGCTTTACAGTATATCACC 1810  
 Qy 561 ThrSerSerMetThrIleAlaProIlyGlyArgGluLeuValValPhePheSerLeuArg 580  
 Db 1811 ACTAGTTCTATGACCATTTGCCCAAGCGCGAGAGCTGGTAGTGTCTTCAGTCTCGCT 1870  
 Qy 581 ValAlaAspMetAlaPheSerAspLeuPheAsnLysSerSerLeuGluTyrArgAla 600  
 Db 1871 GTTGCTACATGGCTTTCTCCACAGACCTGTTCCACAGAGCTCTCTGGATACCGAGCT 1930  
 Qy 601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
 Db 1931 CTGGAGCAACAATTCACAGCTGTGCTGCTTCCATATCTACGATCCAAATCTTACAGGATTT 1990  
 Qy 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
 Db 1991 AAGCAACTTGAATACTTAACCTTCAGAACGGAGGTGATGATGTAATAGCAAAATGAAG 2050  
 Qy 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660  
 Db 2051 TTTGCTAAGTCTGTCCGTAACCTCAACAGGCTGTGCGACGGGTCTTGAGGATTTT 2110  
 Qy 661 ArgSerAlaAlaAlaGlnGlnLeuHsiLeuGluIleAspSerTyrSerLeuAsnIleGlu 680  
 Db 2111 CGTTCTGTGTCAGGCCAACCAATCTCATCTCGGAATAGACAGCTACTCTCTCAACATTTGAA 2170  
 Qy 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
 Db 2171 CCAGCTGATCAAGCAGATCCCTGCAAGTCTCTGCGCTCGCGGAATTTGCCCAATGTGA 2230  
 Qy 701 LysAsnGluArgThrGluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGly 720  
 Db 2231 AAGAACGAACGAGCTGAGAGCGGAGTGTGCTGCAAAACAGGATATGACAGCCAGGGG 2290

Qy 721 SerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrIlyGlnCysGluValLeu 740  
 Db 2291 AGCCTGACGCTGTGAACACGAGCCTCTGTGGCCCTGGCACAAAGGAATCGGAGTCTCTC 2350  
 Qy 741 GlnGlyLysGlyValaProCysArgLeuProAspHisSerGluAsnGlnAlaTyrLysThr 760  
 Db 2351 CAGGGAAGGAGCTCTATGCAGTTGCCAGATCACTCTGAAAATCAGCATACAAACT 2410  
 Qy 761 SerValLysLysPheGlnAsnGlnGlnAsnLysValIleSerLysArgAsnSerGlu 780  
 Db 2411 AGTGTAAAAAGTTCCAAAATCAACAAAATAACAGGTAATCAGTAAAAAGAAATCTGAA 2470  
 Qy 781 LeuLeuThrValGluTyrGluGluPheAsnHisGlnAspTyrGluGlyAsn 797  
 Db 2471 TTACTGACCGTAGAATATGAAGAATTTAAACCATCAAGATTGGGAAGAAAT 2521

## RESULT 2

AB047844  
 LOCUS Bos taurus mRNA 3552 bp mRNA linear MAM 30-AUG-2000  
 DEFINITION Bos taurus mRNA for MLGAPC core protein, complete cds.  
 ACCESSION AB047844  
 VERSION AB047844.1 GI:9955919  
 KEYWORDS  
 SOURCE Bos taurus (cow)

## ORGANISM

Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.

## REFERENCE

1 (sites)  
 Uehara, F., Ohba, N. and Ozawa, M.  
 Isolation and characterization of mucinlike glycoprotein associated  
 with photoreceptor cells

## JOURNAL

Invest. Ophthalmol. Vis. Sci. 41 (9), 2759-2765 (2000)

## MEDLINE

20391374  
 PUBMED 10937595

## REFERENCE

1 (bases 1 to 3552)  
 Uehara, F., Ohba, N. and Ozawa, M.  
 Direct Submission

## AUTHORS

Submitted (28-AUG-2000) FumiYuki Uehara, Kagoshima University  
 Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,  
 Kagoshima 980-8520, Japan  
 E-mail:fuehara@med5.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5402,  
 Fax:81-99-265-4894

## FEATURES

Location/Qualifiers  
 1..3552  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /cell\_type="retina"  
 155..2539  
 /standard\_names="core protein of mucinlike glycoprotein  
 associated with photoreceptor cells"  
 /codon\_start=1  
 /product="MLGAPC core protein"  
 /protein\_id="BAB12254.1"  
 /db\_xref="GI:9955920"  
 /translation="MHLEAARVIFLWTFLOVQIKDLISIKYSGSEIKDIDNAPTEA  
 TKNATKVTWTRRIFDLAKTRSRFAFFPTGVKVCQESMEQILASIQAYRLRVC  
 QAVAEVRI FLDRLEPGEYQDWSVCOQETFLCDI GKNFSNQEHLDLQORMKO  
 RNFLEKDRVTKETLSELGQTPGLQOOLTPVSHPGCLSLPMTAQRNPOLHPSPTR  
 VTRREKTEFTDAADALEQVELSLSLANCKSELDNSQSPYVLEVAKSOLOMOK  
 IFKPKGFBIHVSGFRPKERDGSSTEMQTALPKGKAESAKSPADPLSLDSNKL  
 ESEGPRTGTEEEKRELYPTASLEKLI SRALEEDQSLDVGTIQTDEIVSLPSLD  
 PPTQVLPTLLDTITKDALSPELGQPLRTVDRAGHSPGASPTGWSPEAMTST  
 SISELTPFTASSVPFQDQSDATIMSQITVLI PRLTVPTDDYSAISPLVEI SHLP  
 TSESWLSTSQDTMEYLDGVLTPTTSSGPRNSVGMFPAMI FLENITPDGRLSR  
 ITTSTAARAGRELVPFSLRVANVPSTDLFNKSLSEYQLEORFTOLLVPLNLSR  
 LFGVQLEILNFRNGSVLNSKVPYVNLTKAVRGVLEDFSTAAQQLDLIDS  
 YSLDELPAQADPCFLACGEFAQCVRNTEEAECRCSTGQALVLPFIEDCEDIPGK  
 GTFCELDQSKQNVYEPGVKFKFOODKNVTKRKFELLITIGYEEFNQDWEGN"

## CDS

155..2539  
 /standard\_names="core protein of mucinlike glycoprotein  
 associated with photoreceptor cells"  
 /codon\_start=1  
 /product="MLGAPC core protein"  
 /protein\_id="BAB12254.1"  
 /db\_xref="GI:9955920"  
 /translation="MHLEAARVIFLWTFLOVQIKDLISIKYSGSEIKDIDNAPTEA  
 TKNATKVTWTRRIFDLAKTRSRFAFFPTGVKVCQESMEQILASIQAYRLRVC  
 QAVAEVRI FLDRLEPGEYQDWSVCOQETFLCDI GKNFSNQEHLDLQORMKO  
 RNFLEKDRVTKETLSELGQTPGLQOOLTPVSHPGCLSLPMTAQRNPOLHPSPTR  
 VTRREKTEFTDAADALEQVELSLSLANCKSELDNSQSPYVLEVAKSOLOMOK  
 IFKPKGFBIHVSGFRPKERDGSSTEMQTALPKGKAESAKSPADPLSLDSNKL  
 ESEGPRTGTEEEKRELYPTASLEKLI SRALEEDQSLDVGTIQTDEIVSLPSLD  
 PPTQVLPTLLDTITKDALSPELGQPLRTVDRAGHSPGASPTGWSPEAMTST  
 SISELTPFTASSVPFQDQSDATIMSQITVLI PRLTVPTDDYSAISPLVEI SHLP  
 TSESWLSTSQDTMEYLDGVLTPTTSSGPRNSVGMFPAMI FLENITPDGRLSR  
 ITTSTAARAGRELVPFSLRVANVPSTDLFNKSLSEYQLEORFTOLLVPLNLSR  
 LFGVQLEILNFRNGSVLNSKVPYVNLTKAVRGVLEDFSTAAQQLDLIDS  
 YSLDELPAQADPCFLACGEFAQCVRNTEEAECRCSTGQALVLPFIEDCEDIPGK  
 GTFCELDQSKQNVYEPGVKFKFOODKNVTKRKFELLITIGYEEFNQDWEGN"

## ORIGIN



```

QY 671 luileaspserTyrSerLeuAenilleGluProAlaaspGluAlaaspProCysValyspHel 691
Db 2190 AAATAGATAGTACTCTCTCGAGTGTGAACCGAGCGATCAAGCAGATCCCTGCAAAATCC 2249

QY 691 euAlaCysGlyGluPheAlaGlnCysValysAenGluArgThrGluGluAlaGluCysA 711
Db 2250 TGGCCTGGCGGCGAATTCGCCAGTGTGAGGATGAGTGGACCGAGGAGCGAGTGTG 2309

QY 711 tGcyslyspProGlyTyrAspSerGlnGlySerLeuAaspGlyLeuGluProGlyLeuCysG 731
Db 2310 GCTGTCGATCGGGA-----ACCCAGGCCCTGTGCTTCCCATAGAG----- 2350

QY 731 lyProGlyThrlyspGlyCysGluValLeuGlnGlylyysGlyValaProCysArgLeuProA 751
Db 2351 -----GACGTGTGAAGACATCCCGGGAAGGAGACACCGTGTGAGATCACTAG 2396

QY 751 sPHiSerGlnasnGlnAlaTyrlyspThrSerVallyspPheGlnasnGlnGlnAsnA 771
Db 2397 ACCAACTAAAATCAAGTGTATGAACCTGGTGTATAAAAGATTCCAACTGAGCAAGATA 2456

QY 771 snlyspValileSerlyspArgAenSerGluLeuLeuThrValGluTyrGluGluPheAenH 791
Db 2457 ACAAGTAACTATGAAGAATAATTGTAATTACTGACTATAGGATATGAAGAAATTAAC 2516

QY 791 isGlnAspTyrGluGlyAen 797
Db 2517 ATCAAGATTGGGAAGAAAT 2536

RESULT 3
LOCUS AF266478 3668 bp mRNA linear ROD 18-AUG-2000
DEFINITION Mus musculus IPM 150 proteoglycan mRNA, complete cds.
ACCESSION AF266478
VERSION AF266478.1 GI:9844921
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3668)
Kuehn,M.H., Wietekki,D.T. and Hageman,G.S.
Molecular characterization of the murine orthologue of the human
retinal proteoglycan IPM 150
Mol. Vis. 6 (2000) In press
2 (bases 1 to 3668)
Kuehn,M.H., Wietekki,D.T. and Hageman,G.S.
Direct Submission
Submitted (10-MAY-2000) Ophthalmology, University of Iowa, 2501
Crosspark Rd., Coralville, IA 52241, USA
FEATURES
Location/Qualifiers
1..3668
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
196..2592
/codon_start=1
/product="IPM 150 proteoglycan"
/protein_id="AAG00796.1"
/db_xref="GI:9844922"
translation="MNFQIKHAFVFGTFLQVGQIKDTSIKIFSSEIKNIDKTPRIET
ESTSTVHKVSTKMRKIDFLPKLRKSRALPAANI CPOESLRQITLASLQEVYRLVCO
EVWEAVRIPLDRIPDTEEYQDWVSLQCKETFCFLDIGNKFSNSOEHLLQORIKOR
SFGCKDETASWETLEAPTEAPVVPDVSMSLGPPLPSDDTDLKEILSVTLKDIQK
PTTSKTEPIHVSFESEKVEFSISLPHRFKAELNNGSPYQELVGSQSLQLOKQ
FKLPGFEIRVLGFRPKKEEDGSSSTEIQMAIFKRDHABAKSPSHLSNKNIE
SERIHGVIEDQKQETITATDLKLIQLDGLSLVEGKIPFGDEVTGLFRPVE
PDLPKPLADVEDATLSPDLFPVPELREAVDRGSLPMSKDSMSPPVSAISRS
ENLPSFPIESLDAGPPPLMTPTALPKPLTDIYSTTRQLPLESSHWPASSS
DRELITSSHDITRDLGDWVSDTPALSEISLGYSDASQGLEMTTPIPTVRFITTS
SETATGQELVFLSVANWMPSYDLFPKSSLEYQALQRFTDLLVPLRLSNLQGP
KQELSLFRNGSVIVNSKRVAKAVPINTQAVRGVLEUDELTAAQGLNLEISYLD
LEPADQADPKCLLDGCPAQCVKWEETBAECRCQGHESHGTLDTYQNLNCPGKTC
VAGREQATPCRPDPSTNQAEQPCVKKLRQONKVKYKCRNSKLSAIGFEEDQDQWGN

```

## ORIGIN

## Alignment Scores:

Pred. No.: 4,66e-168 Length: 3668  
 Score: 2548.50 Matches: 528  
 Percent Similarity: 75.12% Conservative: 79  
 Best Local Similarity: 65.35% Mismatches: 180  
 Query Match: 61.90% Indels: 21  
 DB: 10 Gaps: 9

US-10-007-270-2 (1-797) x AF266478 (1-3668)

QY 1 MetTyrLeuGluThrArgAlaIlePheValPheThrIlePheLeuGlnValGlnGly 20  
 Db 196 ATGAATTTCAATTAATTAATCATGCTATCTTTTGGGATTTTCTCCAGTTCAAGA 255  
 QY 21 ThrLyAspIleSerIleAenIleTyrHisSerGluThrLyAspIleAenProPro 40  
 Db 256 ATCAAGATACCTCTATTAAATATATTCAGTTCTGAAATTAATAAATACATAGCAAAACCCCA 315  
 QY 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgAlle 60  
 Db 316 AGAATCGAAACAAATTGAAAGTACTTCAACAGTGCACAAAGTGTCAACCATGAACAAATA 375  
 QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValysVal 80  
 Db 376 TTGGATTTCGAAGGCTTCGAACCAAAAGATCAGCACATTTTCCCA---GCTGCTAACATC 432  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAaspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 Db 433 TGTCCACAGGAATCTCTTGAGACAGATTTTGAAGTCTTCAAGAATATATTATAGACTGAGA 492  
 QY 101 ValCysGlnGluAlaValTyrGluAlaTyrArgGlyPheLeuAaspArgIleProAspThr 120  
 Db 493 GTATGTCAAGAAGTCTGTGGGAAGCATATCTTCTTCTGGACGAATTTCTGCACACA 552  
 QY 121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 Db 553 GAGGAATATCAAGACTGGGTGAGCTTCCAGCAAGAAAGAACCTTCTGCTCTTTGACATT 612  
 QY 141 GlyLyAsnPheSerAsnSerGlnGluHisLeuAaspLeuGlnGlnArgIleLysGln 160  
 Db 613 GGGAAAACTTCAAGCACTCCAGGAGCACCTAGATCTTCTTCAGCAGAGATATAAACAG 672  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 Db 673 AGAAGCTTCCCTGGGAGGAAGATGAGACAGCCTCCATGGAGACACTGGAACCACTACT 732  
 QY 181 GluThrIleValIleSerThrAspValAlaAenValSerLeuGlyProPheProLeuThr 200  
 Db 733 GAAGCCCTGTGTATCCACAGATGTTTCCAGGATGTCCTCCCTGGGCCCCCTTCCCACTTCT 792  
 QY 201 ProAspAspThrLeuLeuAsnGluIleLeuAaspAenThrLeuAasnAspThrLysMetPro 220  
 Db 793 TCTGATGACACAGACTCAAGAGAGATTCTCAGTGTCCCTCAAGGACATTCAAAAGGCC 852  
 QY 221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGln 234  
 Db 853 ACAACAGAAAGTAAACAAACAACTATTACGTGTCTGAATTTCTCA-----TCAGAGGAG 906  
 QY 235 ArgValGluLeuSerValSerLeuValAenGlnLysPheLysAlaGluLeuAlaAaspSer 254  
 Db 907 AAGGTGGAATTCAGCATCTCTCTGCAAAACCAAGGTTCAAGGCGAGACTTACCAACTCT 966  
 QY 255 GlnSerProTyrTyrGlnIleLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274  
 Db 967 CGGTCAACATACATACAGGAACCTGGTGGACAGTCCCAACTGCAGTTCGAAAGATATTT 1026  
 QY 275 LysLysLeuProGlyPheLysLysIleHisValIleGluGlyPheArgProLysLysGluLys 294  
 Db 1027 AAGAAACTTCCAGGATTCGGAGAAATCCGTGTATTAGGATTTAGACCAAGAAAGAAAGAA 1086

QY 295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLeuArgHisSerAlaGlu 314  
 Db 1087 GATGGTTCAAGCTCCACAGAATAACAGCTTTAGGCCATCTTTAAGAGGGACCATGCAGAA 1146  
 QY 315 AlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGlu 334  
 Db 1147 GCAAAAAGCCCTGATAGTCATCTACTGCTCTTGATTCCACAAAAATTGAAAGTGAAGA 1206  
 QY 335 ValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAsp 354  
 Db 1207 ATCCATCATGGAGTCATA---GAAGACAACAAACAGAAACCTACCTCACAGCTACAGAC 1263  
 QY 355 LeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAspValGlyThrIle 374  
 Db 1264 CTCAAAAAACTCATATCAACTACTAGATGAGACCTGTCTTGGTAGAAGGGAAATT 1323  
 QY 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394  
 Db 1324 CCATTCCGTGTAGTGAAGTTACTGGGACACTC-----TTTCAGACCTGTCACTGAACCCAGAT 1377  
 QY 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414  
 Db 1378 CTGCCCAAGCCCTTGCTGATGTACAGAGGATGCCACTTTGAGTCCAGAACTTCCTTTC 1437  
 QY 415 ValGluProGlnLeuLeuThrValAspGlyAlaGluHisGlyLeuPro----- 430  
 Db 1438 GTTGAGCCTTAGCTTGAGGACGTGGACAGAGAGGATCTGAGTCGCTGGAATGTCTCTCC 1497  
 QY 431 ---AspThrSerTrpSerProProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449  
 Db 1498 AAAGACAGTTCTTGCTGCTCCACTGTATCAGCCTCAATTTCCCGATCAGAAATCTACCT 1557  
 QY 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469  
 Db 1558 TCGTTT---ACACCTAGCATCTTCTCTAGATGCTCAAGCCCCCTCCCTTGATGACC 1614  
 QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIle 489  
 Db 1615 ACTGCCCAACAGCATCATCCCAAGCCCACTCTCCCACTATCGATTATTTACCATC 1674  
 QY 490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArgSerSer 509  
 Db 1675 CCGCAATTGCTCTGGATCGTCACATGGCTGATCTCTCCAGTGACAGAGCTGATC 1734  
 QY 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529  
 Db 1735 ACAAGCAGCATGACACAAATCCGAGACCTAGATGCGATGGATGCTCTGACAGCCAGCC 1794  
 QY 530 ProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAsp 549  
 Db 1795 TTGTCAGAAATATCAGAACTGAGTGGATACGATTCTGCTCGGGTCAGTTCTTGAGATG 1854  
 QY 550 ThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLys 569  
 Db 1855 ACCACACCATCCCAACAGTACGGTTTCATCCACCAGCTCCGAGACCATTTGCCACCAAG 1914  
 QY 570 GlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAsp 589  
 Db 1915 GGCCAGGAGCTAGTGGTATTCTTCAGCTCGCTGTTGTGTAACATCCGCTTCTCTATGAC 1974  
 QY 590 LeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnPheThrGlnLeuLeu 609  
 Db 1975 CTGTTCCAAAGAGTCTCTGGAGTATCAAGCCCTGGAAACAGATTCACAGCTCGGTG 2034  
 QY 610 ValProTyrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg 629  
 Db 2035 GTTCCCTATCTACGATCGAATCTTACGGGATTTAAGCAACTGGAATACTCAGCTTCAGA 2094  
 QY 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeu 649  
 Db 2095 AACGGAGGTGATCGTGAACAGCAAGTGGGTGTTGCAAGCGGTACCTTACAACTC 2154  
 QY 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669

Db 2155 ACCAGCGCGTGGCGGGGCTCTTGAGGATCTTCGGTCCACCGCAGCTCAAGGGCTCAAT 2214  
 QY 670 LeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689  
 Db 2215 CTGGAATCGAAAGCTACTCCCTCGACATTTGAACACAGCTGATCAGCGGATCCCTGCAAA 2274  
 QY 690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThrGluGluAlaGlu 709  
 Db 2275 CTCCTAGATGTGGCAATTTGCCAGTGTGTAAAGATGATGGACAGAGGAAGCAGAG 2334  
 QY 710 CysArgCysLysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729  
 Db 2335 TGTGCTGCAGCAGGACATGAGAGCCACGGACCTGCACTACCCAGACCTGAACTC 2394  
 QY 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749  
 Db 2395 TGTCCCTCCCTGGA---AAGACTTGTGTGGCGCCGAGAACAAAGCAACTCCATGACGCCA 2451  
 QY 750 ProAspHisSerGluAsnGlnAlaTyrLysThrSerValLysPheGlnAsnGlnGln 769  
 Db 2452 CCAGATCACTCTACAAACCAAGCTCAGGAACCTGGTGTATAAAGCTA-----CGTCAG 2505  
 QY 770 AsnAsnLysValIleSerLysArgAsnSerGluLeuThrValGluTyrGluGluPhe 789  
 Db 2506 CAAATTAAGTAGTACTCAAGAAAAAGAAATCTAAACTATCAGCTATAGGATTTGAAGAAATTT 2565  
 QY 790 AsnHisGluAspTrpGluGlyAsn 797  
 Db 2566 GAAGACAGACTGGAGGGGAAT 2589  
 RESULT 4  
 BC022970  
 LOCUS  
 DEFINITION Mus musculus interphotoreceptor matrix proteoglycan 1, mRNA (cdna  
 clone MGC:35847 IMAGE:5366008), complete cds.  
 ACCESSION BC022970.1 GI:18606432  
 VERSION BC022970.1  
 KEYWORDS MGC.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 2924)  
 AUTHORS Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,  
 Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Ketteman, M., Maman, A., Rodriguez, S.,  
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 2388257  
 12477932  
 REFERENCE 2 (bases 1 to 2924)  
 AUTHORS Strausberg, R.  
 Direct Submission  
 Submitted (04-FEB-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,



REMARK  
COMMENT

USIA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
Series: IRAK Plate: 53 Row: k Column: 15  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 11528499.  
Location/Qualifiers

Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,  
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanaivati,  
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 53 Row: k Column: 15  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 11528499.

## FEATURES

source  
1..2924  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="MGC:35847 IMAGE:5366008"  
/tissue\_type="Eye, retina, mouse strain C57BL/6"  
/clone\_lib="NIH-MGC\_94"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
1..2924  
/gene="Impg1"  
/note="synonyms: SPACK, IMP150"  
/db\_xref="LocusID:63859"  
/db\_xref="MGI:1926878"  
138..2534  
/codon\_start=1  
/product="Impg1 protein"  
/protein\_id="AAH22970.1"  
/db\_xref="GI:18606433"  
/db\_xref="LocusID:63859"  
/translation="MNQIKHAFVGLGIFLQVQIKDTSIKFSSEIKNDKTPRIET  
IESTVHKVTKMIRIEDLPKLRKRSALPAANICPQESLRQILASLQYRLRVQ  
EVVWEAVIFUDRIPTDEYEDWVSLQKQETFLFDIGKFNFSQHEHLLQORIKQ  
SFGKQDTEAMETLEAPTEAVVPTDVSMSGLPFPDSDTDLKILSVLKDIOK  
PTTSKTEPIHVSFESEKVERSIPLNHRFKAEKLTNSGYPYQELVAGSLOLOKI  
FKLPGGGEIIVLAFRKEEDGSSTEIOLMAIFKEDHAEKSPDHLSDSNKIE  
SERIHGVIEKQETVLTATDLKLIQLLDGLSVGKIPFGDEVITGLFRPVE  
FDLPKPADVTEDATLGPFPFVEPRLEAVDREGSELFGMSKDSWSPVVASIERS  
ENLPSFTPSLDQPPPLMTTGPALPKPLTIDYSTIRQLPLESHWPASS  
DRELTSHDTRIDLDGMDVSDTPALSEISLSDYDSASQGFLEMTPTVPRFITTS  
SETIATQELVWFSLRVAMPFSDYLFNKSLEYQALBORFTDLVPLVRLNLTGF  
KOLBIFRNGSVVNSKVRFAKVPYNTQAVRGVLEDRSTAAQGLNLEIESYSLD  
IEPADQADPKLLDCKGPAOCVKNWTEBAECRCQSHSGHGLDVTNLCPGKTC  
VAGREQATPCRPDHPSTNQAGEPKVKLRQNVKVRKNSKLSAIGFEFEFDQWEN  
"

misc\_feature  
1866..2189  
/note="SEA; Region: SEA domain. Domain found in Sea urchin  
sperm protein, Enterokinase, Agrin (SEA). Proposed  
function of regulating or binding carbohydrate side  
chains"  
/db\_xref="CDD:pfam01390"

## ORIGIN

Alignment Scores:  
Pred. No.: 4,7e-168 Length: 2924  
Score: 2546.50 Matches: 528  
Percent Similarity: 75.12% Conservative: 79  
Best Local Similarity: 65.35% Mismatches: 180  
Query Match: 61.85% Indels: 21  
DB: 10 Gaps: 9

US-10-007-270-2 (1-797) x BC022970 (1-2924)

Qy 1 MetTyrLeuGluThrArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGly 20  
Db 138 ATGAATTTCGAAATTAACATGCTATCTTTTGGGATTTTCTCCAAGTTCAAGGA 197  
Qy 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAspAsnProPro 40  
Db 198 ATCAAGATACCTCTATTAAATATTCAGTTCTGAAATTAATAAATAGACAAACCCCA 257  
Qy 41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgIle 60  
Db 258 AGAATCGAAACCAATTCAGAAAGTACTTCAACAGTGCACAAAGTCTCAACCATGAACGAATA 317  
Qy 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValVal 80  
Db 318 TTGATTTTCCAAAGCTTCGAACCAAAAGATCAGCACTTTTCCCA---GCTGCTAACATC 374  
Qy 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
Db 375 TGTCACACAGATCTCTTGACACAGATTTAGCAAGTCTTCAAGATATTATAGACTGAGA 434  
Qy 101 ValCysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
Db 435 GTATGTCAAGAAAGTCGTGGGAAGCATATCGTATCTTTCTGCACCGAATTCCTGACACA 494  
Qy 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
Db 495 GAGGAATATCAAGACTGGGTGAGCTCTGCCAAGAAAGAACCTTCTGCCCTCTTTGACATT 554  
Qy 141 GlyLysAsnPheSerAsnSerGlnGlnHisLeuAspLeuLeuGlnGlnArgIleLysGln 160  
Db 555 GGGAAAAAATCTCAGCAACTCCCGAGGAGCACTAGATCTTTCTCAGCAGAGAATAAAACAG 614  
Qy 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGluProGly 180  
Db 615 AGAAGCTTCCCTGGGAGGAAAGATGAGACAGCCTCCATGGAGACACTGGAACACCTACT 674  
Qy 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
Db 675 GAAGCCCTGTGGTACCCACAGATGTTTCCAGAGATGTCCTGGGAGCTTCCCACTTCTCT 734  
Qy 201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
Db 735 TCTGATGACACAGACTCTCAAGGAGATTTCTCAGTGTCACTCCTCAAGGACATTCAAAAGCCC 794  
Qy 221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGln 234  
Db 795 ACAACAGAAAGTAACAGACACTATTCTATGTGTCTGAATTTCTCA-----TCAGAGGAG 848  
Qy 235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254  
Db 849 AAGGTGGAATTCAGCATCTCTCTGCCAAACACACAGGTTCAAGGCAGAGGCTCAACCACTCT 908  
Qy 255 GlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274  
Db 909 GGGTCACCATATACAGGAATCTGGGGAGAGTCCCACTCCACTGCATTCGAAAGATATT 968  
Qy 275 LysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysGluLys 294  
Db 969 AAGAACTTCCAGGATTCGGAAGAAATCCGTGTATTAGGATTTAGACCAAGAAAGAGAA 1028  
Qy 295 AspGlySerSerThrThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314  
Db 1029 GATGGTTCAGGCTCCACAGAAATACAGCTTATGGCCATCTTTAAGAGGAGGACCATCGAA 1088  
Qy 315 AlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGlu 334  
Db 1089 GCAAAAGCCCTGATAGTCATCTACTGTCTTCTGATTCCACAAATTTGAAGTGAAGA 1148  
Qy 335 ValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeuThrAlaThrAsp 354  
Db 1149 ATCCATCATGGATGTCATA---GAAGACAAACCAACCAAGAAACCTACCTCACAGCTACAGAC 1205

```

Qy 355 LeuLYeArgLeuIleSerLYsAlaLeuGluGluGlnSerLeuAspValGlyThrIle 374
Db 1206 CTCAAAAACCTCATCACTACTAGATGAGACCTGCTTGGTAGAGGGAAT 1265
Qy 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394
Db 1266 CCATTCCGGTGAAGTACTGGGACAC-----TTGAGACCTGTCAGTGAACACGAT 1319
Qy 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuPro 414
Db 1320 CTGCCCAAGCCCTCTGCTGATGTCACAGAGGATGCCACTTTCAGTCCAGAACTTCCTTC 1379
Qy 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro----- 430
Db 1380 GTTGAGCCCTAGGCTTGAGGACGTGGACAGAGAGGATCTGAGCTGCTGGAATGTCCTCC 1439
Qy 431 ---AspThrSerTipSerProAlaMetAlaSerThrSerLeuSerGluAlaProPro 449
Db 1440 AAGACAGTCTTGCTGCTCCACTGTATCAGCTCNAATTTCCCGATCAGAAATCTACT 1499
Qy 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469
Db 1500 TCGTTT---ACACTAGCATCTCTCTAGATGCTCAAGGCCCTCCCTTCGATGACC 1556
Qy 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTySerAlaIle 489
Db 1557 ACTGGCCCAAGCACTATCCCAAGCCACTCTCCCACTATCGATTATTTACCATC 1616
Qy 490 SerGlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerArgSerSer 509
Db 1617 CGCCATTGCTCTGGAATCGTCACATTGCGCTGCATCTCCAGTGACAGAGCTGATC 1676
Qy 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529
Db 1677 ACAAGCAGCCATGACACAAATCCGAGACCTAGATGCGATGCTGTCGACAGCGCACC 1736
Qy 530 ProSerGluValProGluLeuSerGluTyValSerValProAspHisPheLeuGluAsp 549
Db 1737 TTGTCAGAAATATCAGAACTGATGATACGATTCTGCTCGGGTCAGTTCTTGAGATG 1796
Qy 550 ThrThrProValSerAlaLeuGlnTyIleThrThrSerSerMetThrIleAlaProIys 569
Db 1797 ACCACACCCATCCCAACAGTAGTGTTTCATCACACCGAGCTCGGAGACCATTCGCCACCAAG 1856
Qy 570 GlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAsp 589
Db 1857 GGCAGAGCTAGTGATCTTCACGCTGCGTGTGCTTACATGCGCTTCCTCTATGAC 1916
Qy 590 LeuPheAsnLYsSerSerLeuGluTyArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609
Db 1917 CTGTTCAACAAGAGTTCTCTGGAGTATCAAGCCCTGGAACAACGATTCACAGACCTGCTG 1976
Qy 610 ValProTyLeuArgSerAsnLeuThrGlyPheLYsGlnLeuGluIleuAsnPheArg 629
Db 1977 GTTCCCTATCTAGATCGAATCTTACGGATTTAGCAACTGGAATATCTAGCTTCAGA 2036
Qy 630 AsnGlySerValIleValAsnSerLYsMetLYsPheAlaLYsSerValProTyArgLeu 649
Db 2037 AACGGAAGTGTGATCTGTACACCAAGTCCGCTTTCGAAGCGGTACCTTACAACTC 2096
Qy 650 ThrLYeAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669
Db 2097 ACCAGGCGCTGCGCGGGTCTTTGGAGGATCTTCGGTCCACCGCGAGCTCAAGGGCTCAAT 2156
Qy 670 LeuGluIleAspSerTySerLeuAsnIleGluProAlaAspGlnAlaAspProCysLYs 689
Db 2157 CTGGAATTCGAAGACTTCTCCCTCGACATGAAACGCTGATCAGCGGATCCCTTCGAAA 2216
Qy 690 PheLeuAlaCysGlyGluPheAlaGlnCysValLYsAsnGluArgThrGluGluAlaGlu 709
Db 2217 CTCCTAGACTGTGCCAAATTTGCCAGTGTGTAAAGAAATGATGTCGACAGAGGACGAG 2276

```

```

Qy 710 CysArgCysLYsProGlyTyAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729
Db 2277 TGTGCTGTCACAGAGGACATGAGACCCAGGACCTGGACTACCCAGACCTTGAACCTC 2336
Qy 730 CysGlyProGlyThrLYsGluCysGluValLeuGlnGlyLYsGlyAlaProCysAsnLeu 749
Db 2337 TGTCCCTCTGGA---AAGACTTGTGGCGCGCGAGAACCAAGCAACTCTCATCGAGCCA 2393
Qy 750 ProAspHisSerGluAsnGlnAlaTyLYsThrSerValLYsLYsPheGlnAsnGlnGln 769
Db 2394 CCAGATCACTCTACAAACCAAGCTCAGGAACCTGGTGTATAAAAGCTA-----CGTCAG 2447
Qy 770 AsnAsnLYsValIleSerLYsArgAsnSerGluLeuLeuThrValGluTyGluGluPhe 789
Db 2448 CAATAATAGTAGTCAAGAAAGAAATTTCTAAACTATCAGCTATAGATTGAAGATTT 2507
Qy 790 AsnHisGlnAspTyrGluGlyAsn 797
Db 2508 GAAGACCAGACTGGGAGGGAAT 2531

RESULT 5
AB047843
LOCUS
DEFINITION
AB047843
ACCESSION
AB047843.1 GI:9955917
VERSION
KEYWORDS
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (sites)
Uehara, F., Ohba, N. and Ozawa, M.
Core Protein of rat Mucinlike Glycoprotein Associated with
Photoreceptor Cells
Published Only in DataBase (2000)
2 (bases 1 to 2850)
Uehara, F., Ohba, N. and Ozawa, M.
Direct Submission
Submitted (28-AUG-2000) Fumiyuki Uehara, Kagoshima University
Faculty of Medicine, Ophthalmology; 8-35-1 Sakuragaoka, Kagoshima,
Kagoshima 890-8520, Japan
(E-mail: f.uehara@med5.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5402,
Fax:81-99-265-4894)
FEATURES
Location/Qualifiers
1..2850
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/cell_type="retina"
127..2523
/standard_name="core protein of mucinlike glycoprotein
associated with photoreceptor cells"
/codon_start=1
/product="MUGAPC core protein"
/protein_id="BAB1253.1"
/db_xref="GI:9955918"
/translation="NNLEIKHAILVLWIFLQVQIKDSTKTHSSGKTQNKDAPRIET
TESTSAVHKATMTKRLFAVAKLNKESALFPVAVNICPRESLROIILSLOEYVRLRVCO
EYVWEAYRFLDRVPTEEVQDWVSLCOKETCLEFDIKNFSNSQSHLDLLOORIQR
SFGKNDMSPIELGVTTAPVLPIDVSSMSLRPFPPDPDITDKEVTKIQAQTPIA
IRAELESPEPTHVTIISSEKEVPSISLPNHRFKAEUTNKRSPYIQSLVGSQQL
OKIFKLPFGFIRVLGPKKEEDGSSTETQLVAIFKRDHAEKSPGSDLLSDSN
KIEREIRHGAIEDKQPEAYLTAADLKLIIRLLDGDPLVGTVFSDVTEPLFRP
TIOSELPKLTIDVTEDVTLSPLEPSEPLSEVDIYGYLPDSSWSRPTASTSGVGN
LPSTFPIALDDQSSPPLMATGPTAFIPTLPIISDYSTVQWPLEVSHWPSSDR
ELSTTSHTIDRLDEMVDSPALSEIAELSGVDSAPDRFLEMTPIPLQVTVKSS
ETIAAGHLELVVFFSURVNMFPESYDLFNKSLSEYQALQRTDILLYLRNLTGFK
QLEILDFRNGSVIVNSKVFAPAYNLTQAVRGVLEDKRSTAAQELNLEIYSUDI
EPADQPKFLDCGKPAQCIKNELTEAEKCRQGHSHGSHGLYQELNLCPPGKTC
ASQGOATPCRPDPHSTNQARQPSVKLQKQKQNVKKNRSELSATDFELDDQWEGN
"
```

## ORIGIN

## Alignment Scores:

Pred. No.: 7,346-168 Length: 2850  
 Score: 2543.50 Matches: 516  
 Percent Similarity: 75.15% Conservative: 92  
 Best Local Similarity: 63.78% Mismatches: 178  
 Query Match: 61.78% Indels: 23  
 DB: 10 Gaps: 10

US-10-007-270-2 (1-797) x AB047843 (1-2850)

QY 1 MetTyrLeuGluThrArgAlaPheValPheThrPheLeuGlnValGlnGly 20  
 DB 127 ATGAATTGGAGATTAACATCATCTGTTTGTGGATTTTCTCAAGTTCAGGA 186  
 QY 21 ThrLysAspIleSerIleAsnIleTyrHisSerGluThrLysAspIleAsnProPro 40  
 DB 187 ATCAAGATACCTCTACTAAACACACACAGTTCGGAACATAAAACATAGACAAAGCCCA 246  
 QY 41 ArgAsnGluThrGluSerThrGluLysMetTyrLysMetSerThrMetArgGly 60  
 DB 247 AGAATTGAACAACTGAAGCACTTCAGCAGTGCACAAAGCGTCAACCATGAAGCAGCTG 306  
 QY 61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValLysVal 80  
 DB 307 TTCGCTGTGGCAAGCTTCGAAACAAAGATCGGCACCTGTTCCCA--GCTGTGAACATC 363  
 QY 81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100  
 DB 364 TGTCCGCGGGAATCTTGAGGAGAGATTTAGAAAGTCTTCAAGATATATTATCGACTGAGA 423  
 QY 101 ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120  
 DB 424 GTATGTCAGAAATAGTGTGGAGCATATCGATCTTCTGGATCGGTTCTTGACACA 483  
 QY 121 GlyGluTyrGlnAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140  
 DB 484 GAGGAATATCAAGACTGGGTGAGCTCTGCCAGAGGAGAGACTTCTGCTCTTTCACATT 543  
 QY 141 GlyLysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnArgIleLysGln 160  
 DB 544 GGGAAATCTTCAGCACTCCAGGAGACCTTGGATCTTTCACAGAGAAATTTTCAG 603  
 QY 161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180  
 DB 604 AGAAGCTTCTGGGAGAAAAGATGATATGTCCTCCCATAGAGATACTGGGAGTGCTACC 663  
 QY 181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200  
 DB 664 ACAGCCCTGTGTTACCCATAGATGTTCCAGTATGTCACTGAGGCCCTTCCCACTCCCT 723  
 QY 201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220  
 DB 724 CTGTATGACACAGACTCAAGAGGTC-----ACCATCAAGAGATCCAGAGCGCC 774  
 QY 221 ThrThrGluArgGluThrGluPhe-----AlaVal 230  
 DB 775 ATAGCAATAAGAAAGAGCTGAGTTGGAAAGTAAACACAGAGCCCTACTCAGCTGACATAATC 834  
 QY 231 LeuGluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGlu 250  
 DB 835 TCATCCGAGGAGAAAGTGGAGTTGAGCATCTCTGCCCCAAACCCAGAGTTCAAGCGAGAG 894  
 QY 251 LeuAlaAspSerGlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMet 270  
 DB 895 CTCACCAACTCCAGATCCCATACTACACAGGAACCTGGTGGACAGCTCCCAACTCGATTG 954  
 QY 271 GlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgPro 290  
 DB 955 CAARAAGATATTAAAGAACTTCAGGATTCGAGAAATCCCGGTGTAGGATTTAGACCA 1014  
 QY 291 LysLysGluLysAspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArg 310

DB 1015 AAGAAAGAGAGGATGTTCAAGCTCCACAGAATAACAATCATGCGCCATCTTTAAGAGG 1074  
 QY 311 HisSerAlaGluAlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIle 330  
 DB 1075 GACCATGCGAATCAAAAGGCCCTGAGAGTGTCTCTCTGCTCGATTCCACAAAAATT 1134  
 QY 331 GluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnProGluIleTyrLeu 350  
 DB 1135 GAAAGTGAAGAATCCATCAGGAGCCATA--GAAGACAAACACAGAGCCTACCTC 1191  
 QY 351 ThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGluGluGlnSerLeuAsp 370  
 DB 1192 ACAGCTGCAGACCTCAAAAACCTCATCACTAGTAGTAGGAGACACAGCCCTTGGTA 1251  
 QY 371 ValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAsp 390  
 DB 1252 GAGGGAGCAGTTCATTCAGTGTATGAAGTT-----ACTGAGCCACTCTTCAGACCTGTC 1305  
 QY 391 ThrGlnSerGluLeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerPro 410  
 DB 1306 ACCAATCAGAGTGCACAGCCCTTACTGTGTACAGAGATGTCTACTTTGAGTCCA 1365  
 QY 411 GluLeuProProValGluProGlnLeuGluThrValAspGlyValAlaGluHisGlyLeuPro 430  
 DB 1366 GAGCTTCTTTCAGTGAACCTAGGCTTGAGAGTGTGCACATATATGTCGTAACCTGCCT 1425  
 QY 431 AspThrSerTrpSerProAlaMetAlaSerThrSer---LeuSerGluAlaProPro 449  
 DB 1426 GACAGTCTTGTGCTCGTCTGTAAACAGCTCGACTTCGGAGTGGGAAATCTACCTTCC 1485  
 QY 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469  
 DB 1486 TTT-----ACGCTAGCATCTTCGCTCTCGATGATCAAAAGCTCCCTCCCTTGTAGGCC 1539  
 QY 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspThrSerAlaIle 489  
 DB 1540 ACTGGGCCAACAGCATTCATCCCAAGCTCACTCTCCCATCTCGGATTTATTCTACCGTC 1599  
 QY 490 SerGlnLeuAlaLeuGlyIleSerHis---ProProAlaSerSerAspAspSerArgSer 508  
 DB 1600 CGCAATGCGCGCTAGAGTGTACATTCGCTGTAGTCTTCCAGTGCAGAGAGTGTGCG 1659  
 QY 509 SerAlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrPro 528  
 DB 1660 ACCACAAAGCAGCCACACACAATCAGAGACTAGTAGAAATGATGTGTCCGACACGCT 1719  
 QY 529 AlaProSerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGlu 548  
 DB 1720 GCCTTGTGGAATAGCAGAACTGAGTGGATATGACTCTGCCCGCGATCGGTTTTTGGAG 1779  
 QY 549 AspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaPro 568  
 DB 1780 ATGACCACGCCATCCGACATTTACAGTATGTCAACCCAGCTCTGAGACCATTTGCGCC 1839  
 QY 569 LysGlyArgGluLeuValValPheSerLeuArgValAlaAsnMetAlaPheSerAsn 588  
 DB 1840 AAGGGCCAGCAGTAGTGTATTTTCAGTCTGCGCGTCTGCTAAACATGCGTTCTCTAT 1899  
 QY 589 AspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeu 608  
 DB 1900 GACTTGTTCATAAGAGTTCCTGGAGTACCAAGCTTGGACACAGATTCACAGACCTG 1959  
 QY 609 LeuValProTyrIleuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPhe 628  
 DB 1960 TTGGTTCCATATCTACGATCGAATCTTACGGGCTTTAAGCAACTGGAATCTACGCTTC 2019  
 QY 629 ArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsn 648  
 DB 2020 AGAAACGGAAGTGTATCGTGAACAGAAAGTGGGTTCCCAAGCCCTACCTACAC 2079  
 QY 649 LeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaIleGlnLeu 668

```

Db      2080 CTCACCCAGCGGTGCGGGTCTTGGAGGATCTTCGGTCCACTCGAGCTCAAGAGCTC 2139
Qy      669 HisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCys 688
      ::::::::::::::::::::
Db      2140 AACCTGGAAATCGAAAGTTACTCTCTTGATATCGAACAGAGCTGATCAGGAGATCCCTGC 2199
Qy      689 LysPheLeuAlaCysGlyGluPheAlaGlnCysValIysAsnGluArgThrGluGluAla 708
      ::::::::::::::::::::
Db      2200 AATTCCTAGACTGTGGCAATTCGCCAGTGTATAAAGATGAGTTGACAGAGGAACA 2259
Qy      709 GluCyArgCysIysProGlyTyrAspSerGlnGlySerLeuAspGlyLeuGluProGly 728
      ::::::::::::::::::::
Db      2260 GAGTGTGCTGCAGACAGGACATGAGACCGGACCGCTGGAATACAGGAAGTGAAC 2319
Qy      729 LeuCyGlyProGlyThrIysGluCysGluValLeuGlnGlyIysGlyAlaProCysArg 748
      ::::::::::::::::::::
Db      2320 CTTGTGCTCCCTGGA---AAGACTTGTGAAGCCAGTCAAGGACAAACCCATGCAAG 2376
Qy      749 LeuProAspHisSerGluAsnGlnAlaTyrLysThrSerValIysLysPheGlnAsnGln 768
      ::::::::::::::::::::
Db      2377 CCACCAAGATCACTCTACAAACCCAGCTCGGCAACCTAGTGTAAAGACTACAGCTCAG 2436
Qy      769 GlnAsnAlnIysValIleSerIysArgAsnSerGluLeuLeuThrValGluTyrGluGlu 788
      ::::::::::::::::::::
Db      2437 CAA---ATAAGGTGCTCAAGAAAGAAATCTGAATCTCAGCTACACAGATTTTGAAGA 2493
Qy      789 PheAsnHisGlnAspTyrGluGlyAsn 797
      ::::::::::::::::::::
Db      2494 TTGGATGACAGGATTTGGAGGGAAT 2520

RESULT 6
AF229929
LOCUS      3675 bp mRNA linear ROD 15-NOV-2000
DEFINITION Mus musculus sialoprotein associated with cones and rods SPACR
            mRNA, complete cds.
ACCESSION AF229929
VERSION    1
KEYWORDS   GI:11177167
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3675)
AUTHORS   Lee,J.W., Chen,Q., Rayborn,M.E., Shadrach,K.G., Crabb,J.W.,
            Rodriguez,I.R. and Hollyfield,J.G.
TITLE     SPACR in the interphotoreceptor matrix of the mouse retina:
            molecular and biochemical characterization
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 3675)
AUTHORS   Rodriguez,I.R., Lee,J.W. and Hollyfield,J.G.
TITLE     Direct Submission
JOURNAL   Submitted (31-JAN-2000) LRCMB, NEI-NIH, 6 Center Drive MSC2740
            6/304, Bethesda, MD 20892, USA
FEATURES   Location/Qualifiers
            1..3675
            /organism="Mus musculus"
            /mol_type="mRNA"
            /db_xref="taxon:10090"
            229..2457
            /note="retina specific protein present in the
            interphotoreceptor matrix"
            /codon_start=1
            /product="sialoprotein associated with cones and rods
            SPACR"
            /protein_id="AAC32162.1"
            /db_xref="GI:11177168"
            /translation="WKRIFDLPKLRKRSALFPAAINICPQESLRQILASLOEYVRLRV.
            COEVWEAYRIFLDIPDTEYVDVSLCOKEFTCLFDIGKNFSNSOBHLLQORIK
            ORFQGRKDETAMSELTAPVPTVDVSMSLGPPPLSDPDLDLKEILSVTLKDI
            QPTTESITPHVSEFSEKEVERESISLPHRFAXELTNSGPYQELVQSQSLQK
            KIFKLPFGGEIRVJGFPRKDEGSSSTEIQLMAFKRDHBAKSPDHLSDSNK
            IESERIHGVIEDKPTVLTATDLKLIQLDGLSLVEGKIPFGDEVGTGTFRPV
            TEPDLPKPLADVTEATLSPFLPFVEPRLEAVDREGLPQMSKSDSWSPPVASIS

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 2,15e-161 Length: 3675
Score: 2453.00 Matches: 516
Percent Similarity: 73.27% Conservative: 76
Best Local Similarity: 53.86% Mismatches: 174
Query Match: 59.58% Indels: 43
DB: 10 Gaps: 10

US-10-007-270-2 (1-797) x AF229929 (1-3675)

Qy      1 MetTyrLeuGluThrArgArgAlaIlePheValPheTyrIlePheLeuGlnValGlnGly 20
      ::::::::::::::::::::
Db      125 ATGAATTTTCAATTAACATGCTATCTTTTGGGATTTTCTCAAGTTCAAGGA 184
Qy      21 ThrIysAspIleSerIleAsnIleTyrHisSerGluThrIysAspIleAspAsnProPro 40
      ::::::::::::::::::::
Db      185 ATCAAAACA-ATT----- 195
Qy      41 ArgAsnGluThrThrGluSerThrGluLysMetTyrLysMetSerThrMetArgArgGlie 60
      ::::::::::::::::::::
Db      196 -----GAAAGTACTTCAACAGTGCACAAAGATGTCACCAACCATGAACAAATA 240
Qy      61 PheAspLeuAlaLysHisArgThrLysArgSerAlaPhePheProThrGlyValIysVal 80
      ::::::::::::::::::::
Db      241 TTGGAITTCGCAAGCTTCGAACCAAAAGATCAGCACTTTTCCCA---GCTGTAACATC 297
Qy      81 CysProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArg 100
      ::::::::::::::::::::
Db      298 TGCCCCCAGGAATCCTTGACAGAGATTTTAGCAAGTCTTCAAGAAATATTATAGACTGAGA 357
Qy      101 ValCysGlnGluAlaValTyrGluAlaTyrArgIlePheLeuAspArgIleProAspThr 120
      ::::::::::::::::::::
Db      358 GTATGTCAGAAAGTCTGTGGAGAGATATCGTATCTTTCTGGACCGAATTCCTGACACA 417
Qy      121 GlyGluTyrGlnAspTyrValSerIleCysGlnGlnGluThrPheCysLeuPheAspIle 140
      ::::::::::::::::::::
Db      418 GAGGAATATCAAGACTGGGTGAGCTCTGCGAAGAAAGAACTTCTGCTCTTTGACATT 477
Qy      141 GlyIysAsnPheSerAsnSerGlnGluHisLeuAspLeuGlnGlnArgIleLysGln 160
      ::::::::::::::::::::
Db      478 GGGAAAAACTTCAGCAACTCCCGAGAGCACCTAGATCTTCTTCAGCAGAGATAAAGACAG 537
Qy      161 ArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGluProGly 180
      ::::::::::::::::::::
Db      538 AGAAGCTTCCTCGGAGGAAAGATGAGACAGCTCCATCGAGACACTGGAAGCACCTACT 597
Qy      181 GluThrIleValIleSerThrAspValAlaAsnValSerLeuGlyProPheProLeuThr 200
      ::::::::::::::::::::
Db      598 GAAGCCCTGTGTGTACCAAGATGTTTCCAGATGTCCTCGGGCCATTCCTCCACTTCCT 657
Qy      201 ProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeuAsnAspThrLysMetPro 220
      ::::::::::::::::::::
Db      658 TCTGATGACACAGACCTCAAGAGATCTTCAGTGTCCACTCAAGGACACTTCAAGAGCCC 717
Qy      221 ThrThrGluArgGluThr-----GluPheAlaValLeuGluGluGln 234
      ::::::::::::::::::::
Db      718 ACAACAGAAAGTATAACAGAACCTATTTCAGTGTCTTGAATTTCTCA-----TCAGAGGAG 771
Qy      235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254
      ::::::::::::::::::::
Db      772 AAGTGGAGTTTCAAGATCTCTCTGCCAAACACAGGTTCAAGCAGAGCTTCAACCACTCT 831
Qy      255 GlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnIysIlePhe 274
      ::::::::::::::::::::

```

```

RSNLSPTSFISLDAQPPPLMTTGTPTALIPKPTLPTIDYSTRIQLEPLESHPAS
SSRELTASHDTRDQMDVSDTPALSEISLGSYQALQSFLEMTTPTFTVRPIT
TSSETIATGQELVFFSRVANMPSYSLFNKSLQALQSFLEMTTPTFTVRPIT
GFKQLRILAFNGSVLNSKVPFAKAPYNLTQAVRGVLEDLRSAAQGLNLEISY
LDLEPDAQDPCKLDCGFAQCVKNWTEAEACRCQGHESHGTLDYQTLNLCPPGK
TCVAGREQATPCRPDPHSINQAFPGVKLRQKNVKKRNSKLSAISGEFEDQDWE
GN"

```

Db 832 GGGTCACCATCTACCGAGAACTGGTGGACAGTCCCAACTGCAGTTGCCAAAGATATTT 891  
Qy 275 IysLysLeuProGlyPheLysLysIleHisValLeuGlyPheArgProLysLysGluLys 294  
Db 892 AAGAAACTCCAGGATTCGGGAAATCCGGTATTTAGGATTTAGACCAAGAAAGAA 951  
Qy 295 AspGlySerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314  
Db 952 GATGTTCAAGCTCCACAGAAATACAGCTTATGGCCATCTTTAGAGGACCATGCCAG 1011  
Qy 315 AlaLysSerProAlaSerAspLeuLeuSerPheAspSerAsnLysIleGluSerGluGlu 334  
Db 1012 GCAAAAGAGCCCTGATAGTCACTACTGCTCTCTGATTCACAAATAATGAAAGTAAAGA 1071  
Qy 335 ValThrHisGlyThrMetGluGluAspLysGlnProGluIleThrLeuThrAlaThrAsp 354  
Db 1072 ATCCATCATGGAGTCAATA---GAACACAAACACAGAAACCTACCTCACAGCTACAGAC 1128  
Qy 355 LeuLysArgLeuLysSerLysAlaLeuGluGlnSerLeuAspValGlyThrIle 374  
Db 1129 CTCAAAAAATCATCATCACTACTAGATGGAGACCTGCTCTGGTAGAGGGAAT 1188  
Qy 375 GlnPheThrAspGluIleAlaGlySerLeuProAlaPheGlyProAspThrGlnSerGlu 394  
Db 1189 CCATTCCGATGATGAAGTTACTGGGACACTC-----TTACAGACCTGTCACCTGAACACGAT 1242  
Qy 395 LeuProThrSerPheAlaValIleThrGluAspAlaThrLeuSerProGluLeuProPro 414  
Db 1243 CTGCCCAAGCCCTGCTGTGTGTACAGAGATGCCACTTTGATGTCGAACTTCCTTC 1302  
Qy 415 ValGluProGlnLeuGluThrValAspGlyAlaGluHisGlyLeuPro----- 430  
Db 1303 GTTGAGCCTAGGCTTAGGCGAGTGGACAGAGAGATCTGAGCTGCCTGGAAATCTCCTCC 1362  
Qy 431 ---AspThrSerTrpSerProAlaMetAlaThrLeuSerProGluLeuProPro 449  
Db 1363 AAAGACAGTTCTGCTCTCCACCTGTATCAGCCTCAATTTCCCGATCAGAAATCTACCT 1422  
Qy 450 PhePheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAla 469  
Db 1423 TCGTTT---ACACCTPAGCATCTCTCTAGATGCTCAAGCCCTCCCTTCGATGACC 1479  
Qy 470 ThrAspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspThrSerAlaIle 489  
Db 1480 ACTGCCCAACAGCAGCACTCATCCCAAGCCCACTCTCCCACTATCGATATTTACCATC 1539  
Qy 490 SerGlnLeuAlaLeuGlyLysSerHisProProAlaSerSerAspSerSerSer 509  
Db 1540 CGCCAAATTCCTGGATCTGCATCTGCATGGCTGCATCTCCAGTGACAGAGCTGATC 1599  
Qy 510 AlaGlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAla 529  
Db 1600 ACAAGCAGCCATGACAAATCCGAGACCTAGATGGCATGGATGTCTGACACGCCAGCC 1659  
Qy 530 ProSerGluValProGluLeuSerGluThrValSerValProAspHisPheLeuGluAsp 549  
Db 1660 TTGTCAGAAATATCAGAACTGAGTGGATGATTCCTGCTCGGTCAGTCTTCGAGATG 1719  
Qy 550 ThrThrProValSerAlaLeuGlnThrIleThrThrSerSerMetThrIleAlaProLys 569  
Db 1720 ACCACACCCATCCCAACAGTAGGTTTCATCACCAGCTCCGAGACCATTCGCCACCAAG 1779  
Qy 570 GlyArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAsp 589  
Db 1780 G3CCAGGAGCTAGTGGTATCTTCAGCCCTGGGTGTGCTAACATGCCGCTTCCTCATGAC 1839  
Qy 590 LeuPheAsnLysSerSerLeuGluThrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609  
Db 1840 CTGTTTCACACAGATTCTCTGGAGTATCAAGCCCTGGACACACGATTCACAGACTCTGCT 1899  
Qy 610 ValProThrLeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArg 629  
Db 1900 GTTCCCTATCAGCATGAAATCTTACGGGATTTAAGCAATGGAATCTCAGCTTCAGA 1959

Qy 630 AsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerValProThrAsnLeu 649  
Db 1960 AACGGAGTGTGATCGTGAACAGCAAGTGCGGTTTGCAGAGCGGTACCTACACACCTC 2019  
Qy 650 ThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHis 669  
Db 2020 ACCAGCGCGTGGCGGGGTCTTGGAGGATCTTCGGTCCACCGCAGCTCAGGGCTCAAT 2079  
Qy 670 LeuGluIleAspSerThrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLys 689  
Db 2080 CTGAAATCGAAAGCTACTCCTCGACATTGAACACGATGATCAGCGGATCCCTGCAAA 2139  
Qy 690 PheLeuAlaCysGlyGluPheAlaGlnCysValLysValLysAsnGluArgThrGluAlaGlu 709  
Db 2140 CTCCTAGACTGTGGCAATTTGCCAGTGTGTAAAGATGATGGACAGGAAGCAGAG 2199  
Qy 710 CysArgCysLeuProGlyThrAspSerGlnGlySerLeuAspGlyLeuGluProGlyLeu 729  
Db 2200 TGTGCTGCAGACAGGACATGAGAGCCAGCGGACCTCGACTACCCAGACCTCGAACCTC 2259  
Qy 730 CysGlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArgLeu 749  
Db 2260 TGTCCCTCCGGA---AAGACTTGTGTGCCGCCGCGAGAACCAAGCACTCCATCGAGCCA 2316  
Qy 750 ProAspHisSerGluAsnGlnAlaThrLysThrSerValLysLysPheGlnAsnGlnGln 769  
Db 2317 CCAGATCATCTTCAACACCAAGCTCAGGAACCTGGTGTATAAAGCTA-----CGTCAG 2370  
Qy 770 AsnAsnLysValIleSerLysArgAsnSerGluLeuLeuThrValGluThrGluGluPhe 789  
Db 2371 CAAATTAAGGTAGTCAAGAAAGAAATTTCTAAACTATCAGCTATAGGATTTGAAGATTT 2430  
Qy 790 AsnHisGlnAspTrpGluGlyAsn 797  
Db 2431 GAAGACCAGATCTGGAGGGAAT 2454  
RESULT 7  
LOCUS AB070714 4953 bp mRNA linear VRT 10-JUL-2002  
DEFINITION Gallus gallus mRNA for SPACR, complete cds.  
ACCESSION AB070714  
VERSION AB070714.1 GI:21623676  
KEYWORDS  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
REFERENCE 1  
AUTHORS Zako, M., Iwaki, M., Yoneda, M., Miyaiishi, O., Zhao, J., Suzuki, Y., Takeuchi, M., Miyake, G., Ikagawa, H. and Kimata, K.  
TITLE Molecular Cloning and Characterization of Chick Sialoprotein Associated with Cones and Rods, a Developmentally Regulated Glycoprotein of Interphotoreceptor Matrix  
J. Biol. Chem. 277 (28), 25592-25600 (2002)  
JOURNAL  
PUBMED 11991949  
REFERENCE 2 (bases 1 to 4953)  
AUTHORS Zako, M. and Iwaki, M.  
TITLE Direct Submission  
JOURNAL  
Department of ophthalmology; Nagakute-cho, Aichi-gun, Aichi 480-1195, Japan (E-mail:zako@aichi-med-u.ac.jp, Tel:81-52-264-4811 (ex.2181), Fax:81-561-63-7255)  
FEATURES  
source  
1. .4953  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/tissue\_type="retina"  
1. .4953  
/gene="cspacr"  
1. .225  
5'UTR





```

Db 1774 GATAGCAATGACTTAATCACCAGATGAGTCTCCACAGACAGAGGTTATCACACGGCAGTT 1833
Qy 440 AlaSerThrSerLeuSerGluAlaProProPhePheMetAlaSerSer----- 455
Db 1834 TACACACAGAGGTAGCTTTTACCTTACCTTCTTCTCAGACCCACACATAAGGATAGTAA 1893
Qy 456 ----- 1952
Db 1894 GCTGAGATGAAGAAAGNAGTCTGTTGGAGTAAACAGAACCACTTTTCAAGAAAGCTGATGA 1953
Qy 462 ----- 462
Db 1954 GACAGCCTGTCTGGCAAGCAGTGAAGATGATGATGAATAGAAATCATCATGATGATGAC 2013
Qy 463 ----- 467
Db 2014 ATTTTGGTTACACACAGCAGCTTACAAAACATTCCTTCTTATCGGTTCAAGCAGATCTC 2073
Qy 468 MetAlaThr----- 475
Db 2074 TTTTGTACGAGCGCGAGGTCACTTTTGCGAGCAGCACTGCCACACAGACCAACTCTGCTG 2133
Qy 476 ValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeuGly 495
Db 2134 -----CCACAGTACACAGCCACTTTCACAGCCACTCTGTGTC----- 2172
Qy 496 IleSerHisProPro----- 505
Db 2173 ATTGACCACTCCCGAAGTACCAGACACTTGATGCCAGCAGCTGCCAGCGCTTCTCT 2232
Qy 506 SerArgSerSerAlaGlyGluAlaMetValArgHisLeuAspGluMetAspLeuSer 525
Db 2233 GACCGTGCCAGCAGCAGAGTGCAGACATTTGCTGAGTGGCGCTGCTGTGAAG 2292
Qy 526 AspThrProAlaProSerGluValProGluLeuSerGluTyrValSerValProAspHis 545
Db 2293 AGCAGCAGCTGCTGGATGAGCAGCAGCAGTGCAGCTGCTATCTCAGTGCAGACAACT 2352
Qy 546 PheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThr 565
Db 2353 GAACCTGCAGAAAGTACCCAGGCTCCACGCTGAAGTATGTAACCAACAGCTCCATGACA 2412
Qy 566 IleAlaProGlyArgGluLeuValPhePheSerLeuArgValAlaAsnMetAla 585
Db 2413 ACAGCAGCAAGGCAAGAGCTGTGGTTTCTTCAGCGTGGAGGTAAACCAACATGCAC 2472
Qy 586 PheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnPhe 605
Db 2473 TTTCTCGATGATCTTTCAACCGGAGCTCGCAGGATACAAAGCACTAGAACACAGTTC 2532
Qy 606 ThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPheLeuGlnLeuGluIle 625
Db 2533 ATGCAATTGCTACTTCCATACCTCAGTCCACCTTACAGGTTTAAAGCACTGGAATA 2592
Qy 626 LeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLysPheAlaLysSerVal 645
Db 2593 CTTAATCTCAGAAATGAAGTGTGATGTCACAGTAAATGAATTTGCCAGCAACAGTG 2652
Qy 646 ProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPheArgSerAlaAlaAla 665
Db 2653 CCATATAATATCACAGACAGCAGTACACTCGGTTTTTGGAGACTTCTGTGACGCTGCCGC 2712
Qy 666 GlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGluProAlaAspGlnAla 685
Db 2713 CAACACCTCAATTTGGAGATTCAGAGCTACTCCCTAGATATTGAGCCAGCTGATCAGCA 2772
Qy 686 AspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysValLysAsnGluArgThr 705
Db 2773 GACCATGCAATTCATGCGATGTCAGCAATTTTCAATATGCAATGAATGATGAGTGA 2832
Qy 706 GluGluAlaGluCysArgCysLysProGlyTyrAspSerGlnGly----- 720
Db 2833 AAAGAGGCTGACTGCTTTGTAAAGCCCGGTTATGCAAGCCAGGAGGATTCGCCCTGCCG 2892

```

```

Qy 721 SerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLysGluCysGluValLeu 740
Db 2893 AGCCTGTGTGAATGAAGAACACACACTCTTTGTGACAAATGTTGGGAAG---TGTGAGTTAGTT 2949
Qy 741 GlnGlyLysGlyAlaProCysArgLeuProAspHis----- 752
Db 2950 CCAGGAAGAGAGCTGTCTGCAGGTCCACAGACAGGTTTACAGAGCCAGAGTACACAAGT 3009
Qy 753 ---SerGlu-AsnGlnAlaTyrLysThrSerValLysPheGlnAsnGlnGlnAsnAs 771
Db 3010 TAGTCTGTGAATTTCTGCAATTTCCAGCATCATTCAGACAAACACCAAGTATTACAGATAA 3069
Qy 771 nLysVal 773
Db 3070 GGAGGTC 3076

RESULT 8
AF157624 3989 bp mRNA linear PRI 06-MAR-2000
LOCUS Homo sapiens Spacrcan mRNA, complete cds.
DEFINITION AF157624
ACCESSION AF157624
VERSION AF157624.1 GI:6467402
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3989)
AUTHORS Acharya,S., Foletta,V.C., Lee,J.W., Rayborn,M.E., Rodriguez,I.R.,
Young,W.S. III and Hollyfield,J.G.
TITLE SPACRCAN, a novel human interphotoreceptor matrix
hyaluronan-binding proteoglycan synthesized by photoreceptors and
pinealocytes
JOURNAL J. Biol. Chem. 275 (10), 6945-6955 (2000)
MEDLINE 20167166
PUBMED 10702256
REFERENCE 2 (bases 1 to 3989)
AUTHORS Foletta,V.C. and Young,W.S.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1999) SNGE, NIMH, 36 Convent Dr, MSC 4068,
Bethesda, MD 20892-4068, USA
FEATURES
Location/Qualifiers
source
1..3989
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3q11.2"
15..3740
/notes="hyaluronan-binding proteoglycan; interphotoreceptor
matrix component"
/codon_start=1
/product="Spacrcan"
/protein_id="AAPI3154.1"
/db_xref="GI:6467403"
/translation="MIMFLFGKISLIGILFVLIRGDFPSLTAQTVLSTIEEIQEPKSA
VSPFLPESTDLATKKKQPTDRRTEROMLTRRRSLFPNGVKICPDESVAEAVA
NVKVPKRVCOEAVWEAFRTWDRLPGRSEVYVWNLCEGVTSTIFEMGTNFSSEVA
HSLIMKLTAKETVSSSELSPYVGDSTLTGDTTISVPHPVEDVAGASESSLER
PRESINENIENIEATRPAGEQIAFPIHLKQKQRELDQSSSFHROHLEEFISE
VNAFTGLPGYKEIRVLPRSPKENDSGVDVTVYAVTFNGEAISSNTWDLISHSNKE
NGLVLEDDKPTVVYITNFRDYIATLQONFLGNSLNPDPDSLQINVRGLRHQ
TDFLVNTOSSSLQATPSSILNDTPAAMPSEDESITSSIPPLDFSSPPSAGRELW
SSPLGLDLYSTHKLAFPPSKMGLSSSPVEVLSLTHSVTPAVLOTGLPVAEBERTSG
SHLVEDGLANVESDFLSIDSLPSSSTQPVKETIPSMEDSDVLSLTPSSIP
FGLDSITSKVKDQKVSPPLPDASMEKELIPDGLGSGGQKVDLTWPMSETSEKS
ASPLKPLWEDDDSLIPAEIEDKVLVDMDSDTQISKHSKYVHDDSKDPSDEPL
SGAPVPIADTAESASITLPHISEVGVDDISVTKAPLITLTSASTDPSQD
ATLRDEMOITESSNYEWFDSVSNKPDQMTLMTLPESERVWTRTSLEKLSRDL
ASTPQADRLMTSVTQSTKLPTTITLLEDEVMGVQDISELDRIQIDTGYQPQVQ
EQNGKVGSVEMSTSVHSTEMVSWAPTEGGDLSYTOTSGALVVFSLRVNMFSE
DLFNKNSLEYKALEQRFLELLVPLQSLNTGFQNLLEIFNNGSIIVNSRKNFANSPV

```

CDS





FGLDLSLTKVKDQKQVSPFLPDASMEKELIFDGLGSGSKQKVDLITWPSSETSSEKS  
 AEPLSRMLEDDSLIPAEIEDKLVIVDMSTDOIISKSKYKHEDHRTHTPEPEPL  
 SGPAVPIADTAESASLTLFKHISEVGVDDCSVTKAPLITVSVAISATDKSDQAD  
 AILKREDEQILTESNEMFDFSEVMKPMQMTLWITLIPESRVMTRTSLEKLSRDIL  
 ASIPQADRIQLWLSVTQSTKLPTTITLLEDEVMGVODISLELDRTGDIYQPEQVQ  
 EQNGKSVYVEMTSVHSISTEMVAVPTGDDLSYTQTSGLVVPFSLRVNMFSE  
 DLFNKLSLEYALEQRLPFLLELLVPLQSNLTGFONLEILNFRNGSIVVNSRMKPFANSVP  
 PVNNAVYMTLEDFTAYNTMLAIDKYSLDVSDGEANPKCFQACNEFSCLYNPW  
 SGEAKRCFPGLYSVERPCQSLDLPQFCLNDKCDIMPFGHAIACRVRGENWYWR  
 GKICEFVSPVIGITIASVGLLVIFSAIYFFRTLOAHDHRSERSPFSGSRQ  
 PDLSSLENAVKNTPVESHRAKCEKIEGYPPOHPFYSSAGSDVIGGUSREIRQYVE  
 SSLSREBIEQRMVLELYANDDEFAAFVREQQVEV"

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,66e-55 Length: 4165  
 Score: 927.00 Matches: 297  
 Percent Similarity: 39.71% Conservative: 145  
 Best Local Similarity: 26.68% Mismatches: 267  
 Query Match: 22.52% Indels: 405  
 DB: 9 Gaps: 36

US-10-007-270-2 (1-757) x AF173155 (1-4165)

QY 2 TyrluGluThrArgAlaIlePheValPheTrpIlePheLeuGlnValGlnGlyThr 21  
 DB 202 TTCTCTTTTGGAGCATTTCTGGGTATTTTG-ATATTCTCTGATAGAAGGAGAC 260  
 QY 22 ---LysAspIleSerIleAsnIleTyHISerGluThrIleAspIleAspAsnPro--- 39  
 DB 261 TTCCCATATACAGCACAAACCTACTATCT-ATAGAGGAGATCAAGAACCCAAAG 317  
 QY 40 -----ProArgAsnGluThr-----ThrGluSer 47  
 DB 318 AGTGCACTTTCTTCTCTGCTGCTGAGAAATCAACAGACCTTTCTCTAGCTACCAAAAG 377  
 QY 48 ThrGluIleMetTyrluMetSerThrMetArgArgIlePheAspLeuAlaIleHisArg 67  
 DB 378 AAACAGCCTCTGACCGCAGAGAACTGAAGACACAGTGGTGA-ATCAGA 425  
 QY 68 ThrLysArgSerAlaPheProThrGlyValIleValCysProGlnGluSerMetLys 87  
 DB 426 AGCGGAGATCTATTCTGTTCTCTATGAGTGAGAAATCTGCCAGATGAAGTGTGCA 485  
 QY 88 GlnIleLeuAspSerLeuGlnAlaTyrluArgLeuArgValCysGlnGluAlaValTrp 107  
 DB 486 GAGGCTGTGCAAAATCATGTGAAGTATTTTAAAGTCCGAGTGTGTGAGAACTGTCTGG 545  
 QY 108 GluAlaTyrluArgIlePheLeuAspArgIleProAspThrGlyIleTyrluGlnAspTrpVal 127  
 DB 546 GAAGCTTTCAGGACTTTTGGATCGACTCTCCGGCGGTGAGGAATATCATTTACTGGATG 605  
 QY 128 SerIleCysGlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSer 147  
 DB 606 AATTGTGTGAGGATGAGTCAAGATATATTGAATGGCACAAATTTTAGTGAATCT 665  
 QY 148 GlnGluHisLeuAspLeuGlnGlnArgIleLysGlnArgSerPheProAspArgLys 167  
 DB 666 GTGGACATAGAAGCTTAATCATGAAGAACTGACTTAT-----GCAAG 710  
 QY 168 AspGluIleSerAlaGluIleThrLeuGlyGluPro-----GlyGluThrIleVal 184  
 DB 711 GAAACTGTAGACACTCTGAA---CTGTCTCTCCAGTTCCTGTGTTGTTGATCTTCARCA 767  
 QY 185 IleSerThrAspValAlaIleValSerLeuGlyProPheProLeuThr----- 200  
 DB 768 TTGGGACACACTACTCTCAGTGT-----CCACATCCAGGTGAGCGCTATGAA 818  
 QY 201 -----ProAspAspThrLeuLeuAsnGlnIleLeuAsp 211  
 DB 819 GTGCGCTCAGAGACGCTTGGAAAGCCAGAGAGATATTAGCATGAAATTT---GAG 875  
 QY 212 AsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGluPheAlaValLeu 231

DB 876 AATGTGATAGAAGAGCCACAAAACCCAGCAGGTGAACAGATTGCAGAAATTC----- 926  
 QY 232 GluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeu 251  
 DB 927 -----AGTATCCACCTTTTGGGGAAGCAGTACAGGGAAGAACTA 965  
 QY 252 AlaAspSerGlnSerProTyrluGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGln 271  
 DB 966 CAGGATTCCTCCAGCTTTACCACACAGCCTTGAAGAAGAAATTTATTCAGAGTTGAA 1035  
 QY 272 LysIlePheLysLeuProGlyPheLysIleHisValLeuGlyPheArgProLys 291  
 DB 1026 AATGCAATTACTGGTTACCAGGCTACAGGAATTCGTACTTGAATTAGTCTCCCCC 1085  
 QY 292 LysGluIleAspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHis 311  
 DB 1086 AAGGAAATATGAC-----AGTGGCGTAGATGTTTACTATGACGTACTCTTC----- 1130  
 QY 312 SerAlaGluAlaLysSerProAlaSer---AspLeuLeuSerPheAspSerAsnLysIle 330  
 DB 1131 AATGGTGAGCCCATCAGCAATACCACCTGGGACCTCATTAGCCTTCACTCCACAGGTG 1190  
 QY 331 GluSerGluGluValTyrluHisGlyThrMetGluGluAspLysGlnProGluIleTyrlu 350  
 DB 1191 GAAATC-----CATGGCCTTGTGAACCTGGATGATTAACCCACTGTTGTTTAT 1238  
 QY 351 ThrAlaThrAspLeuLysArgLeuIleSerLysAlaLeuGlu----- 365  
 DB 1239 ACAATCAGTAACTCAGAGATATATTGCTGAGACATTCAGCAGAAATTTTTCCTGGG 1298  
 QY 365 ----- 365  
 DB 1299 AACTCTCTTGAATCCAGATCTCTGCTGAGCTTATCAATGTGAGAGGATTTTG 1358  
 QY 366 ---GluGlnSerLeuAspVal-----GlyThrIleGlnPheThr--- 377  
 DB 1359 CGTCACCAAACTGAAGATCTAGTTTGGAAACACCCAAAGTTCAAGTCTTCAGGCAACCG 1418  
 QY 378 -----AspGluIleAla 381  
 DB 1419 TCATCTATTCTGGATAATACCTTTCAAGTGCATGCTGCCCTCAGCAGATGAATCATCACC 1478  
 QY 382 GlySerLeuPro-----AlaPheGlyProAspThr 391  
 DB 1479 AGCAGTATTCACCACTTGATTTGAGTCTGCTCTCCCTCAGCCTCAGCAGGAACTC 1538  
 QY 392 GlnSerGluLeuPro----- 396  
 DB 1539 TGGTCAGAAAGTCTTTGGGTGATTTAGTGTCTACACAAATTAGCTTCCCTCGAAG 1598  
 QY 396 ----- 396  
 DB 1599 ATGGGCTCAGCTCTTCCACAGAGTTTATAGAGTTAGAGCTTGACGTGACTTTCATCTGTC 1658  
 QY 397 -----ThrSerPheAlaValIleThrGluAspAlaThrLeuSerPro 410  
 DB 1659 ACCCGGCGAGTCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1718  
 QY 411 GluLeuProValGluProGlnLeuGluThrValAspGlyAlaGlu----- 426  
 DB 1719 CACTTG-----GTAGAAGATGGATTAGCCAAATTTGAAGAGTACAGAGATTTCTTTCT 1772  
 QY 427 ---HisGlyLeuProAspThrSerTrpSerProAlaMetAlaSerThr----- 442  
 DB 1773 ATTGATTCATTGCTTCAAGTTCACTTCACTCAACCTGTGCCAAAGAAACAATACCATCC 1832  
 QY 443 -----SerLeuSerGluAlaPro-----ProPhe 450  
 DB 1833 ATGGAAGACTCTGATGTGCTTAAACATCTTACCATATCTGACCTTCTTACCTTTT 1892  
 QY 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470

Db 1893 GGCTTGGACTCTTGACCTCCAAAGTCAAAGACCAATTAATAAGTGAAGCCCTTTCCTGCGCA 1952  
Qy 471 AspGlnThrMet----- 474  
Db 1953 GATGATCCATCGAAGAAAGAGTAAATATTGACGGTGGTTAGTTCAGGCTCTGGCGAA 2012  
Qy 475 LeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAlaLeu 494  
Db 2013 AAGGTAGATCTGATTACTTGGCCATGGAGTGAAGTTCATCA--GAGAAGAGCCCGAA 2069  
Qy 495 GlyIleSerHisProProAlaSerSerAspSerArgSerSerAlaGlyGlyLeuAsp 514  
Db 2070 CCAGTGTCCAGCCGCTGGTGAAGATGATGATTCATCTTTGCCAGCTCGAGATTGAAGAC 2129  
Qy 515 MetValArgHisLeu--AspGluMetAspLeuSerAsp----- 526  
Db 2130 AGAAACTAGTTTTAGTTGACAAATAGATCCAGACCAAAATAGTAAGCACTCAAAA 2189  
Qy 527 -----ThrProAlaProSerGluValPro----- 534  
Db 2190 TATGAACATGATGACAGATCCACACACTTCCAGAGGAAGAGCCTCTTGTAGTGGGCTGCT 2249  
Qy 535 -----GluLeuSerGluTyrValSerValProAspHisPhe 546  
Db 2250 GTGCCCATCTTCGAGATGATCGAGCTGAATCTGCGTCTTAACCTCCCAAGCACAATA 2309  
Qy 547 LeuGlu-----AspThr 550  
Db 2310 TCAGAAGTACCTGGTGTGATGATGCTCAGTTACCAAGACCTCTTATACTGACATCT 2369  
Qy 551 ThrProValSerAla----- 555  
Db 2370 GPAGCAATCTCTGCTCTACTGATAAAATCAGATCAGCAGATGCCATCTTAAGGAGGAT 2429  
Qy 556 LeuGlnTyrIleThrSerSer----- 563  
Db 2430 ATGGACAAATTAAGTATGATGATCACTCACTATGATGTTTGACAGTGAAGTTCAATGTA 2489  
Qy 564 -----MetThrIleAlaProGlyGlyArgGlu----- 572  
Db 2490 AAGCCAGATATGCAAACTTTGTGGACTATATGCGCAGATCATGAGAGAGTTTGACAGA 2549  
Qy 572 ----- 572  
Db 2550 ACTTCTCCCTAGAGAAATTTGCGAGACATATTTGCGCAAGTACACACAGAGTGTGAC 2609  
Qy 572 ----- 572  
Db 2610 AGGCTCTGTTATCTGTGACACAGTCTACCAAAATGCGCTCCCAACCAATCTCCACCTG 2669  
Qy 572 ----- 572  
Db 2670 CTAGAGATGAAGTAAATTTAGTGTACAGGATATTTCTGTAGAACTGGACCGGATAGGC 2729  
Qy 572 ----- 572  
Db 2730 ACAGATTACTATCAGCTTGAGCAAGTCCAGAGCAAAATGCCAAGTTGTTAGTTATGTG 2789  
Qy 572 ----- 572  
Db 2790 GAAATGTCAACAAGTGTCTCACTCCACAGATAGTGTAGTGTGGCTTGCGCCACAGAGA 2849  
Qy 573 -----LeuValValPhePheSerLeuArg 580  
Db 2850 GGAGATGATCTGAGTTATACCGAGATTCAGAGCTTTGGGGTTTCTTCAGCCTCCGA 2909  
Qy 581 ValAlaSerMetAlaPheSerAsnAspLeuPheAsnLysSerSerLeuGluTyrArgAla 600  
Db 2910 GTGACTAATCATGATCTTTTCAAGAGATCTGTTTAAATAAAACTCTCTGGAGTATAAAGCC 2969  
Qy 601 LeuGluGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSerAsnLeuThrGlyPhe 620  
Db 2970 CTGGAGCAAGATCTTGAATATGCTGTTCCCTATCTCCAGTCAAAATCTCACGGGGTTC 3029

Qy 621 LysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleValAsnSerLysMetLys 640  
Db 3030 CAGAACTTAGAAATCTCAACTTCAGAAATGGCAGCATTTGTGTGACAGTTCGAATGAAG 3089  
Qy 641 PheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGlyValLeuGluAspPhe 660  
Db 3090 TTTGCCAATCTCTCTCTCTTAACGTCACAAATGCGGTGATCATGATTCTGGAGACTTT 3149  
Qy 661 ArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyrSerLeuAsnIleGlu 680  
Db 3150 TGTACACTGCTTACATAATACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3209  
Qy 681 ProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGluPheAlaGlnCysVal 700  
Db 3210 TCAGGTGATGAACCAACCTTCAAGTTTTCAGGCTCTGAATGAATTTTCAGAGTGTCTG 3269  
Qy 701 LysAsnGluArgThrGluGluAlaGluCysArgCysGlyAspProGlyTyrAspSerGln--- 719  
Db 3270 GTCAACCCCTGGAGTGGAGAGCAAGTGCAGATGCTTCCCTGGATACCTGAGTGTGAA 3329  
Qy 720 -----GlySerLeuAspGlyLeuGluProGlyLeuCysGlyProGlyThrLys 735  
Db 3330 GAACGCCCTGTGAGTGTCTGTGACCTACAGCCTGACTTCTGCTTGAATGATGGAAG 3389  
Qy 736 GluCysGluValLeuGlnGlyLysGlyAlaProCysArg 748  
Db 3390 ---TGTGACATTATGCTGGCAGCGGGCAATTTGTAGG 3425

## RESULT 10

AY174061

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .4010

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/chromosome="16"

/note="specifically expressed in retina and pineal gland;

detectable as early as E15"

226. .3809

/note="SPACKCAN; similar to Rattus norvegicus PGI0.2 and

Homo sapiens IPM200; retinal-specific protein present in

the interphotoreceptor matrix"

/codon\_start=1

/product="sialoprotein associated with cones and rods

proteoglycan"

/protein\_id="AA021221.1"

/db\_xref="GI:27802105"

/translation="MFLPVGRMSLGILFLITGNGLVSSASERQEPMAHVSVLSPKAS

TDLSPTRKQLLDATETGRWLLRRRSILFPNGVKICSSETVAEAVANHYKPKAR

VCOEAIWEAFRTFDRLPQRDREYHWMNLCEGVTSTVFEMGAHPSQSVSEHRLNLMKKL  
 AYTRAESSCKDCQCPPLSPFPIGISTLTGAVSSAYVGLASESSAASPOESIS  
 NREUNTEPTPAEQIAEISFQILKRAYSEELDPDSALYRLIVERPISVEKAPT  
 GUPGYAKVLEFRAPFEEENDSGIDVHIAVTFNGEAISNTTMDLISLHSENKVENHGLVE  
 MODKPAVTIISNFDYIAIBTHQNFQMGNSLNPDKSLQNLINAVLQDLPVAPBGR  
 TSGFLEDTGLASTELETSIDGLPSPLIQPVKETVPWEDSDTALLSTPHLTS  
 AIEDTKDTGTPSGLESASNDQLEVPWPDTSVKDKRIFESGLGSGGKQDVVI  
 DWPWSTSEKTKPLKSWSEQDALLPTEGREKLHIDGRVDSYEQIIESSERYGD  
 RPIHTEBSHVRSITPIFVESATPPTSPIFSKTHSDVPDIDSDYSLSLTKPRLPTVIAL  
 PASTKTDVLEKDVHTESSKSLDSEVPVSRPDMOPVMTLPESDVATVTRSSLG  
 KLSRDTLASTPSTEDBMLKASTQSTELPSTHSTQLEBEVINAVQDISELQVGT  
 KYIQSLTEBQKADSYVEMSTSVHYTEMPIVALTPQGVLSHTQTAGALVYFSLR  
 VTNMFSDPKNLSLEKSFQLELLVPYQNSLGSFQNLLEISFRNGSIYVNSR  
 VFAPASPNVANKYRIIELEDFCTAYQTMNLDIDKSLDVSSEDEANPCKFOACNEF  
 SECLNVNWSGEAKCKCPYGLSVDELPCQSLDQDFCLNDKGDIMPGRHACRCR  
 VGSNMYRGOHCBEFVSEPFVIGITIASVUSFLVAVSVFVFLKMLQAOVNREROR  
 PTTSSRHPDLSLVSANMKNYPAYBSHLAGELYEKSQHPFVSSASEVIGLSRE  
 EIRQWYESSDLKSEIQRMRILELYANDPEFAGFRERA<sup>a</sup>

ORIGIN

## Alignment Scores:

Pred. No.: 8,77e-54 Length: 4010  
 Score: 911.50 Matches: 279  
 Percent Similarity: 42.43% Conservative: 136  
 Best Local Similarity: 28.53% Mismatches: 272  
 Query Match: 22.14% Indels: 291  
 DB: 10 Gaps: 35

US-10-007-270-2 (1-797) x AY174061 (1-4010)

Qy 31 SerGluThrLysAspIleAspAsnProProArgAsnGluThrThrGluSerThrGluLys 50  
 Db 295 TCAGCCTCAGAGAGAGAGACAAGACCCATGCGTCTCTGCTCTCCTCCTCAGGAG 354  
 Qy 51 MetTyrLysMetSer-----ThrMetArgArgIlePheAspLeuAlaLysHis--- 66  
 Db 355 TCAACAGACCTTTCCTGCTACCAGGAGAGAGCGAGCTTTTGGATGCCACGAGACTGG 414  
 Qy 67 -----ArgThrLysArgSerAlaPhePheProThrGlyValLysValCys 81  
 Db 415 AGGAGGTGGCTGCTTGAAGGGCGGCGATCTATTCTTCCCAATGGAGTAAATTTGC 474  
 Qy 82 ProGlnGluSerMetLysGlnIleLeuAspSerLeuGlnAlaTyrTyrArgLeuArgVal 101  
 Db 475 TCCAGTGAACCGTTCCAGAGGCTGGGCAACCATGTGAAGTATTTAAAGCCGAGTG 534  
 Qy 102 CysGlnGluAlaValTrpGluAlaTyrArgIlePheLeuAspArgIleProAspThrGly 121  
 Db 535 TGCAGGAAAGCCATCTGGGAAGCCTTCAGGAGCTTTGGGATCGACTTCTCGGGCGTGT 594  
 Qy 122 GluTyrGluAspTrpValSerIleCysGlnGlnGluThrPheCysLeuPheAspIleGly 141  
 Db 595 GAATATCGTCACGTGAATGAATTTATGTAGGATGGAGTCCAAAGTCCAAAGTATTTGAAATGG 654  
 Qy 142 LysAsnPheSerAsnSerGlnGluHisLeuAspLeuLeuGlnGlnArgIle----- 158  
 Db 655 GCCCATTTTGTAGTCAGTCTGTGGAACATACAAACCTAATCATCAGAAACCTGCTTACACA 714  
 Qy 159 LysGlnArgSerPheProAspArgLysAspGluIleSerAlaGluLysThrLeuGlyGlu 178  
 Db 715 AGGGAAGCTCAGAGACGACTCCTGCAAGGATCAG---TCCTGTGGGCGCTGAGTTCCTTT 771  
 Qy 179 Pro-----GlyGluThrIleValIleSerThrAspValAlaAsnValSerLeuGly 195  
 Db 772 CCAGTTCCTATTGGTAGACC-----TCAACACTGACAGGTGCTGTCTCCAGTCT 822  
 Qy 196 ProPhePro-----LeuThrProAspAspThrLeuLeuAsn 207  
 Db 823 TCCTATCCAGGGTTGGCTTCGAGAGACGCGCAGCGGTCAACCGCAGGAGAGTATCAGCAAT 882  
 Qy 208 GluIleLeuAspAsnThrLeuAsnAspThrLysMetProThrThrGluArgGluThrGlu 227  
 Db 883 GAAATTT---GAGAAATGTGACAGAGGAGCCACACAAACCGAGTCTGCTGAAACAGATTCGGAA 939

Qy 228 PheAlaValLeuGluGluGlnArgValGluLeuSerValSerLeuValAsnGlnLysPhe 247  
 Db 940 TTC-----AGCATCCAACTTCTGGGGAAGCGATAC 969  
 Qy 248 LysAlaGluLeuAlaAspSerGlnSerProTyrTyrGlnIleLeuAlaGlyLysSerGln 267  
 Db 970 AGTGAAGAACTCGGGATCCCTCCAGCGCCTCTACCGGCTCTCTGGGAAGAGTTATT 1029  
 Qy 268 LeuGlnMetGlnLysIlePheLysLysLeuProGlyPheLysLysIleHisValLeuGly 287  
 Db 1030 TCAGGGCTGAAAAGACATTTCACAGGTTTACCTGGCTACAGGGCATCCGTGTTCGGAA 1089  
 Qy 288 PheArgProLysLysGluLysAspGlySerSerSerThrGluMetGlnLeuThrAlaIle 307  
 Db 1090 TTCAGGGCCCGGAGGAAATGACATGGATAGATGTTCACTATGCAGTTACC----- 1143  
 Qy 308 PheLysArgHisSerAlaGluAlaLysSerProAlaSer---AspLeuLeuSerPheAsp 326  
 Db 1144 -----TCAATGGCGAAGCCATCAGCAATACCACCTGGGACCTCTAAGCCTTCAC 1194  
 Qy 327 SerAsnLysIleGluSerGluGluValTyrHisGlyThrMetGluGluAspLysGlnPro 346  
 Db 1195 TCCACAGAGTAGAAGAAC-----CATGGCTTGTAGAGATGATGATAACCC 1242  
 Qy 347 GluIleTyrLeuThrAlaThrAspLeuLysArgLeuLysSerLysAlaLeuGluGlu 366  
 Db 1243 ACTGCTGCTATACAATTAGTAACCTTCAGAGATTATATCGCTGAGACGCTG-----CAC 1296  
 Qy 367 GlnSerLeuAspValGlyThrIleGlnPheThrAspGluIleAlaGlySerLeuProAla 386  
 Db 1297 CAGAACTTTTGTATGGGAAATTCCTCTTGAATCCAGAT---CCCAAGTCTCTCCAGTCT 1353  
 Qy 387 PheGlyProAspThrGlnSerGluLeuPro-----ThrSerPheAla 400  
 Db 1354 ATCAATCAGTGTCTCAGCCTGACCTGCTGTGGCTCTGAGGGAAGGACTTCTGGATCG 1413  
 Qy 401 ValIleThrGluAspAlaThrLeuSerProGlu----- 411  
 Db 1414 TTCATATTAGAGATGGTTAGCCAGCAGCTGAAGATTAAGAAGATCTTCTATTGATGGA 1473  
 Qy 412 -----LeuProValGlu--- 416  
 Db 1474 TTGCCTTCAGCCCATTAATTCACCTGTGCCAAAAGAAACAGTACCACTATGGAAGAC 1533  
 Qy 417 -----ProGlnLeuGlu-----Thr 421  
 Db 1534 TCTGACACGGCTCTCTTGTCCACACCATCTGACCTTCTTCTATAGAAGACCTTACT 1593  
 Qy 422 ValAsp---GlyValaGluHisGlyLeu----- 429  
 Db 1594 AAAGACATAGGGACACCTTCTGGCTTGGAGTCTTGGCTTCCACATCTCAGACCAAGTTG 1653  
 Qy 430 -----ProAspThrSer----- 433  
 Db 1654 GAAAGTATCCCATGGTTTCCAGACACCTCTGTGGAAAAAGAACTTCACTTTTGAAGTGGC 1713  
 Qy 434 -----TrpSerProAla 438  
 Db 1714 TTGGTTCTGGGTCTGGGAAAGATGTAGATGATTTGATGGCCATGGAGTGAGACTTCA 1773  
 Qy 439 MetAlaSerThr-----SerLeuSerGluAlaPro----- 448  
 Db 1774 TTAGAGAGACCACTAAACCCTGTCAAAGTCTATGCTCTGAGAGAACAGGATGCCTATT 1833  
 Qy 448 ----- 448  
 Db 1834 CCAACTGAGGGTAGAGAAAAATTACATATAGATGGCAGATAGATTCCACAGAACAAATT 1893  
 Qy 448 ----- 448  
 Db 1894 ATTGAATCATCAGAACATAGATATGGAGATAGGCCCATACATTTTATAGAGGAGAAATCC 1953



```
QY 449 -----ProPheMetAlaSerSer-----tile 456
Db 1954 CATGTAGATCTACTATACCAATCTTTGTAGAGTCGCAACTCCCACTACATCTCCAATC 2013
QY 457 PheSer-----LeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGlnThrMet 474
Db 2014 TTTTCAAAACACACTTTCAGATGTACAGATGTACAGATGTATCTTCTACTCTACCTTACCAACACACC 2073
QY 475 LeuValPro---ClyLeuThrIleProThrSerAspTyrSerAlaIleSerGlnLeuAla 493
Db 2074 TTTTACCGGTAACTATAGCAATCCCTGCTTCCACTTAAGAAACAGATGAGTACTCAAG 2133
QY 494 LeuGlyIleSerHisProAlaSerSerAsp-----AspSerArgSerSerAla 510
Db 2134 GAAGATATGTCATACAGATCATCCAGTCACAAAGAACTTGACAGTGCAGTTCAGTG 2193
QY 511 GlyGlyGluAspMet-----515
Db 2194 TCAAGGCCAGATATGAGCGCTGTGTGGACCATGTTGCCAGATTCAGATACAGTTTGGACA 2253
QY 516 -----ValArgHisLeuAspGluMetAspLeuSerAspThrPro-----528
Db 2254 AGAATCTTCTTAGGAAATGTCAGAGACACATTTGGCAAGTACACAGAGAGACT 2313
QY 529 -----AlaProSerGluValPro-----534
Db 2314 GACAGACTCTGTTGAAGCTTCCATGACACAGCTCCACTGAATGCTTCAACACCCACC 2373
QY 535 -----GluLeuSerGlnTyrValSerVal-----542
Db 2374 TCCACCCAGCTAGAGGAGGAAGTAATATGCGGTCCAGATATTTTCATTAGAAGTATAG 2433
QY 543 -----ProAsp 544
Db 2434 CAGGTAGGCACAGATTTATTCAGTCCGAGCTAACTGAAGACACATGGCAGCTGCAC 2493
QY 545 HisPheLeuGluAspThrThrProValSerAlaLeuGlnTyrIleThrThrSerSerMet 564
Db 2494 AGCTATGTGGAATGTCTACCACTGTT-----CACTACACAGAGATGCTATTGTG 2544
QY 565 ThrIleAlaProIleGly-----ArgGluLeuValVal 575
Db 2545 GCTCTGCCCAAAAGAGAGGTCTTGTAGTCACCCAGACTGCAGGAGCATGTGTGTGTT 2604
QY 576 PhePheSerLeuArgValAlaIleMetAlaPheSerAsnAspLeuPheAsnLysSerSer 595
Db 2605 TTCTTCAGCTCCGCTGACAAACATGTTGTTTTCAGAGACTGTTTAAACAAAACCT 2664
QY 596 LeuGluTyrArgAlaLeuGlnGlnPheThrGlnLeuLeuValProTyrLeuArgSer 615
Db 2665 TTGGAAATAAAGCCCTGGAACAAAGATTTCTAGAACTGCTGTTCCCTATCTCCAGTCA 2724
QY 616 AsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySerValIleVal 635
Db 2725 AATCTGTCAAGGTTCAGAACCTAGAAATCTCTGAGTTTCAGAAACGGCAGCATTTGTGTG 2784
QY 636 AsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAlaValHisGly 655
Db 2785 AACAGCCGAGTGAAGTTCGCCAGTGTGCCCTCTCTAATGTCAACAAAGCCATGTATAGG 2844
QY 656 ValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHisLeuGluIleAspSerTyr 675
Db 2845 ATCTGTGAAGATTTTGTACCACTGCTTACCAACCAACCACTGATATCGATATGAATGATC 2904
QY 676 SerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAlaCysGlyGlu 695
Db 2905 TCCCTGAGCTGGAATCAGGTATGAGGCCAACCTTGCAGTTTCAGGCTGTGAATGAA 2964
QY 696 PheAlaGlnCysValLysAsnGluArgThrGluGluAlaGluCysArgCysLysProGly 715
Db 2965 TTTTCTGAGTGTGTTGTAATTCATGAGTGAGAGCAAGTGAATGTACCTCTGG 3024
QY 716 TyrAspSerGlnGly-----SerLeuAspGlyLeuGluProGlyLeuCys 730
```

```
Db 3025 TACCTGAGTGTGGATGAAGTCCCTTGTCAAAAGTCTCTGTGATCTACAGCTGACTTCTGC 3084
QY 731 GlyProGlyThrLysGluCysGluValLeuGlnGlyLysGlyAlaProCysArg 748
Db 3085 TTGAACGATGGAAG---TGTGACATTATGCTGGGCGATGGAGCCATTGTAGA 3135

RESULT 11
LOCUS HSIMPG13 816 bp DNA linear PRI 28-OCT-1998
DEFINITION Homo sapiens interphotoreceptor matrix gene (IPM150), exon 13.
ACCESSION AF017772
VERSION AF017772.1 GI:3800727
KEYWORDS
SEGMENT
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 816)
AUTHORS Felbor,U., Gehrig,A., Sauer,C.G., Marquardt,A., Kohler,M.,
Schmid,M. and Weber,B.H.
GENOMIC ORGANIZATION AND CHROMOSOMAL LOCALIZATION OF THE
INTERPHOTORECEPTOR MATRIX PROTEOGLYCAN-1 (IMPG1) GENE: A CANDIDATE
FOR 6G-LINKED RETINOPATHIES
Cytogenet. Cell Genet. 81 (1), 12-17 (1998)
JOURNAL
MEDLINE 98358139
PUBMED 9891169
REFERENCE 2 (bases 1 to 816)
AUTHORS Gehrig,A., Felbor,U., Kelsell,R., Hunt,D.M., Maumenee-Hussels,I.E.
and Weber,B.H.F.
TITLE Assessment of a novel interphotoreceptor matrix gene (IPM150)
localized to 6q14.2-q15 in autosomal dominant Stargardt-like
macular dystrophy, progressive bifocal choriorretinal atrophy
(PBCRA), and North Carolina macular dystrophy (MCDRI)
Unpublished
JOURNAL
AUTHORS Felbor,U., Kuehn,M., Hageman,G.S. and Weber,B.H.F.
TITLE Direct Submission
SUBMITTED (09-AUG-1997) Humangenetik, Universitaet Wuerzburg, Am
Hubland, Wuerzburg D-97074, Germany
FEATURES
source
1. 816
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6q14.2-q15"
144..676
/genes="IPM150"

exon

ORIGIN

Alignment Scores:
Pred. No.: 7,24e-54 Length: 816
Score: 899.00 Matches: 178
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.44% Mismatches: 0
Query Match: 21.84% Indels: 0
DB: 9 Gaps: 0

US-10-007-270-2 (1-797) x HSIMPG13 (1-816)
QY 431 AspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProPhe 450
Db 143 GACACTTCTTGGTCTCCACCTGCTATGGCTCTTACCTCCCTGTCAGAGCTCCACCTTC 202
QY 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470
Db 203 TTTATGGCATCAGCATCTCTCTGATGATCAAGGCCACACATACATATGGCCACT 262
QY 471 AspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSer 490
Db 263 GACCAGACATGTAGTACCAGGGCTCAGCATCCCAAGGATGATTATTCTGCAATCAGC 322
```

QY 491 GlnLeuAlaLeuGlyIleSerHisProProAlaSerSerAspSerAspSerSerAla 510  
 Db 323 CAACTGGCTCGGAATTCATCCACTGCATCTTCAGATGACGCCGATCAAGTGCA 382  
 QY 511 GlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaPro 530  
 Db 383 GGTGGCGAAGATATGGTCAGACACCTAGATGAATGATGCTGTCTGACACTCCTGCCCA 442  
 QY 531 SerGluValProGluLeuSerGluTyrrValSerValProAspHisPheLeuGluAspThr 550  
 Db 443 TCTGAGGTACACAGACTCAGCGAATATGTTTCTGCCAGATCATTTCTTGAGGATACC 502  
 QY 551 ThrProValSerAlaLeuGlnTyrrThrThrSerSerMetThrIleAlaProLysGly 570  
 Db 503 ACTCTGCTCAGCTTTACAGTATATCACCCTAGTCTATGACCATTCGCCCAAGGC 562  
 QY 571 ArgGluLeuValValPhePheSerLeuArgValAlaIleMetAlaPheSerAspLeu 590  
 Db 563 CGAGAGCTGGTAGTGTCTTCTCAGTCTGGTGTGTTGCTAACATGGCTTCTCCACGACCTG 622  
 QY 591 PheAsnLysSerSerLeuGluTyrrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609  
 Db 623 TTCACAGAGCTCTCTGGATACCGAGCTCTGGAGCAACATTCACACAGCTGGTG 679

RESULT 12  
 AL392166/c  
 LOCUS Human DNA sequence from clone RP11-758J17 on chromosome 6, complete  
 DEFINITION  
 ACCESSION AL392166  
 VERSION HTG.  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (Bases 1 to 90766)

REFERENCE  
 AUTHORS Direct Submission  
 TITLE Submitted (15-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 JOURNAL CB10 USA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk

COMMENT  
 On Mar 20, 2001 this sequence version replaced gi:13234983.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em, EMBL; Swi,  
 SWISSPROT; Tr, TREMBL; Wp, WORMPEP; information on the WORMPEP  
 database can be found at

http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping  
 Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr6  
 RP11-758J17 is from the library RP11-11.3 constructed by the group  
 of Pieter de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm

VECTOR: pBAC3.6  
 IMPORTANT: This sequence is not the entire insert of clone  
 RP11-758J17. It may be shorter because we sequence overlapping  
 sections only once, except for a 100 base overlap.

The true left end of clone RP11-62L18 is at 24664 in this sequence.  
 The true left end of clone RP11-453C2 is at 90667 in this sequence.  
 The true right end of clone RP3-472A9 is at 100 in this sequence.

## FEATURES

source  
 1..90766  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="6"  
 /clone="RP11-758J17"  
 /clone\_lib="RPC1-11.3"  
 64..483  
 /note="match: GSS: Em:AQ037329"  
 misc\_feature  
 171..463  
 /note="AluSg repeat: matches 1..294 of consensus"  
 repeat\_region  
 464..666  
 /note="L1PB3 repeat: matches 5941..6140 of consensus"  
 repeat\_region  
 1963..2000  
 /note="19 copies 2 mer gt 84% conserved"  
 repeat\_region  
 2002..2286  
 /note="AluSx repeat: matches 1..285 of consensus"  
 repeat\_region  
 5357..5715  
 /note="L1MA6 repeat: matches 5423..5788 of consensus"  
 repeat\_region  
 5720..6039  
 /note="160 copies 2 mer ta 55% conserved"  
 repeat\_region  
 5732..6097  
 /note="6 copies 61 mer 69% conserved"  
 misc\_feature  
 5896..6073  
 /note="Weak data. Digests checked and match."  
 repeat\_region  
 6105..6587  
 /note="L1MA6 repeat: matches 5785..6293 of consensus"  
 repeat\_region  
 6878..6992  
 /note="AluJc/FLAM repeat: matches 1..115 of consensus"  
 repeat\_region  
 6996..7297  
 /note="AluSx repeat: matches 1..305 of consensus"  
 repeat\_region  
 9105..9153  
 /note="12 repeat: matches 2645..2698 of consensus"  
 repeat\_region  
 9525..9807  
 /note="AluSx repeat: matches 25..308 of consensus"  
 repeat\_region  
 9846..9955  
 /note="HY1 repeat: matches 1..110 of consensus"  
 misc\_feature  
 9875..110328  
 /note="match: GSS: Em:AQ407990"  
 repeat\_region  
 10385..10760  
 /note="L1ME repeat: matches 5303..5714 of consensus"  
 repeat\_region  
 10761..11036  
 /note="L1PA4 repeat: matches 5867..6146 of consensus"  
 repeat\_region  
 11037..11094  
 /note="29 copies 2 mer aa 72% conserved"  
 repeat\_region  
 11096..11316  
 /note="L1M4 repeat: matches 4823..5039 of consensus"  
 repeat\_region  
 12031..12187  
 /note="MERSA repeat: matches 5..186 of consensus"  
 repeat\_region  
 12708..12880  
 /note="MERSA repeat: matches 1..179 of consensus"  
 repeat\_region  
 14029..14333  
 /note="AluSg repeat: matches 1..305 of consensus"  
 repeat\_region  
 15129..15266  
 /note="MIR repeat: matches 114..251 of consensus"  
 misc\_feature  
 16761..17159  
 /note="match: GSS: Em:AQ018572"  
 repeat\_region  
 17011..17215  
 /note="ORSL repeat: matches 203..443 of consensus"  
 repeat\_region  
 17794..17851  
 /note="12 repeat: matches 2648..2705 of consensus"  
 misc\_feature  
 complement(18194..18664)  
 /note="match: GSS: Em:AQ728325"  
 misc\_feature  
 18506..18856  
 /note="match: GSS: Em:AQ493517"  
 misc\_feature  
 18514..18752  
 /note="match: GSS: Em:AQ825405"  
 misc\_feature  
 18582..18939  
 /note="match: GSS: Em:AQ090573"

```
misc_feature
/notes="match: GSS: Em:AQ698147"
misc_feature
/notes="match: GSS: Em:AQ692558"
repeat_region
/notes="AluSx repeat: matches 1. .311 of consensus"
repeat_region
/notes="MER67D repeat: matches 1. .44 of consensus"
repeat_region
/notes="AluJb repeat: matches 1. .295 of consensus"
repeat_region
/notes="L1PA4 repeat: matches 5742. .6142 of consensus"
repeat_region
/notes="MER67C repeat: matches 60. .331 of consensus"
repeat_region
/notes="L2 repeat: matches 1263. .1720 of consensus"
repeat_region
/notes="L2 repeat: matches 2685. .2750 of consensus"
repeat_region
/notes="L1PA7 repeat: matches 2. .79 of consensus"
repeat_region
/notes="MER58 repeat: matches 21. .101 of consensus"
repeat_region
/notes="MER58 repeat: matches 2363. .2459 of consensus"
repeat_region
/notes="WSTB repeat: matches 20. .405 of consensus"
repeat_region
/notes="AluSx repeat: matches 1. .312 of consensus"
repeat_region
/notes="WTR repeat: matches 3. .146 of consensus"
repeat_region
/notes="L1PA7 repeat: matches 108. .393 of consensus"
repeat_region
/notes="match: GSS: Em:AQ470494"
repeat_region
/notes="MER41A repeat: matches 1. .554 of consensus"
repeat_region
/notes="AluSg/x repeat: matches 132. .286 of consensus"
repeat_region
/notes="L1PA1 repeat: matches 1. .365 of consensus"
repeat_region
/notes="L1PA7 repeat: matches 5814. .6140 of consensus"
repeat_region
/notes="L1PA7 repeat: matches 3084. .6143 of consensus"
repeat_region
/notes="AluSg repeat: matches 1. .305 of consensus"
repeat_region
/notes="L1PA7 repeat: matches 4. .3084 of consensus"
repeat_region
/notes="MER33 repeat: matches 1. .96 of consensus"
misc_feature
/notes="match: GSS: Em:AQ067266"
misc_feature
/notes="match: GSS: Em:AQ442060"
repeat_region
/notes="L2 repeat: matches 2379. .2750 of consensus"
repeat_region
/notes="L1PA1 repeat: matches 757. .1038 of consensus"
repeat_region
/notes="AluJb repeat: matches 2. .293 of consensus"
repeat_region
/notes="L1MA9 repeat: matches 6263. .6307 of consensus"
repeat_region
/notes="L1A1 repeat: matches 864. .1043 of consensus"
repeat_region
/notes="L1A1 repeat: matches 1161. .1225 of consensus"
repeat_region
/notes="AluSx repeat: matches 1. .300 of consensus"
repeat_region
/notes="L1A1 repeat: matches 1224. .1257 of consensus"
repeat_region
/notes="L1A1 repeat: matches 1332. .1669 of consensus"
repeat_region
/notes="L1A1 repeat: matches 1332. .1669 of consensus"

/notes="L1MD2 repeat: matches 6271. .6336 of consensus"
44847. .45554
/notes="L1M4 repeat: matches -10. .721 of consensus"
45557. .45727
/notes="L1WB5 repeat: matches 6004. .6176 of consensus"
45730. .46038
/notes="AluSg repeat: matches 1. .310 of consensus"
46044. .46936

Alignment Scores:
Pred. No.: 4,87e-51 Length: 90766
Score: 899.00 Matches: 178
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.44% Mismatches: 0
Query Match: 21.84% Indels: 0
DB: 9 Gaps: 0

US-10-007-270-2 (1-797) x AL392166 (1-90766)
Qy 431 AspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProPhe 450
Db 32428 GACATCTTTGGTCTCCACCTGCTATGGCTCTTACCTCCCTGTCAGAGCTCCACCTTC 32369
Qy 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470
Db 32368 TTTATGSCATCAAGCATCTTCTCTGACTGATCAAGGCACACAGATCAATGGCCACT 32309
Qy 471 AspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSer 490
Db 32308 GACCAGACAATGTAGTACCAGGGCTCACCATCCCGCAGTGATTTATTCTGCAATCAGC 32249
Qy 491 GlnLeuAlaLeuGlyIleSerHisProAlaSerSerAspSerSerSerAla 510
Db 32248 CAATGGCTCTGGGAATTTTCATCCACTCCCTGCTTCAGATGACAGCCGATCAATGCA 32189
Qy 511 GlyGlyGluAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaPro 530
Db 32188 GGTGGGGAAGATATGTCAGACACCTAGATGAATGGATCTGTCTGACACTCTCGGCCCA 32129
Qy 531 SerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThr 550
Db 32128 TCTGAGGTACCAGCTCAGCGAATATGTTCTGCTCCAGATCATTTCTTGGAGGATACC 32069
Qy 551 ThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGly 570
Db 32068 ACTCTGTCTCAGCTTTACAGTATATCACCACTAGTTCTATGACCATGCCCCAGGCG 32009
Qy 571 ArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeu 590
Db 32008 CGAGAGCTGGTAGTGTCTTCAGTCTGCGTGTGTGCTTAACATGGCTTCTCCAACGACCTG 31949
Qy 591 PheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609
Db 31948 TTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGACACATTCACACAGCTGGTG 31892

RESULT 13
AL359817
LOCUS Homo sapiens chromosome 1 clone RP11-505B21, 26 unordered pieces.
DEFINITION AL359817
ACCESSION AL359817
VERSION AL359817.6 GI:12225447
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Mclay, K.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT On Jan 14, 2001 this sequence version replaced gi:12214326.
```

```

----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA505B21
----- Summary Statistics
Assembly program: XGAP; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 117761 bases at least Q40
Consensus quality: 123343 bases at least Q30
Consensus quality: 126505 bases at least Q20
Insert size: 129645; sum-of-contigs
Insert size: 166195; 8.3% error; agarose-fp
Quality coverage: 3.05x in Q20 bases; sum-of-contigs Quality
coverage: 2.65x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 8912: contig of 8912 bp in length
* 8913 9012: gap of 100 bp
* 9013 12665: contig of 3653 bp in length
* 12666 12765: gap of 100 bp
* 12766 16825: contig of 4060 bp in length
* 16826 16925: gap of 100 bp
* 16926 22958: contig of 6033 bp in length
* 22959 23058: gap of 100 bp
* 23059 23080: contig of 2022 bp in length
* 23081 25180: gap of 100 bp
* 25181 27272: contig of 2092 bp in length
* 27273 27372: gap of 100 bp
* 27373 40754: contig of 13382 bp in length
* 40755 40854: gap of 100 bp
* 40855 45147: contig of 4293 bp in length
* 45148 45247: gap of 100 bp
* 45248 48493: contig of 3246 bp in length
* 48494 48593: gap of 100 bp
* 48594 52881: contig of 4288 bp in length
* 52882 52981: gap of 100 bp
* 52982 57112: contig of 4131 bp in length
* 57113 57212: gap of 100 bp
* 57213 60637: contig of 3425 bp in length
* 60638 60737: gap of 100 bp
* 60738 62745: contig of 2008 bp in length
* 62746 62845: gap of 100 bp
* 62846 70684: contig of 7839 bp in length
* 70685 70784: gap of 100 bp
* 70785 74560: contig of 3776 bp in length
* 74561 74660: gap of 100 bp
* 74661 77242: contig of 2582 bp in length
* 77243 77342: gap of 100 bp
* 77343 81104: contig of 3762 bp in length
* 81105 81204: gap of 100 bp
* 81205 83750: contig of 2546 bp in length
* 83751 83850: gap of 100 bp
* 83851 92962: contig of 9112 bp in length
* 92963 93062: gap of 100 bp
* 93063 106093: contig of 13030 bp in length
* 106093 106192: gap of 100 bp
* 106193 110995: contig of 4803 bp in length
* 110996 111095: gap of 100 bp
* 111096 114862: contig of 3767 bp in length
* 114863 114963: gap of 100 bp
* 114963 118927: contig of 3865 bp in length
* 118928 118927: gap of 100 bp

```

```

fragment_chain:8"
misc_feature      106193..110995
                  /note="assembly_fragment:00353"
misc_feature      111096..114862
                  /note="assembly_fragment:00726"
misc_feature      114963..118827
                  /note="assembly_fragment:00964"
misc_feature      118928..124084
                  /note="assembly_fragment:01042"
misc_feature      124185..128603
                  /note="assembly_fragment:01274"
misc_feature      128704..132145
                  /note="assembly_fragment:01290"

ORIGIN
Alignment Scores:
Pred. No.:      8.18e-51      Length:      132145
Score:          899.00      Matches:      178
Percent Similarity: 100.00%      Conservative: 1
Best Local Similarity: 99.44%      Mismatches: 0
Query Match:    21.84%      Indels:      0
DB:            2      Gaps:      0

US-10-007-270-2 (1-797) x AL1539817 (1-132145)
Qy 431 AspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProProPhe 450
Db 14959 GACACTTCTGGTCTCCACCTGCTATGCGCTTACCTCCCTGTGTCAGAGTCCACCTTTC 15018
Qy 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470
Db 15019 TTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGCACCAACATCAATGGCCACT 15078
Qy 471 AspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSer 490
Db 15079 GACCAGCAATGCTAGTACACAGGCTCACCATCCACCAGTATTTCTGCAATCAGC 15138
Qy 491 GlnLeuAlaLeuGlyIleSerHisProAlaSerSerAspSerArgSerAla 510
Db 15139 CAATGGCTCTGGGAATTTCCATATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCA 15198
Qy 511 GlyGlyLeuAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaPro 530
Db 15199 GTGGCGAAGATATGTCACACACCTAGATCAATGGAATGCTGCTGACACTCTCTGCCCA 15258
Qy 531 SerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThr 550
Db 15259 TCTGAGGTACACAGCTCAGCGAATATGTTCTGTCCAGATCATTTCTGGAGGATACC 15318
Qy 551 ThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProGlyGly 570
Db 15319 ACTCTGTCTCAGCTTTACAGTATATACCCACTAGTTCATGACCATTCGCCCAAGGCG 15378
Qy 571 ArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeu 590
Db 15379 CGAGAGCTGTAGTGTCTTCTTCACTGCGGTGTTGCTAACATGGCTTCTCCAGACCTG 15438
Qy 591 PheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609
Db 15439 TTCAACAAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACAATTCACACAGCTGGTG 15495

RESULT 14
AL157379/c      160719 bp      DNA      linear      HTG 11-SEP-2001
LOCUS          Homo sapiens chromosome 6 clone RPI-62L18.
DEFINITION     AL157379
ACCESSION     AL157379
VERSION       AL157379.14 GI:15590763
KEYWORDS      HTG; HTGS PHASE2; HTGS_CANCELLED.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1

```

# AUTHORS TITLE JOURNAL

## COMMENT

Wall, M.  
Direct Submission  
Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone  
requests: clonerequest@sanger.ac.uk  
On Sep 12, 2001 this sequence version replaced gi:11991356.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: dj62L18  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 160382 bases at least Q40  
Consensus quality: 160493 bases at least Q30  
Consensus quality: 160578 bases at least Q20  
Insert size: 160719; sum-of-contigs  
Insert size: 158939; 9.3% error; agarose-fp  
Quality coverage: 8.32x in Q20 bases; sum-of-contigs Quality  
coverage: 8.41x in Q20 bases; agarose-fp  
-----

\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

## FEATURES source

1..160719  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/clone="RPI-62L18"  
/clone\_lib="RPI-1"  
1..160719  
/note="assembly\_fragment:02758"  
clone\_end:SP6  
vector\_side:left  
clone\_end:T7  
vector\_side:right

## misc\_feature

## ORIGIN

## Alignment Scores:

Pred. No.: 1.07e-50 Length: 160719  
Score: 899.00 Matches: 178  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.44% Mismatches: 0  
Query Match: 21.84% Indels: 0  
DB: 2 Gaps: 0

US-10-007-270-2 (1-797) x AL157379 (1-160719)

Qy 431 AspThrSerTrpSerProAlaMetAlaSerThrSerLeuSerGluAlaProProPhe 450  
Db 7762 GACACTTCTGGTCTCCACCTGCTATGCGCTTACCTCCCTGTGTCAGAGTCCACCTTTC 7703  
Qy 451 PheMetAlaSerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThr 470  
Db 7702 TTTATGGCATCAAGCATCTTCTCTGACTGATCAAGGCACCAACATCAATGGCCACT 7643  
Qy 471 AspGlnThrMetLeuValProGlyLeuThrIleProThrSerAspTyrSerAlaIleSer 490  
Db 7642 GACCAGCAATGCTAGTACACAGGCTCACCATCCCACTGATTTCTGCAATCAGC 7593  
Qy 491 GlnLeuAlaLeuGlyIleSerHisProAlaSerSerAspSerArgSerAla 510  
Db 7592 CAATGGCTCTGGGAATTTCCATATCCACCTGCATCTTCAGATGACAGCCGATCAAGTGCA 7523  
Qy 511 GlyGlyLeuAspMetValArgHisLeuAspGluMetAspLeuSerAspThrProAlaPro 530

Db 7522 GGTGGCAAGATATGGTCAGACACCTAGATGAAATGGATCTGTCTGACACTCTCTGCCCCA 7463

Qy 531 SerGluValProGluLeuSerGluTyrValSerValProAspHisPheLeuGluAspThr 550

Db 7462 TCTCAGGTACAGAGCTCAGCAATATGTTCTGTGCCAGATCATTTCTTGGAGGATACC 7403

Qy 551 ThrProValSerAlaLeuGlnTyrIleThrThrSerSerMetThrIleAlaProLysGly 570

Db 7402 ACTCCTGTCTCAGCTTTACAGTATATCACCACCTAGTTCTATGACCATTTGCCCAAGGGC 7343

Qy 571 ArgGluLeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeu 590

Db 7342 CGAGAGCTGGTAGTGTCTTTCAGTCTCGTGTCTTAACTAGCCCTTCTCAACAGCACTG 7283

Qy 591 PheAsnLysSerSerLeuGluTyrArgAlaLeuGluGlnGlnPheThrGlnLeuLeu 609

Db 7282 TTCACACAGAGCTCTCTGGAGTACCGAGCTCTGGAGCAACATTCACACAGCTGGTG 7226

RESULT 15

LOCUS RNU76717 4368 bp mRNA linear ROD 13-NOV-1996

DEFINITION Rattus norvegicus PG10.2 mRNA, complete cds.

ACCESSION U76717

VERSION U76717.1 GI:1667596

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 4368)

AUTHORS Wang,X., Brownstein,M.J. and Young,W.S. III.

TITLE Sequence analysis of PG10.2, a gene expressed in the pineal gland and the outer nuclear layer of the retina

JOURNAL Brain Res. Mol. Brain Res. 41 (1-2), 269-278 (1996)

MEDLINE 97038366

PUBMED 8883960

REFERENCE 2 (bases 1 to 4368)

AUTHORS Wang,X., Brownstein,M.J. and Young,W.S.

TITLE Direct Submission

JOURNAL Submitted (30-OCT-1996) LCMR, NIMH, 36 Convent Drive, MSC 4068, Bethesda, MD 20892-4068, USA

FEATURES

source

1..4368

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/db\_xref="taxon:10116"

1..4368

/gene="PG10.2"

190..3909

/gene="PG10.2"

/notes="expressed in the pineal gland and retina"

/codon\_start=1

/protein\_id="AAC52891.1"

/db\_xref="GI:166759"

/translation="MFLPLGILSIGILILFLTGNLVSVEEIQDRMHAVALSPKES TDLSLPKQLDARETGERPRLRRRLIFENGRI CPSTDTAFAVANVHYKPKAR VCGRAWEARTWRDLPGREEIQYWNLCEDGVTFENGTFQSGVSRHLINKEKL TYTKBAESSCKQACGPELSPVPIGETSTLAGAVSSASYPGAASERAAAPQSEIS NEIENVTQPTPAEQIAEFISQILKQYSEELRDPSSALYELLVEEFISEVEKFT GLPGYKGLHLDPRSPKENGSGIDVHYATFNGEAIENITWDLISLHKNVNHGLIVE LDDKPTAVYIISNFRPIASTHONF.MGNSLNPDPKSLQILINVGVLPPOTETIV NTQSSIQVTTISNLDNTLOAELMSADESITTTTTTIIPFGPSSGPPSATGRELHSE STIGDVIYSTKLASPKVLSLSSPEVLGGSSLLHSTVPAVLQIDLPAPEGRTSGSS ILDDNTEESDVISDIPSSLIQVPKRETVFPFMDSDMLITSSPHUTSVSVIDLA KDITTPGLSLASRSDKLDVDPWFDFTSVEKEFIFESGLSGSGSKNVVDIDWPSL TSLEKTEPLSKWSNEQDITLPTESIEKLHWYFTEQMEPSAHRYGDGP1YFTPEES SAHRTPIFAESATQPSLSKSTSDVDIPDSYVTKAPFLIATANTASTKRETDV NVTLKGMQVTPSSPKGLDSKISVARPDMQPVMTILPESDTWASTSLGKLSRDTL NTPSPESADRLWLKASMTQPAELPSTHSICLEDEVIMAVQNLISLEDQVGYQPEL TQSQNGKVDYSEMPHTVHTENPLVAQPTKGVLSRTQTAGALVVFSLRVNWLPS EDLFNKNSLEYKALEQRLELLPYQSNLSGFGNLEILNFRNGSIVVNSRVKFAESV PPNVNNAIYMLIEDFCTATYQTWNLDIDKYSLDVESGDDANPCKFOACNEFSECLNP

## ORIGIN

## Alignment Scores:

Pred. No.: 5,94e-52 Length: 4368

Score: 886.00 Matches: 281

Percent Similarity: 37.74% Conservative: 127

Best Local Similarity: 25.99% Mismatches: 265

Query Match: 21.52% Indels: 408

DB: 10 Gaps: 33

US-10-007-270-2 (1-797) x RNU76717 (1-4368)

Qy 32 GluThrLysAspIleAspAsnProProArg---AangluThrThrGluSerThrGluLys 50

Db 316 GAGTCAACAGACCTTTCCCTCCCTACCAGGAAGAGACAGACTTTTGGATGCCACAGAG--- 372

Qy 51 MetTyrLysMetSerThrMetArgArgIlePheAspLeuAlaLysHisArgThrLysArg 70

Db 373 -----ACTGGAGGAGG---TGGCCGCTT-----AGAAGCGGACGA 405

Qy 71 SerAlaPhePheProThrGlyValLysValCysProGlnGluSerMetLysGlnIleLeu 90

Db 406 TCTATTCTGTTCCTCCAAATGGAGTAAAGATTTCCTCCCACTGACACTGTTGGCAGAGCTGTG 465

Qy 91 AspSerLeuGlnAlaTyrTyrArgLeuArgValCysGlnGluAlaValTTPGluAlaTyr 110

Db 466 GCACACCATGTGAAGTATTTTAAAGCCGAGTGTGCCAGGAGGCATCTGGAGACCTTC 525

Qy 111 ArgIlePheLeuAspArgIleProAspThrGlyGluTyrGlnAspTTPValSerIleCys 130

Db 526 AGGACATTTTGGGACCGACTTCCTGGCGGTGAGGAATATCAATCTGATCAACTATGT 585

Qy 131 GlnGlnGluThrPheCysLeuPheAspIleGlyLysAsnPheSerAsnSerGlnGluHis 150

Db 586 GAGGATGGAGTCAACAGTGTATTGAAATGGGACCCAGTATTAGTCAATCTGTGGAACAC 645

Qy 151 LeuAspLeuLeuGlnGlnArgIle-----LysGlnArgSerPheProAspArgLys 167

Db 646 AGACACTTATCATGGAGAAATTCACATACACAAAGGAGCTGAGAGCAGCTCTGCAAG 705

Qy 168 Asp-----GluIleSerAlaGluLysThrLeuGlyGluProGlyGluThr 182

Db 706 GATCAGCGCTGTGGACCTGAGTGTCTCAGTCTCAGTCTCCTATTGGCGAG----- 753

Qy 183 IleValIleSerThrAspValAlaAsnValSerLeuGlyProPhePro----- 198

Db 754 -----ACCTCAACATTGGCAGGTGTCTCCAGTCTTCCTATCCAGGGCGGCCTCA 807

Qy 199 -----LeuThrProAspAspThrLeuLeuAsnGluIleLeuAspAsnThrLeu 214

Db 808 GAGAGAAGCGGGCATCACACAGAGAGATATCAGCAATGAAT-----GAG 855

Qy 215 AsnAspThrLysMetProThrThrThrGluArgGluThrGluPheAlaValLeuGluGln 234

Db 856 AATGTGACAGAGACCCACACCCCA-----GCTGCTGGAACAG 894

Qy 235 ArgValGluLeuSerValSerLeuValAsnGlnLysPheLysAlaGluLeuAlaAspSer 254

Db 895 ATAGCTGAATTCAGCATCCAACTTCTGGGGAAGCAGTACACGCAAGAACTCGCGGATCCC 954

Qy 255 GlnSerProTyrTyrGlnGluLeuAlaGlyLysSerGlnLeuGlnMetGlnLysIlePhe 274

Db 955 TCCAGCGCCCTCTACCGGCTCTTGTGGAGAGAGTTATTTTTCAGAGGTGTAAGAAAGCTTTC 1014

Qy 275 LysLysLeuProGlyPheLysIleHisValLeuGlyPheArgProLysLysLysLys 294

Db 1015 ACAGGTTACTTGGCTACAGGGCATCCATGTTCTGATTTTCAGTCTCCAAAGGAAAT 1074

Qy 295 AspGlySerSerSerThrGluMetGlnLeuThrAlaIlePheLysArgHisSerAlaGlu 314



1075 GGCAGTGGGATAGATGTTCACTATGCGATTACT-:::|||||:::---TTCAACGGCGAG 1119  
Qy 315 AlaLysSerProLaseR---AspLeuLeuSerPheAspSerAsnLysIleGluSerGlu 333  
Db 1120 GCCATCAGCAATACCACTGGGACCTCATAGGCTTCACTCCACAAAGGTGGAGAAC-- 1176  
Qy 334 GluValTy-HisGlyThrMetGluGluAspLysGlnProGluIleTyLeuThrAlaThr 353  
Db 1177 -----CATGGCTTGTAGAGCTGGGATGATATAAACCCACGGCGCTCTATACGATCAGT 1227  
Qy 354 AspLeuLysArgLeuLysSerLysAlaLeuGlu----- 364  
Db 1228 AACTTCAGAGATTATATCGCTGAGACACTGCACACGAACTTTTAATGGGAATTCCTCT 1287  
Qy 364 ----- 364  
Db 1288 TTGAATCCAGATCCCAAGTCTCTCCAGCTTATCAATGTGAGAGGAGTTCTGCTCCCCCAA 1347  
Qy 365 -----GluGluGlnSerLeuAspValGlyThrIleGlnPhe 376  
Db 1348 ACGGAGAAATAGTTTGGAAACACCCAAAGTTCAGTCTTCAGGTGACAACTCTCTATT 1407  
Qy 377 ThrAspGluLe----- 380  
Db 1408 CTGGATAATACCTGCAAGCTGAATGGCTCTCAGCAGATGAATCCATCACCACCAACCACC 1467  
Qy 381 -----AlaGlySerLeuProAlaPheGlyProAsp 390  
Db 1468 ACCACCACTATTTCACCAATTTGGTTTCACTCCGGTCTCTCCCTCAGCCACTGGCAGGGAA 1527  
Qy 391 ThrGlnSerGlu-----LeuProThr 397  
Db 1528 CTCCATTGAGAAAGTACTTTGGGTGACATAGTGTCTACACCAAGTAGCTTCTCCCTCG 1587  
Qy 398 SerPhe----- 399  
Db 1588 AAGGTGGTCTCAGTTCTCCCGCAGAGGTTTGGGGGTAGCAGCTTGACTTCTCATTTCT 1647  
Qy 400 -----AlaValIleThrGluAspAlaThrLeuSerProGlu----- 411  
Db 1648 GTTACCCAGCAGTGTCTCAGATTGACCTGCGCTGGCTCTCTGAGGGAAGGACTTCTGGA 1707  
Qy 411 ----- 411  
Db 1708 TCTTCCATATTAGAAGACGACACACAGAAAGATCAGAAGATGTTTCTATTGATGATTG 1767  
Qy 412 -----LeuProProValGlu----- 416  
Db 1768 CCTTCAGCTCATTAATCACTGTGCAAAAGAAACAGTACCACCCATGGGAAGACTCT 1827  
Qy 416 ----- 416  
Db 1828 GACATGATTCTCTGACATCTCCACACATCTGACCTCTCTCTGTGTATAGAGACCTTGCT 1887  
Qy 417 ProGlnLeuGluThrValAspGlyAlaGluHis----- 427  
Db 1888 AAAGACATAACGACACCTTCTGGCTTGGACTCTCTGGCTTCCAGAGTCTCAGACAAGTTG 1947  
Qy 428 -----GlyLeuProAspThrSer----- 433  
Db 1948 GACGTGAGCCCATGGTTTCCAGACACCTCTGTGGAAAAGAGTTCATTTTGAAGTGGC 2007  
Qy 434 -----TyrSerProProAla 438  
Db 2008 TTGGGCTCTGGGTCTGGGAAAAATGTGATGTGATTGTTGGCCATGGAGTGAGACTTCA 2067  
Qy 439 MetAlaSerThr-Ser----- 443  
Db 2068 TTAGAGAGACCACCTGAACCCCTGTCAAAGTCATGGTCTGAAGACGAGATACACTATTA 2127  
Qy 443 ----- 443

2128 CCAACTGAGAGTATAGAAAAATTACATATGTATTTTTCAGAGACAAATGATTGAACCTTCA 2187  
Qy 443 ----- 443  
Db 2188 GCACATAGATATGGAGATGGACCCATATATTTTACAGAGGAAGATCCCATGTTAGATCT 2247  
Qy 443 ----- 443  
Db 2248 ACCATACCCATCTTTGCGAGAGTCTGCAACTCAACCTACATCTCTAAATTTCTTCAAAGCAC 2307  
Qy 444 LeuSerGluAlaPro-----ProPhePheMetAla 453  
Db 2308 ACATCAGATGTACCAGACATTGATTCTTACTCAGTTACCAAGACACCTTCTTACTGGCA 2367  
Qy 454 SerSerIlePheSerLeuThrAspGlnGlyThrThrAspThrMetAlaThrAspGln--- 472  
Db 2368 -----ACTATAGCAAAACACTGCTTCCCAAGGAAGAAACAGATGAGGTG 2409  
Qy 473 ---ThrMetLeuValProGlyLeuThr----- 480  
Db 2410 AATACCTCTCTTAAAAAAGGTATGTGTACAAACAGAACCATCCAGTCCCAAGAGACTTGAC 2469  
Qy 481 -----IleProThrSer 484  
Db 2470 AGCAAGATTTCACTAGCAGGCCAGATATGCAAGCTGTGTGGACCATTTTGCCAGAAATCA 2529  
Qy 485 AspTy-SerAlaIleSerGlnLeuAlaLeuGly-----IleSer 497  
Db 2530 GATACAGTTTGGCGAGGACTTCTTCTTAGGGAATTTGTCCAGGGACACATTGGTGAGT 2589  
Qy 498 HisPro-----ProAlaSerSer 503  
Db 2590 ACACCGAGAGCGCTGACAGACTCTGGTTGAAGCGCTCCATGACACAGCGCTGAAATTG 2649  
Qy 504 AspAspSerArgSerSerAlaGlyGlyGluAsp-----MetValArgHisLeuAsp 520  
Db 2650 CCTCCATCCACCCACTCCATCCAGCTAGAGGATGAAGTTATATATGCTGTCCAGAAATATT 2709  
Qy 521 GluMetAspLeuSerAspThrProAlaProSerGluValProGluLeuSerGlu----- 538  
Db 2710 TCATTAGAACTAGACAGGTCAGGATGATCTACTATCAGCTGAGCTGAGTAAACCCAGAACAA 2769  
Qy 539 -----TyrValSerValProAspHisPheLeuGluAspThrThrPro 552  
Db 2770 AATGGCAAGGTTGATAGCTATGTGAAATGCCTTACCATGTTCACTACACAGAGATGCCT 2829  
Qy 553 ValSerAlaLeuGlnTyIleThrThrSerSerMetThrIleAlaProLysGlyArgGlu 572  
Db 2830 CTTGTAGCT---CAGCCCAAAAGCGGTGTCTTGAGTCGCACCCAGACTGCGAGAGCT 2886  
Qy 573 LeuValValPhePheSerLeuArgValAlaAsnMetAlaPheSerAsnAspLeuPheAsn 592  
Db 2887 TTGGTGGTTTCTTCAAGCTCCGAGTGACAAACATGTTGTTTTCAGAGACCTGTTTAAAC 2946  
Qy 593 LysSerSerLeuGluTyArgAlaLeuGluGlnGlnPheThrGlnLeuLeuValProTyr 612  
Db 2947 AAAAATCTTTGGAGTATAAGCCCTGGAGCAAGATTTCTTAGAAGTCTGGTTCCTCAT 3006  
Qy 613 LeuArgSerAsnLeuThrGlyPheLysGlnLeuGluIleLeuAsnPheArgAsnGlySer 632  
Db 3007 CTCAGTCAATCTGTGAGGTTCCAGAACTTAGAGATCTCTGAACTTCAGAAATGGCAGC 3066  
Qy 633 ValIleValAsnSerLysMetLysPheAlaLysSerValProTyrAsnLeuThrLysAla 652  
Db 3067 ATTGTGTGAACAGCAGGAGTGAAGTTCCGCGAGTCTGTCTCTCTTAATGTCAACAACGCC 3126  
Qy 653 ValHisGlyValLeuGluAspPheArgSerAlaAlaGlnGlnLeuHisLeuGluIle 672  
Db 3127 ATATATGATCTTGAAGACTTTTGTACCCCGCTTACCAACCAACCACTGGATATT 3186  
Qy 673 AspSerTyrSerLeuAsnIleGluProAlaAspGlnAlaAspProCysLysPheLeuAla 692  
Db 3187 GATAAGTACTCTCCCTGGATGGAATCAGGTGTGACGACCAACCCCTTGCAAGTTTCAGGCC 3246

